



OLLI at Illinois
NOVA Study Group June 6th
Roy Campbell

Hunt for the Oldest DNA

NOVA Study Group

Roy Campbell

Thursday, 10:00 a.m. – 11:30 p.m.
Session 6: June 6
Format: In-person

- This week we view and discuss Hunt for the Oldest DNA NOVA Science program Season 51 Episode 4 broadcast on PBS. It's a 53 minutes NOVA program, so we will see the whole show with breaks for discussion. We will leave time to discuss the science presented in more detail at the end.
- PBS Official Nova site <https://www.pbs.org/video/hunt-for-the-oldest-dna-zckys0/>
This site has a transcript of the video.

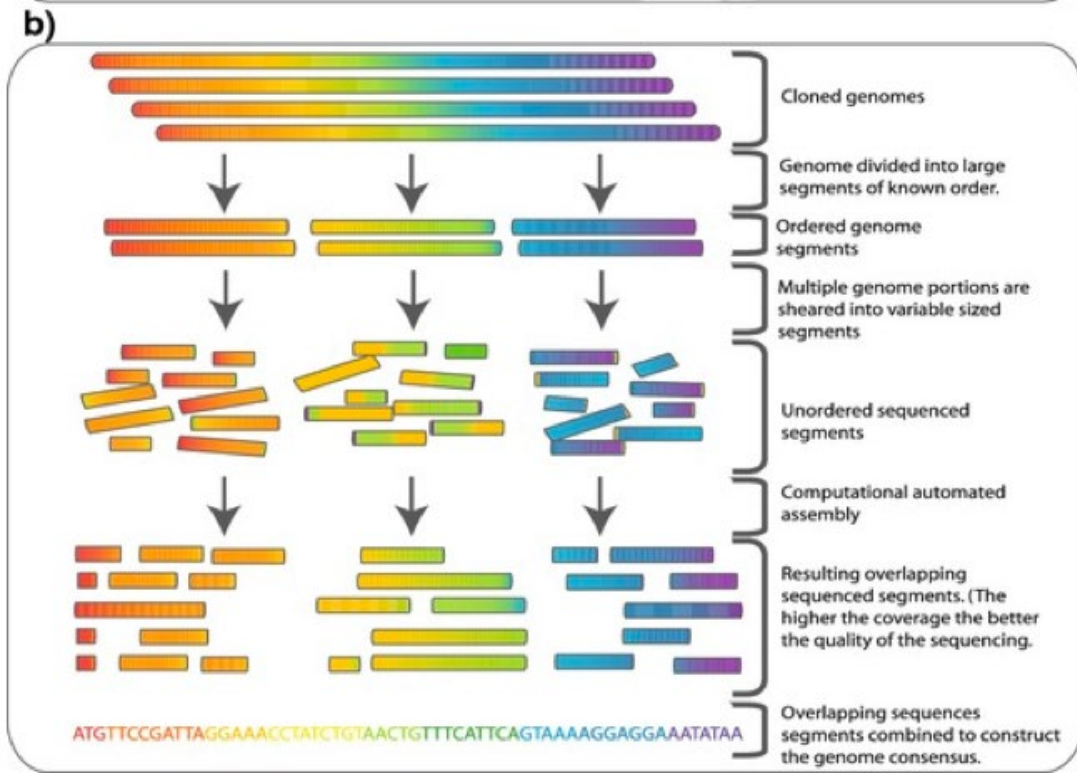
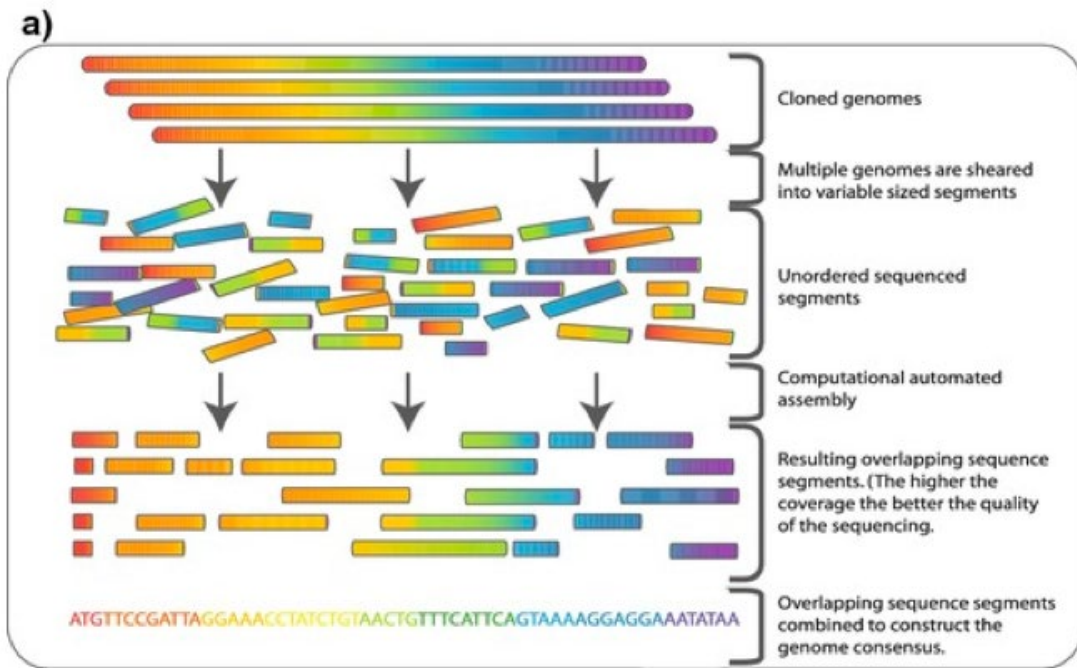


Quick References to Video Content

- ESKE WILLERSLEV https://en.wikipedia.org/wiki/Eske_Willerslev
- MAANASA RAGHAVAN <https://southernasia.uchicago.edu/raghavan-maanasa/>
- BETH SHAPIRO https://en.wikipedia.org/wiki/Beth_Shapiro
- ASTRID SCHMIDT <https://independent.academia.edu/AstridSchmidt>
- Shotgun Sequencing https://en.wikipedia.org/wiki/Shotgun_sequencing
- Kap Kobenhavn Formation https://en.wikipedia.org/wiki/Kap_Kobenhavn_Formation
- A 2-million-year-old ecosystem in Greenland uncovered by environmental DNA <https://www.nature.com/articles/s41586-022-05453-y>
- Natalia Rybczynski https://en.wikipedia.org/wiki/Natalia_Rybczynski
- Maureen Raymo https://en.wikipedia.org/wiki/Maureen_Raymo

Shotgun reads

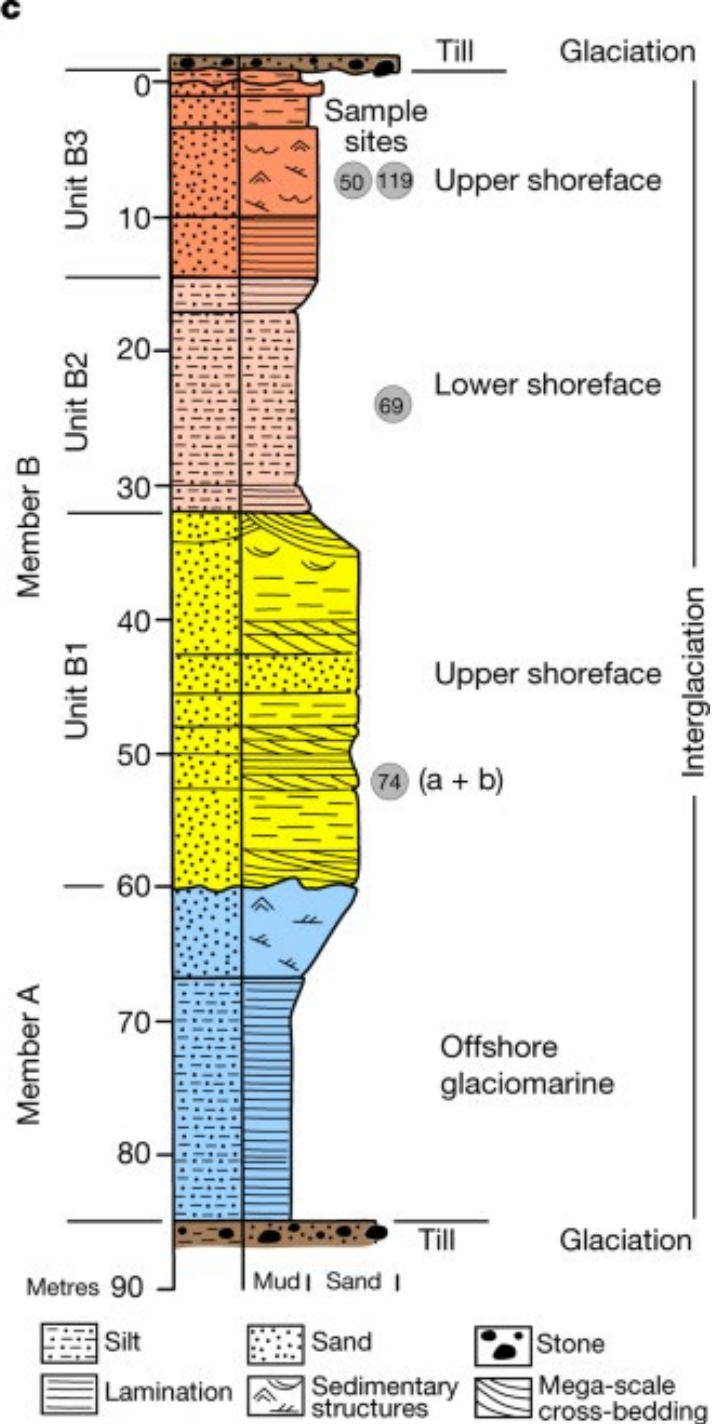
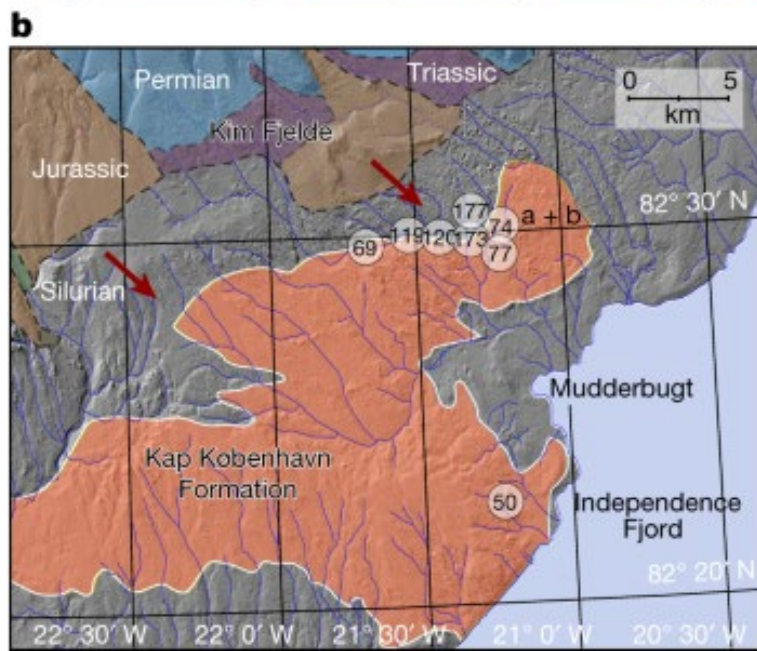
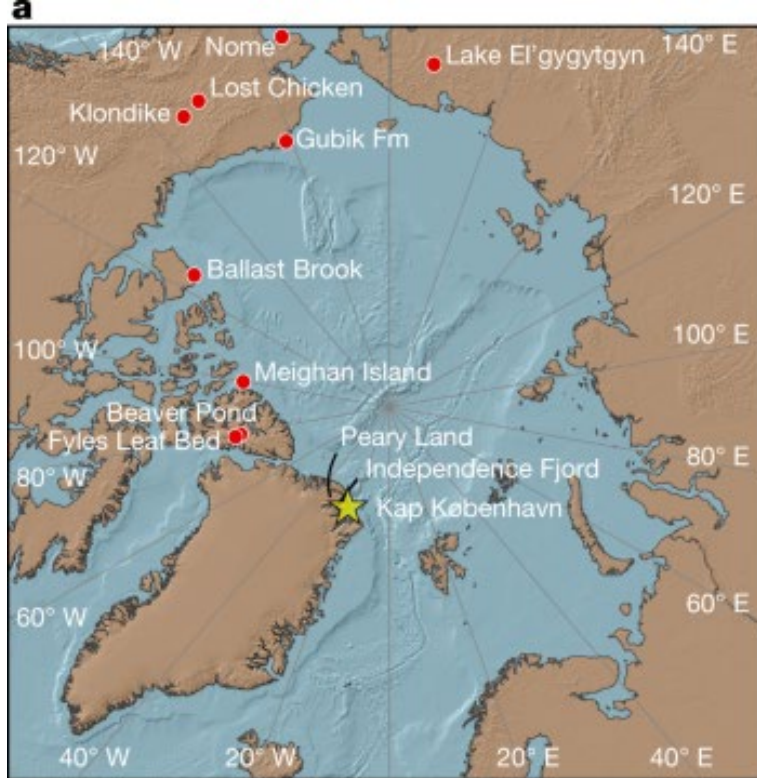
	Strand	Sequence
Original		AGCATGCTGCAGTCATGCTTAGGCTA
First shotgun sequence		AGCATGCTGCAGTCATGCT----- -----TAGGCTA
Second shotgun sequence		AGCATG----- -----CTGCAGTCATGCTTAGGCTA
Reconstruction		AGCATGCTGCAGTCATGCTTAGGCTA



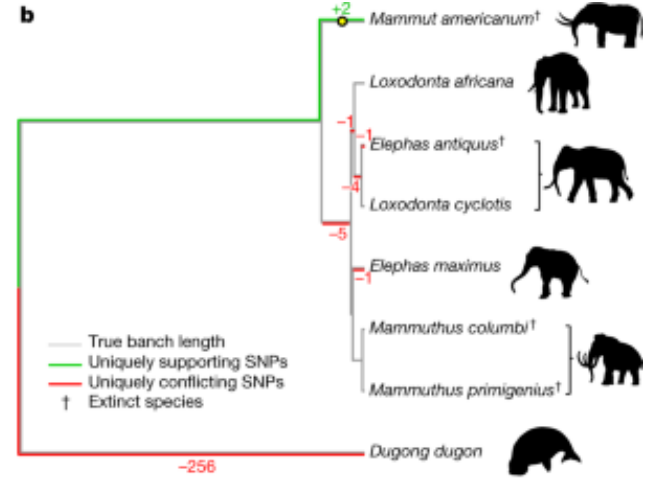
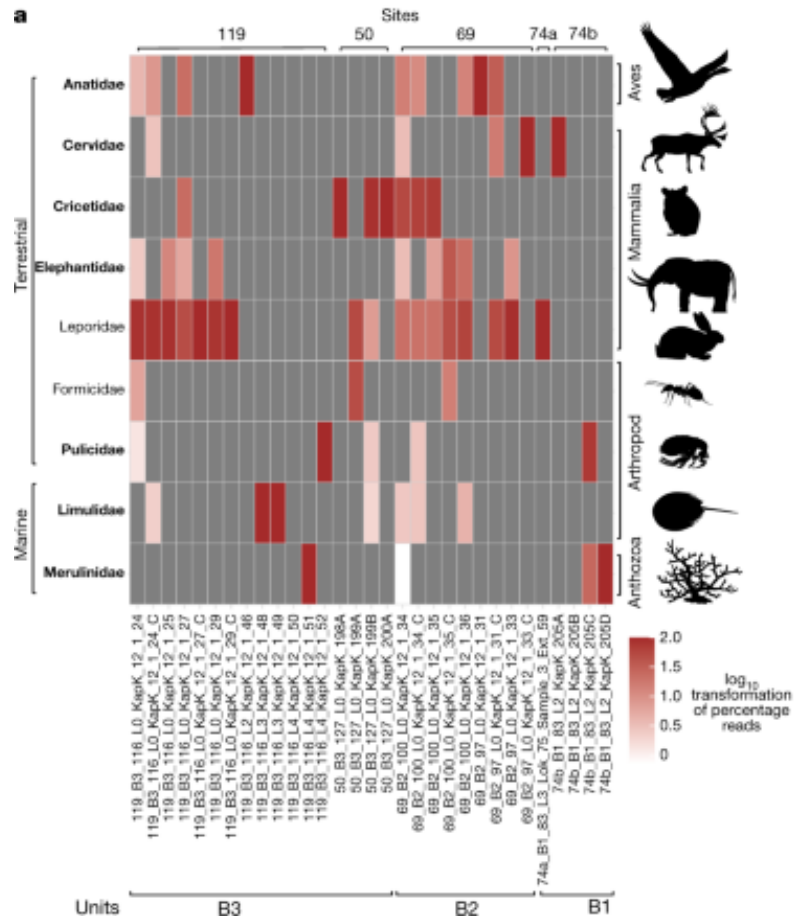
Hierarchical shotgun sequencing

Metagenomic shotgun sequencing

- Having reads of 400-500 base pairs length is sufficient to determine the species or strain of the organism where the DNA comes from, provided its genome is already known, by using for example a [k-mer based taxonomic classifier](#) software.
- With millions of reads from next generation sequencing of an environmental sample, it is possible to get a complete overview of any complex microbiome with thousands of species, like the [gut flora](#).
- Advantages over 16S rRNA [amplicon sequencing](#) are: not being limited to bacteria; strain-level classification where amplicon sequencing only gets the genus; and the possibility to extract whole genes and specify their function as part of the metagenome.^[19]



Animals



Questions

- 1.How long does DNA survive?
- 2.What can ancient DNA tell us about the environment long ago?
- 3.Is a Jurassic Park feasible?
- 4.What can the soil tell us?
- 5.Ancient DNA in ICE?
- 6.Can we paint a picture of the past environment?