Linking genomes, traits and environment across time and space:
a vision for Digitization 2.0

Scott V. Edwards
Department of Organismic and Evolutionary Biology
Museum of Comparative Zoology
Harvard University
Cambridge, MA USA
http://www.oeb.harvard.edu/faculty/edwards
Overview – Genomes, Environment and Digitization

• We know genomes change over time and space…
  – Temporal comparisons
  – Geographic comparisons

• …but thus far we’ve focused on just one dimension of the genome – its sequence
  – Genome expression and changing environments
  – Epigenetics and changing environments

• How do we capture these data and what kinds of research will it enable?
  – Need for renewed collection of diverse resources for genomics
  – Capturing these data and linking it to environmental change
Museum collections in 21st century evolutionary biology
Museum of Southwestern Biology, U. New Mexico

Gothenburg Natural History Museum

Museum of Natural History, Stockholm

Gothenburg Herbarium

Museum für Naturkund, Berlin

Museum of Comparative Zoology, Harvard

Essig Museum of Entomology, Berkeley

Natural History and Science Museum, University of Porto

Universeum, Gothenburg
The Directorate for Biological Sciences (BIO) awards Postdoctoral Research Fellowships in Biology to recent recipients of the doctoral degree for research and training in selected areas supported by BIO and with special goals for human resource development in biology. The fellowships encourage independence at an early stage of the research career to permit Fellows to pursue their research and training goals in the most appropriate research locations regardless of the availability of funding for the Fellows at that site. For FY 2015 and beyond, these BIO programs are (1) Broadening Participation of Groups Under-represented in Biology, (2) Research Using Biological Collections, and (3) National Plant Genome Initiative (NPGI) Postdoctoral Research Fellowships. These areas change periodically as new scientific and infrastructure opportunities present themselves. For this reason, this solicitation will be changed as necessary to reflect the areas being funded.

The fellowships are also designed to provide active mentoring of the Fellows by the sponsoring scientists who will benefit from having these talented young scientists in their research groups. The research and training plan of each fellowship must address important scientific questions within the scope of the BIO Directorate and the specific guidelines in this fellowship program solicitation. Because the fellowships are offered to postdoctoral scientists only early in their careers, NSF encourages doctoral advisors to discuss the availability of these postdoctoral fellowships in biology with their graduate students early in their doctoral programs to ensure potential applicants may take advantage of this funding opportunity. Fellowships are awards to individuals, not institutions, and are administered by the Fellows.
The NSF collections postdoctoral program broadens the collections community*

As a result of your postdoc, have you, do you or are you ....

*Based on a post-conference survey of 35 participants
Museum of Comparative Zoology: a research and teaching museum

From field to digital genome
Whole genomes and variation linked to vouchered specimens

Data generation
Grinnell Resurvey Project
Population genomics over 100 years for chipmunks impacted by climate change

Microsatellites/exon capture from tissues & skins for ~10K exons; 
Rubidge et al. 2012 *Nature Climate Change*; Good et al. in review.
Tracking the effects of a *Mycoplasma* epizootic through time in House Finches

Pre-epizootic tissue collection: priceless!

Ongoing collections During the epizootic

Diverse data types emerging from single study system

Whole-genome sequencing reveals serial bottlenecks due to introductions and disease.

1.3% 2.2%

Pre-MG 10 gens Post-MG Pre-MG 10 gens Post-MG 20 gens Post-MG

western eastern
Whole-genome sequencing reveals subtle signatures of disease-induced natural selection

Shultz et al., in prep.
Whole-genome sequencing reveals subtle signatures of disease-induced natural selection

Shultz et al., in prep.
The genome is dynamically expressed and modified in space and time…

…but museums are unprepared for capturing this dynamism

Rapid phenotypic evolution triggered by the 2013-2014 polar vortex

Rapid sequence and expression evolution triggered by the 2013-2014 polar vortex

Expression comparisons in House Finches are limited to geography, not time.

Comparative Genomics as a Foundation for Eco-evolutionary Studies in Birds
Phil Grayson, Simon Y.W. Sin, Timothy B. Sackton, and Scott V. Edwards
Assay for Transposase-Accessible Chromatin

ATAC-Seq identifies DNA with open chromatin, accessible to transcription factors

Stage HH24-25 chickens and rheas

Chromatin state varies by species, development time...and probably environment.

Ratite noncoding element 1317692 is contained under chicken ATAC peaks...

... but the rhea is missing this peak.
Chromatin state predicts the ability of noncoding regions to drive gene expression
Genomically-informed cryo-collections produce high-quality genomes

Based on 31 reference-quality genomes of birds in Edwards lab
Genomically-informed field collections facilitate a greater diversity of temporal studies.
Genomic data are easy to digitize; linking them to specimens and environments is harder.
Vision: from genomes and epigenomes to global change

Genomes          Environments          Spatial/Temporal Change

Acknowledgements:
Edwards Lab and colleagues
Thank you!

Courtesy J. Tonini, poster