



**DNA DATA
STORAGE**
ALLIANCE
A SNIA TECHNOLOGY AFFILIATE

Creating confidence in preserving digital data in synthetic DNA

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Acknowledgements

Jacques Bonnet, Marthe Colotte, Lee Organick, Chris Takahashi

Library of Congress Seminar
April 2024

DNA Data Storage Alliance

40+ member organizations today

Mission

- Create an interoperable storage ecosystem based on DNA as a data storage medium

Scope

- Educate the market to create awareness and adoption of DNA data storage
- Develop a DNA data storage technology roadmap to drive R&D and funding
- Develop standards and/or specifications to encourage evolution of the ecosystem



DNA Data Storage Alliance Standards Work

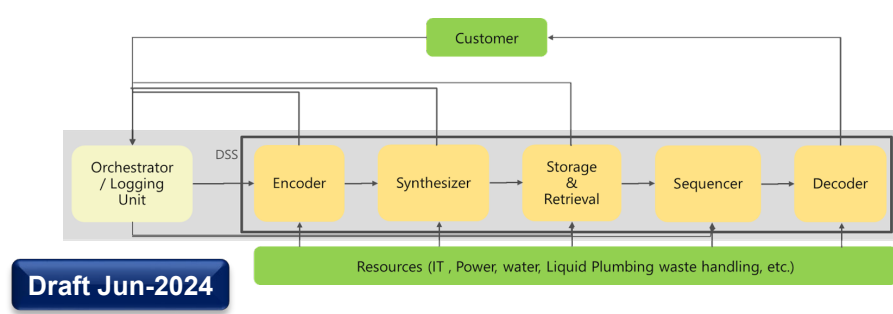
Bootstrap a nascent ecosystem without stifling innovation

1) DNA Archive Rosetta Stone - MBR

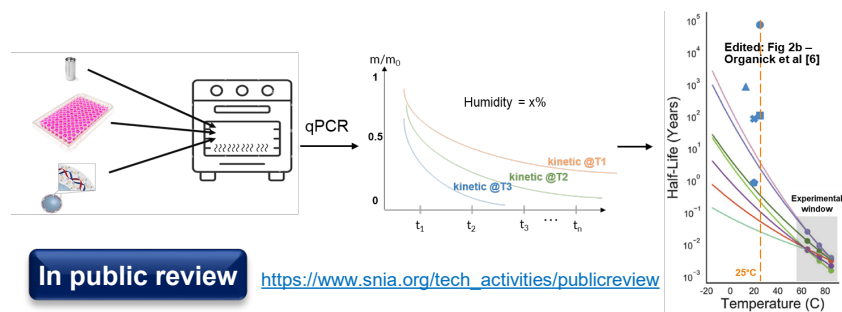
The image shows two SNIA standards documents: 'DNA Data Storage Sector Zero' and 'DNA Data Storage Sector One', both Version 1.0, published on November 11, 2023. To the right is a diagram of a 'DNA Archive' showing various colored bars representing different sectors: Sector 0 (orange), Sector 1 (yellow), and Archive (green). A blue 'Published' badge is at the bottom right.

https://www.snia.org/tech_activities/standards/curr_standards

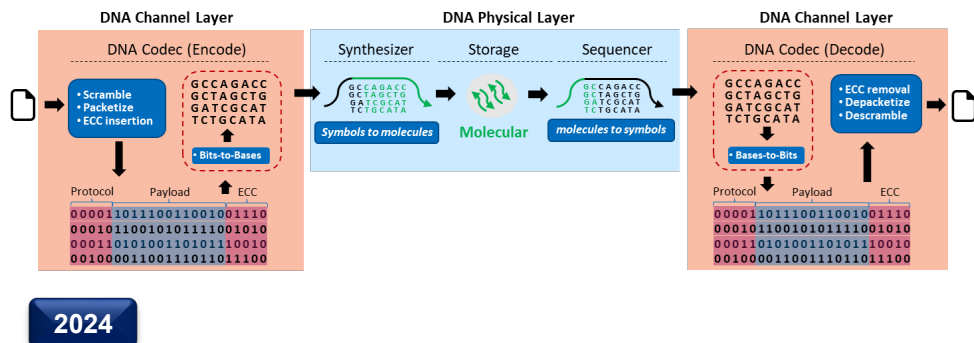
2) Interoperable Interfaces – DNA in the Datacenter



3) DNA Stability Evaluation – Compare Half-Life



4) Open-Source Codecs – DNA Channel

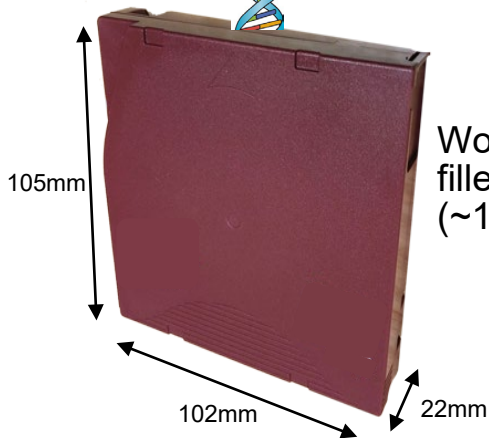
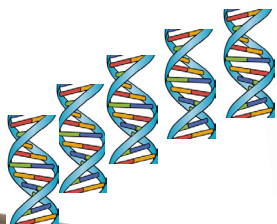




Data Stability Evaluation Spec

Why DNA?

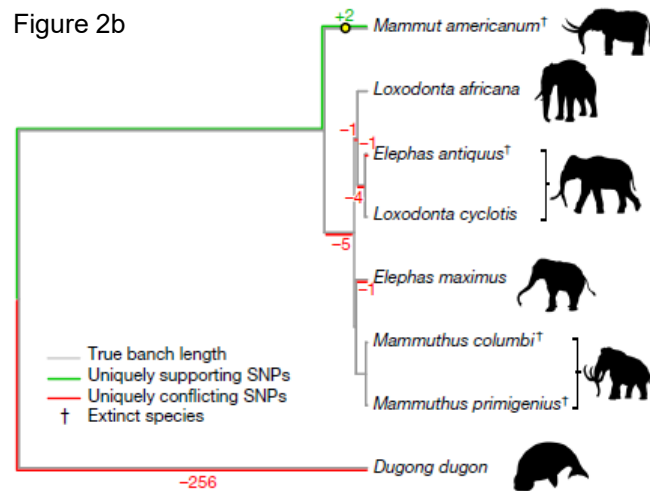
DNA bits are very small, $\sim 1\text{nm}^3$



Would hold ~ 2 exabytes if filled with DNA bits
($\sim 115,000$ LTO9 tapes)

And they are extremely (i.e., 2M+ years) durable and sustainable

Figure 2b

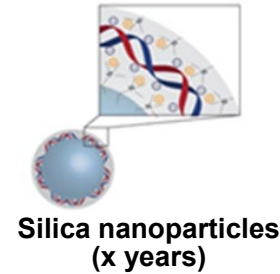


Kjær, K.H., Winther Pedersen, M., De Sanctis, B. et al. A 2-million-year-old ecosystem in Greenland uncovered by environmental DNA. *Nature* 612, 283–291 (2022). <https://doi.org/10.1038/s41586-022-05453-y>

We don't store digital data in DNA using fossils

Must create trust that manufactured DNA Containment Systems work

- Challenge to creating trust
 - Rating the durability enabled by a DNA Containment System (DCS), and enabling apples-to-apples comparison to another DCS, is not possible without a standard method of conducting media aging experiments that yield standard metrics
- Challenges to creating standard methods/metrics
 - Can a DCS be evaluated independent of the other steps in the DNA data storage pipeline?
 - DNA ages very slowly so we need to believe that an accelerated wear methodology won't skew results



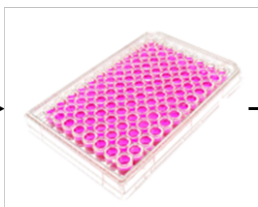
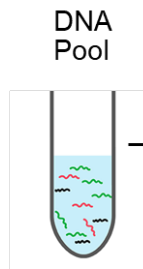
Typical DNA Data Stability Evaluation Experiment

DNA Containment System (DCS)

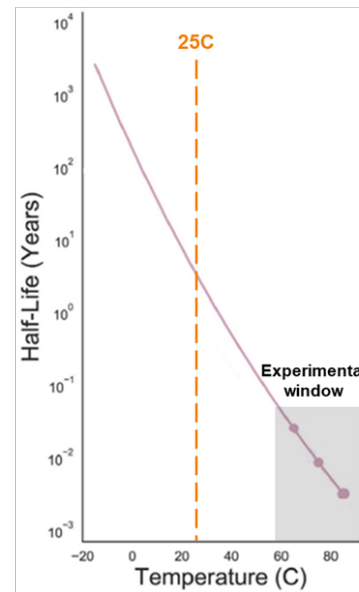
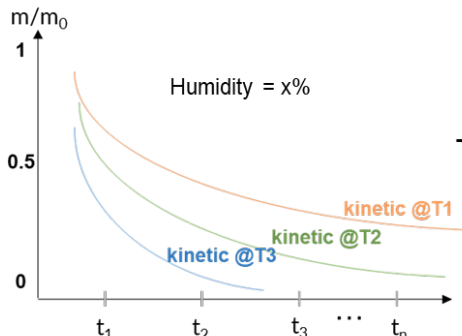
Accelerated aging at various temperature, humidity conditions

Measured % remaining material (i.e., uncut strands over time)

Arrhenius curve fit of degradation data set

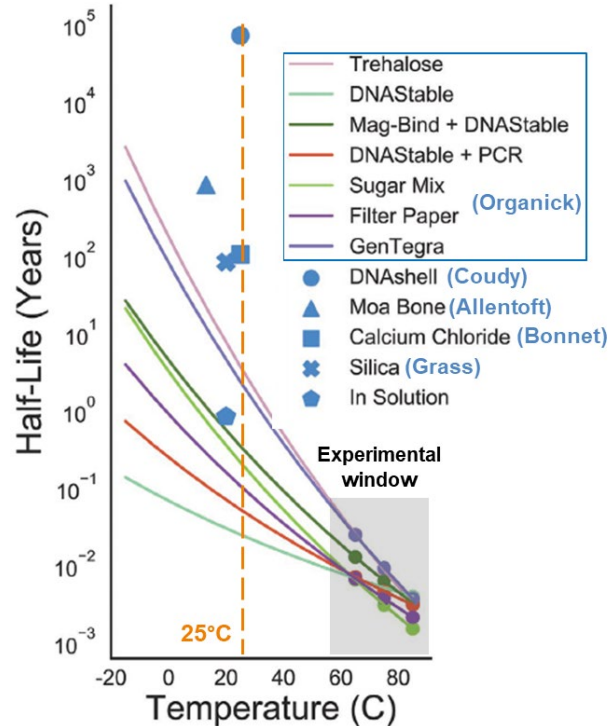


qPCR



What did the research say about durability?

- Possible to, in general, extend the durability of DNA media by using various additives and containment systems
- Containment systems which shield DNA from atmosphere preserve molecular stability for long periods at “room temp” (i.e., 20C-25C)



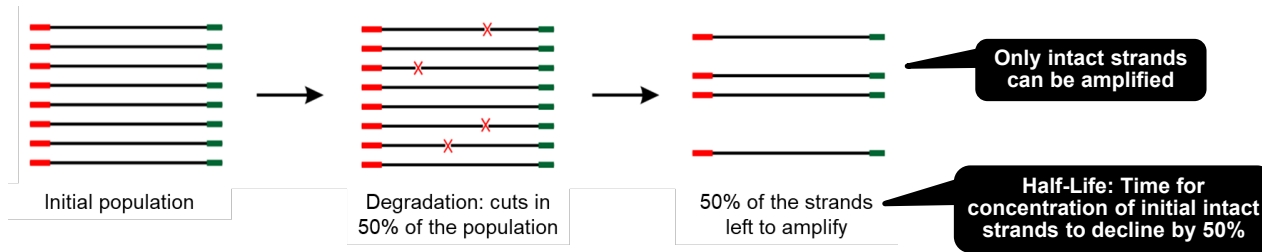
Edited from figure 2b, Organick et al [6]

Presevation Category	Preservation Substrate/Method
Chemical encapsulation	Encapsulation in salts [12, 16]
	Degradable Polymer Microcapsules [32]
	Cationic Diblock Copolymer [33]
Physical encapsulation	Silica nanoparticles [1]
	Stainless steel capsules [3, 7, 30]
	Magnetic silica nanoparticles [13]
Inclusion in a matrix	DNASTable [1, 21]
	Gentegra DNA [1, 22]
	Pullulan [14]
	Silk [15]
	composite nucleic acid-polymer fibers [34]
	300K matrix inclusion [25]
Absorption on paper	FTA paper [1, 23, 24]
	Chitosan treated paper [17]
Dehydration on solid supports	Capillaries [20]
	Glass [26, 27]
	Tube walls [28]
Dissolution in liquid salts	Imidazolium cations [18]
	Imidazolium cations [19]
Living organism	yeast genome [36]
	Ecoli genome [37]
	yeast cells [38]
	Bacteria [29]
DNA beads	Magnetic Bead Spherical Nucleic Acid Microstructure [35]

Source: Bonnet, J., Colotte, M.

What did the research say about **measuring** durability?

- The cited studies measured broken strands (i.e., strands which have at least one break in the sugar-phosphate chain) as a function of concentration of remaining intact DNA



Several studies examined intact strands for data retention

- Read errors did not appear to be affected by the DCS (i.e., preservation method), nor by any particular sequence of bases
- The encoded data in DNA strands that survived accelerated wear aging with no strand breaks appeared recoverable

Indications of relationship between molecular stability and data retention

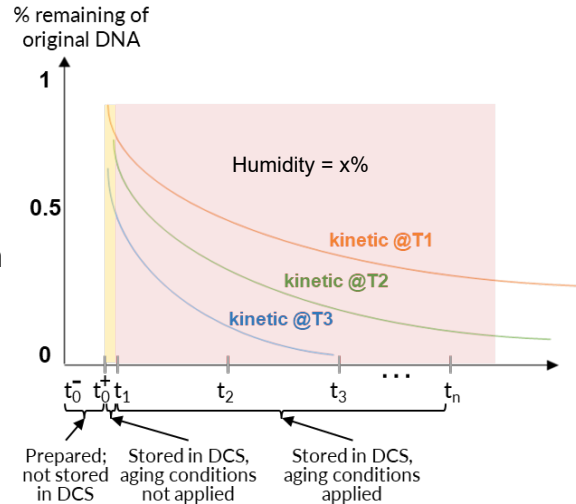
Conclusion

Gaining confidence into how well a DCS preserves data is possible by measuring how well it prevents DNA molecular breakdown, **independent of synthesis/retrieval/sequencing**.

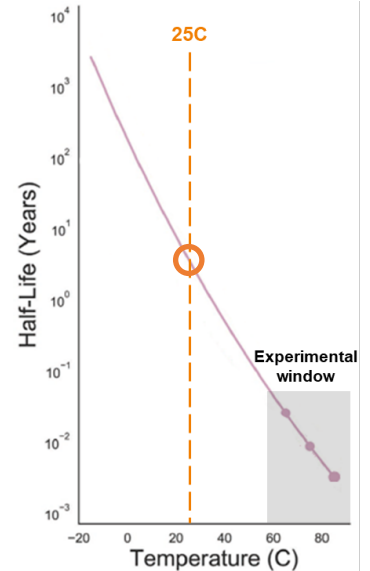
Summary

Standardizing an aging protocol and lifetime metric enables meaningful vendor independent comparisons of durability claims for different DCSs

1. Apply aging conditions (temp/humidity points) to media in a DCS, and count chain breaks as a concentration of intact DNA over time



2. Do an Arrhenius curve fit on the collected data to extrapolate half-life of the media for that DCS at 25°C



Data Stability Evaluation Method for DNA Data Storage Containment Systems

https://www.snia.org/tech_activities/publicreview

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THANK YOU

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BACKUP

Grass et al [1]

Can we recover data in uncut strands that survive accelerated wear?

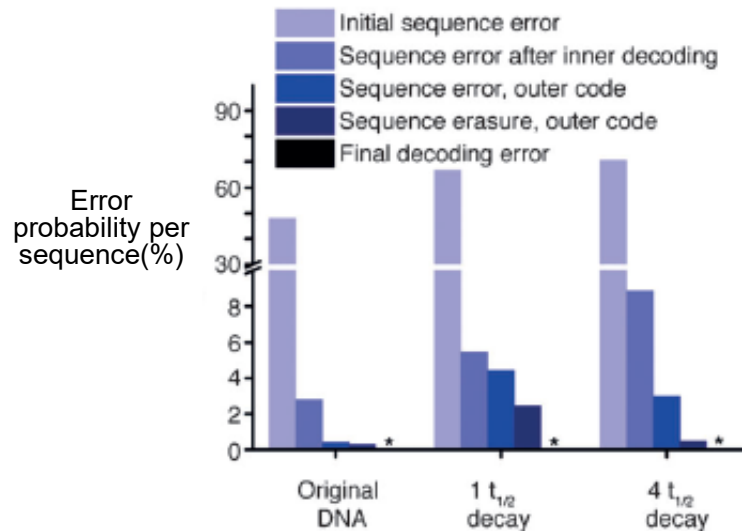
Study observations

- “Inner and outer code of the error correcting scheme had to correct significantly more errors than in the non-heat-treated sample, [but] in both cases the original information could be recovered without final error”

Answer: Yes

- Enough strands survived temperatures used in accelerated wear to validate high temperature stress method

Figure 3
Recovering original data from silica substrate



Organick et al [6]

Do read errors vary due to preservation method?

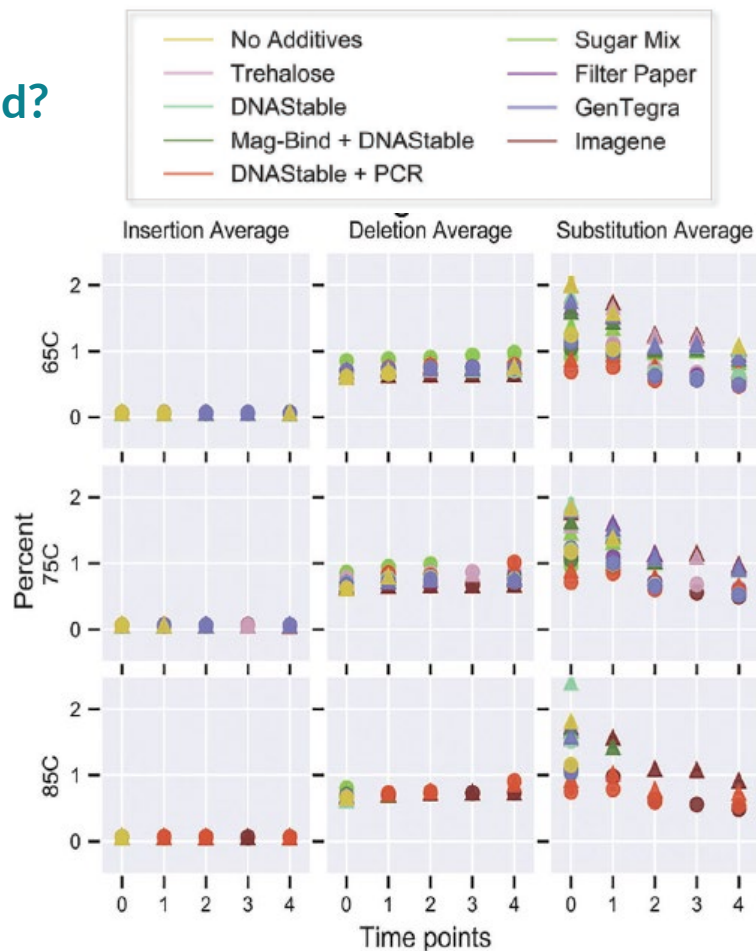
Study observations:

- Minimal (< 1%) variation in error rates across preservation methods, temps, and time points
 - Even substitutions, which show most variance, show this variance before any aging begins
- No one preservation method showed consistently more or fewer errors than any other method across different temperatures and time points
 - Suggests insertion, deletion, substitution errors are independent of storage method

Answer: No

- For the purposes of evaluating and comparing a DCS, errors introduced/corrected by synthesis, retrieval, and sequencing can be ignored

Figure 4 – Observed error rates



Organick et al [6]

Do certain sequences cause read errors with specific preservation methods?

Study Observations

- Total # of sequences found missing during sequencing (across all methods, time points, temperatures) were analyzed for sequence loss
 - Total # missing sequences did not increase over Time 0, indicating no sequence dependent degradation caused by preservation method (i.e., no “storage bias”)
 - This finding reinforced by further finding that individual sequences missing at a particular timepoint had > 90% probability of reappearing and being successfully sequenced later

Answer: No

- Further reinforces that one can define a standard stability evaluation methodology that is independent of the effects of synthesis, retrieval, and sequencing

