

Proteins & Fibers Inquiry I: Animal Histories on the Proteomic Horizon

Organizer: Lisa Onaga

10:00-16:00, 16 May 2018,
Seminar Room 265, Max Planck Institute for the History of Science, Boltzmannstraße
22, 14195 Berlin

This micro-workshop is the first of a series of cross-disciplinary inquiries designed to identify new approaches in the study of animals in history. By forging a conversation around the historical and scientific studies of animal fur, hair, keratin, and silk, the possibilities for reading animal materiality as historical sources are explored. State of the craft biomolecular methods used to characterize ancient to contemporary animal-derived proteinaceous objects are discussed relative to historical challenges that have informed the reliability of, and relatedly, trust in various scientific dating practices. The fruition of new proteomic methods especially prompts workshop participants to explore how new historical puzzles have arisen in animal evolutionary history, textile history, or in the history of scientific analyses of animal proteins.

Space is limited. To register and access the pre-circulated readings and papers that will be discussed in this mini-workshop, please email event_dept3@mpiwg-berlin.mpg.de by 7 May 2018.

Programme

10:00 - 10:30	Welcome & Introduction Lisa Onaga (MPIWG, Nanyang Technological University)
10:30 - 12:00	Hounds of Moctezuma: Dogs, Breeding, and the Columbian Exchange Mackenzie Cooley (Cornell University)
12:00 - 13:00	Lunch Break
13:00 - 15:00	Biomolecular approaches to historical and archaeological hair and animal fibers: Characterizing 100- to 6,000-year-old protein fibers with proteomics Caroline Solazzo (Smithsonian Institution)
15:00 - 15:20	Break
15:20 - 16:00	Wrap-up

Hounds of Moctezuma: Dogs, Breeding, and the Columbian Exchange

As traditionally conceived, the Columbian Exchange consisted of the transportation of plants, animals, and microbes from Europe to the Americas and vice versa following 1492. These foreign elements certainly affected cultures, biospheres, and landscapes in the region to which they were transported. Few accounts, however, focus on how those natural things themselves evolved after their arrival. Because the Eurasian and American biospheres were so different, interbreeding following migration was not often an issue. Indeed, canonical accounts of the exchange focused on how the absence of interbreeding and the limited genetic pool of stock transferred over long distances led to lower genetic diversity in distant populations. Humans and dogs constitute major exceptions to this rule. Both readily interbred with isolated populations of their own species.

This paper considers how systematic dog breeding projects shaped animals in fifteenth and sixteenth century Mesoamerica using the idea of a “quotient of malleability.” It aims to contextualize the interplay between such projects and theories of inheritance prevalent at the time. Recently excavated canine burial sites in former Teotihuacan offer new sources on precolonial Aztec pet-keeping practices and about how systematic breeding shaped traits prized in dogs. During early contact, European explorers reported dogs that could not bark living in the Caribbean, many hairless varieties, and dogs bred for consumption throughout the countryside. The canine genome is famously malleable, meaning that new breeds of dog can be produced in relatively few generations. Thus, the New World dogs of 1490 would have looked markedly different from the dogs of 1530, even without concentrated human intervention. As New World dogs changed shape, natural historians struggled to keep up with the flexibility of the canine form, forcing them to weigh evidence that challenged the limits of the race/species divide and raised the issue of extinction. Dogs themselves were changing too quickly for European natural historians to believe.

How might growing evidence from genomic studies of dogs help trace the extent of interbreeding between Mexican *xoloitcuintli*, Spanish mastiffs, and German herding dogs to create a mixed canine population in the sixteenth century following the conquest of the Americas? By combining archival and bio-archaeological evidence, this paper posits a narrative for how effective early modern European and New World animal experts believed themselves to be when it came to influencing bodies through breeding, and how effective their methods actually were in producing new variations of animals.

Mackenzie Cooley has just completed her Ph.D. in the Stanford University Department of History where she studied history of culture and science in the early modern European and Atlantic world. Her dissertation, “Animal Empires: The Perfection of Nature between Europe and the Americas, 1492-1630,” considered the collection and design of living beings in the expanding Renaissance world, with attention to animals, natural history, and reproduction. She is currently a Presidential Postdoctoral Scholar at Cornell University, a member of the Cornell Society of Fellows, and this spring will be visiting the Max Planck Institute for the History of Science in Berlin throughout May before taking up an assistant professorship in history at Hamilton College. Her research has been supported by Council on Library and Information Resources (CLIR), Fulbright Foundation, Mellon Foundation, and Renaissance Society of America.

Biomolecular approaches to historical and archaeological hair and animal fibers: Characterizing 100- to 6,000-year-old protein fibers with proteomics

Over the past few years, a biomolecular revolution has taken shape in the science of characterizing and identifying the animal origins of textile materials. At the center of this revolution lies the importance of understanding the interaction of the proteins among themselves and with their environment: protein fibers are complex systems constructed from core proteins (alpha-helical keratins for wool and beta-pleated sheets of fibroins for silk) surrounded by smaller amorphous proteins, each one of them having different properties and susceptibility to degradation. In the past, protein substrates in ancient artefacts were identified by their overall amino acid composition or by immunological specificity. However, these techniques offered only a general view of the protein content and were limited by the identification of the major proteins and by the preservation of the protein chains. Starting in the early 2000s and with the arrival of new mass spectrometry techniques, scientists began to identify peptide sequences. In parallel with developments in instrumentation that have increased in sensitivity and accuracy, databases of protein sequences have been growing, allowing access to genetic information (and therefore proteins) for key species (*e.g.* sheep). This has given us access to the complete set of proteins present in a sample (including proteins of multiple origins, even if present in minor concentration), better identification of the animal species through peptide biomarkers, and better evaluation of the protein degradation. Case studies and future directions in the application of proteomics on baleen, wild silk, and dog and goat fiber blend Coast Salish blankets are discussed in order to reflect upon how these new methods have had consequences for conservator goals to identify, date and provenance textiles.

Caroline Solazzo is a research scientist at the Smithsonian's Museum Conservation Institute (MCI) in Washington D.C. She has a master degree in analytical chemistry from the University of Orsay (France), and a PhD in biochemistry from the University of Lille 1 (France). She started at the Smithsonian Institution 15 years ago as a post-graduate fellow working on a variety of conservation and archaeological science projects, and, for her thesis dissertation, on the early development of proteomics techniques for the study of ancient proteins. She quickly became interested in the application of proteomics to the study of textiles, and after joining the BioArCh's team at the University of York led by Prof. Matthew Collins, she was awarded a Marie Curie International fellowship, between the University of York and the Protein and Structure team of AgResearch in New Zealand, a group specialised in wool research. The THREADs project (Textile and Hair proteomics: Re-examination of European wool from Archaeological Deposits) between AgResearch and BioArCh aimed at creating proteome maps for selected breeds and highlighting the differentiation in the protein composition of different fiber types. The fellowship also evaluated protein damage to understand to which extent protein markers can be detected in ancient textiles and how the proteome is affected by diagenesis and wool processing. In 2012, she returned to MCI as a post-doctorate fellow and since 2017 as a research scientist as part of the new Proteomics and Biomolecular Mass Spectrometry Laboratory team.