



BEST: Biomolecule Extraction and Sequencing Technology Utilizing the Station's Miniature Molecular Lab to Create Big Data

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Astromaterials Research and Exploration Science

October 25, 2018 at POIWG in Huntsville, Alabama

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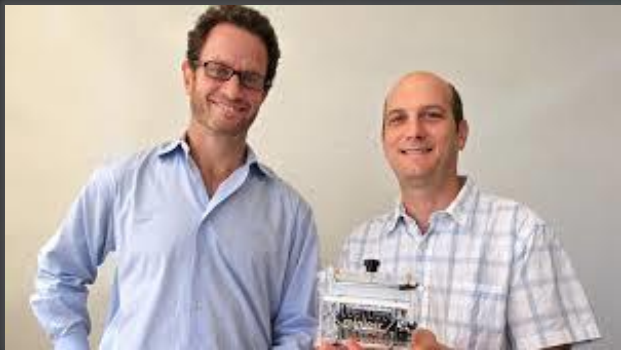


Outline

- Brief background to how we got here
 - miniPCR
 - Genes in Space
 - Biomolecule Sequencer
- Why molecular biology on station?
- Merging the technology
 - NEEMO
- Genes in Space-3
- Biomolecule Extraction and Sequencing Technology (BEST)
 - Swab-to-sequencer
 - Mutation tracking
 - Direct RNA sequencing



Genes in Space: The Molecular Space Age

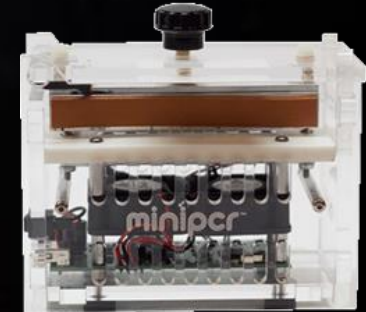


Sebastian Kraves, Ph.D.
and Ezequiel (Zeke) Alvarez Saavedra, Ph.D.,
miniPCR, Genes in Space



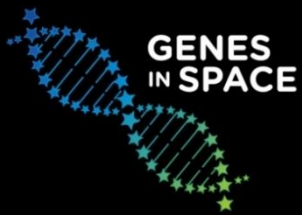
miniPCR

- Copies targeted pieces of DNA in a process known as the polymerase chain reaction (PCR) (amplifies segment of DNA)
- Serves as a heat block for a range of biochemical enzymatic reactions required in molecular biology-based investigations such as whole genome amplifications

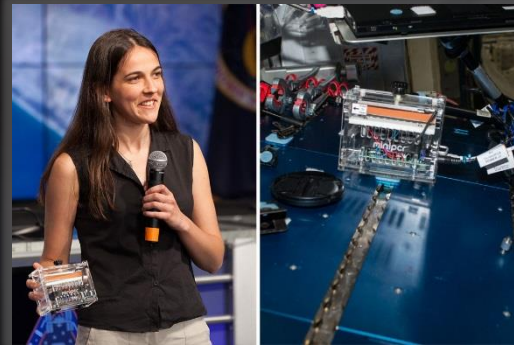


April 19: The first molecular biology assay in space is completed, as DNA is amplified using the miniPCR thermal cycler

2
0
1
6



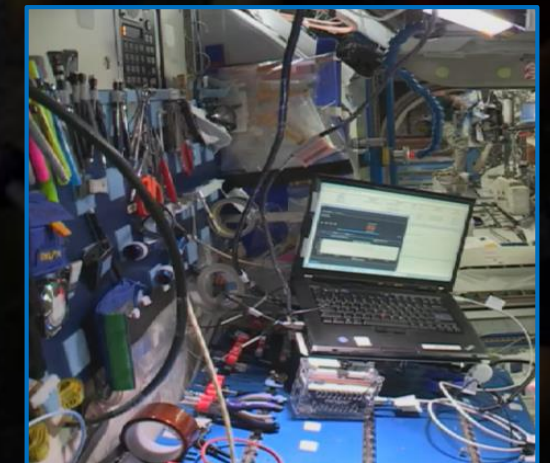
<https://www.genesinspace.org/>



Genes in Space-1 winner Anna-Sophia's investigation was the first molecular biology experiment ever conducted in space, April 19, 2016



Genes in Space-2 winner Julian had his experiment launched to the ISS in March 2017 on OA-7

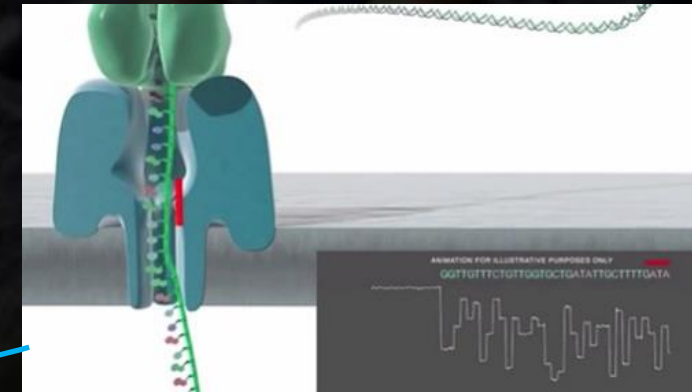




Biomolecule Sequencer



- The first device to assess the capability of DNA sequencing in the microgravity environment of space
- Enabled by the MinION, developed by Oxford Nanopore Technologies
- COTS miniature DNA Sequencer
- 3 3/4 x 1 1/4 x 5/8 inches
- Less than 120 grams (with USB cable)
- Powered via USB connection
- Capable of DNA, RNA, and protein sequencing
- First launched July 18, 2016 (SpaceX-9)

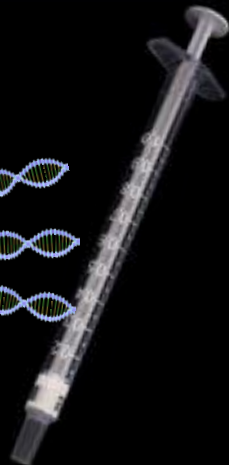
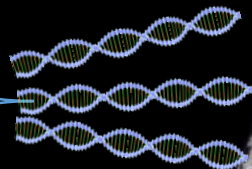
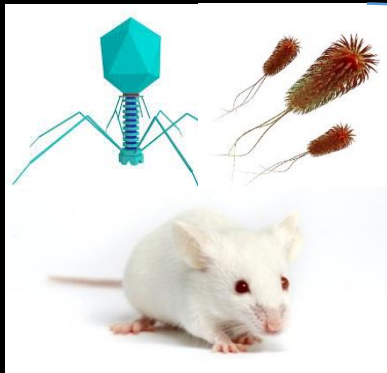
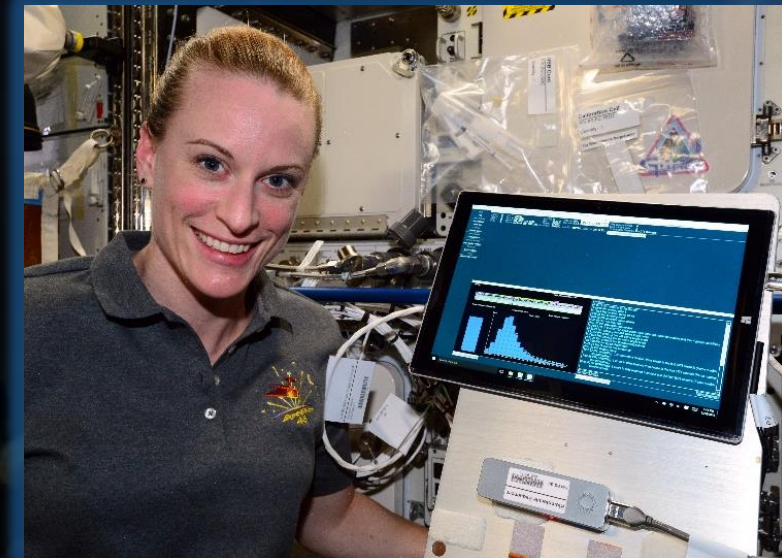
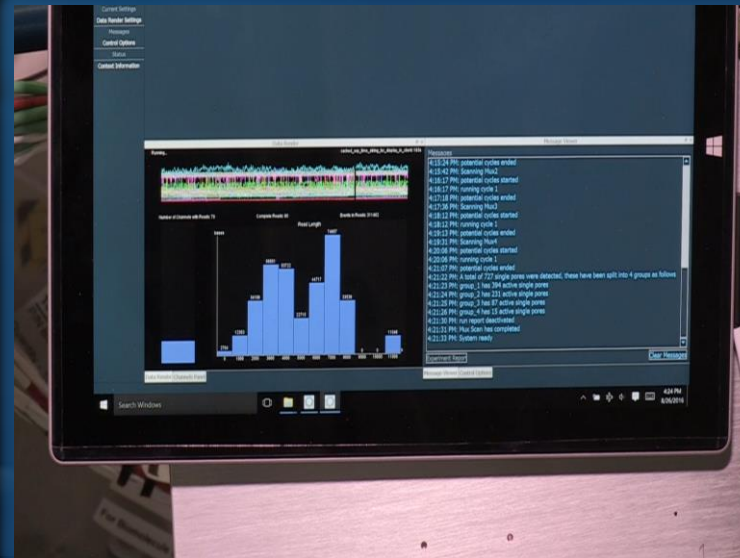


MinION by Oxford
Nanopore Technologies

Nanopore-based sequencers measure changes in current caused by DNA strands migrating through the pore. The changes in current are characteristic of the sequence of migrating DNA.



Biomolecule Sequencer



August 26th, 2016

“Welcome to systems biology in space.” – Astronaut Kate Rubins, Ph.D.

On orbit operations:

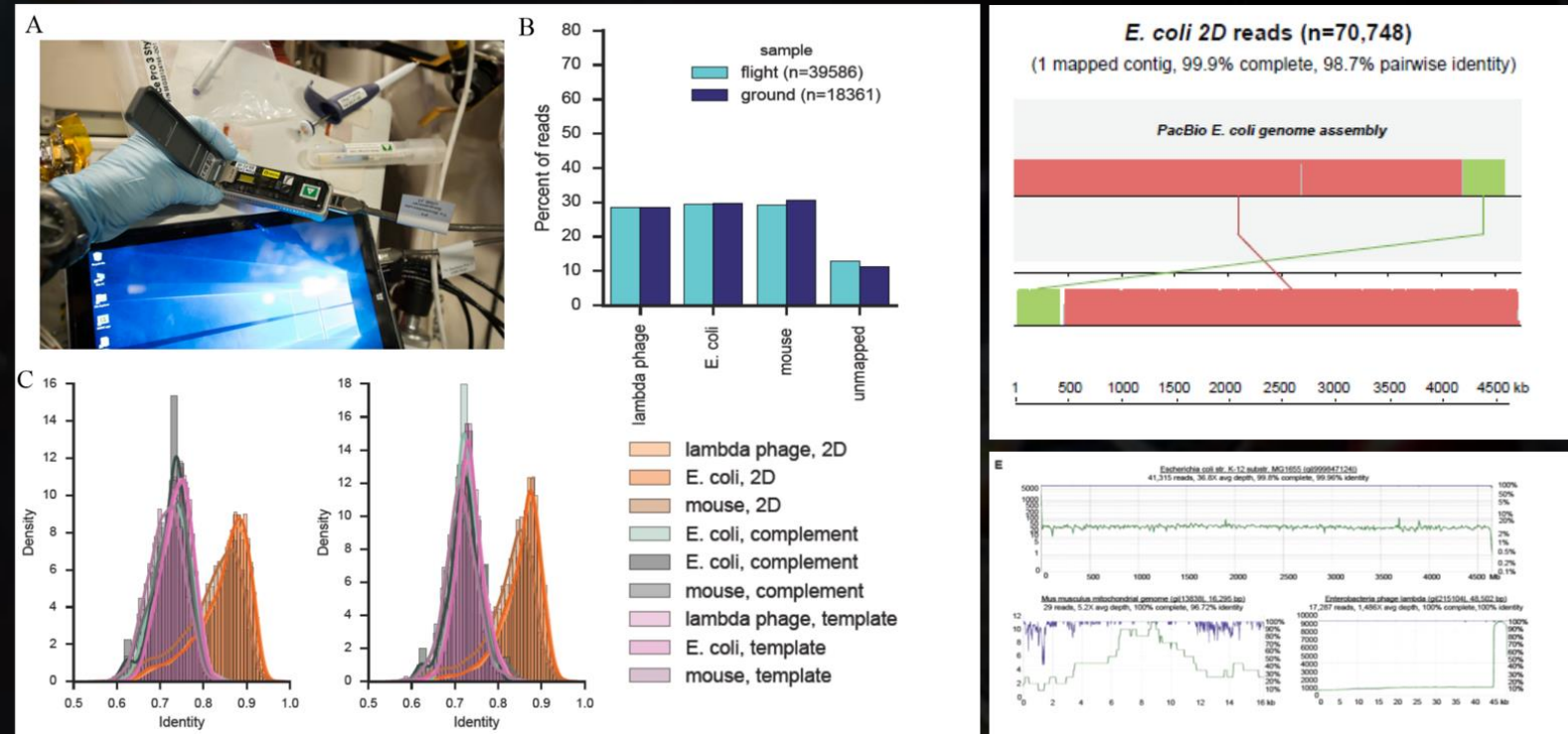
- August 26, 2016
- September 3, 2016
- September 7, 2016
- September 13, 2016
- October 18, 2016
- October 25, 2016
- October 26, 2016
- November 26, 2016
- January 9, 2017



Biomolecule Sequencer



- No decrease in sequencing performance
- Over 284,000 reads were generated on the ISS
- Directed genome assemblies of:
 - Bacteriophage lambda
 - *E. coli*
 - Mouse mitochondrial genome
- de novo genome assemblies of:
 - Bacteriophage lambda
 - *E. coli*
- Demonstrated flow cell reuse and shelf-life stability to at least 6 months in space



Castro-Wallace et al. <https://www.nature.com/articles/s41598-017-18364-0>

Why Molecular Biology in Space?

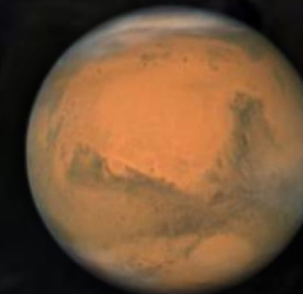


Why do we need molecular biology tools to support the human exploration of space?

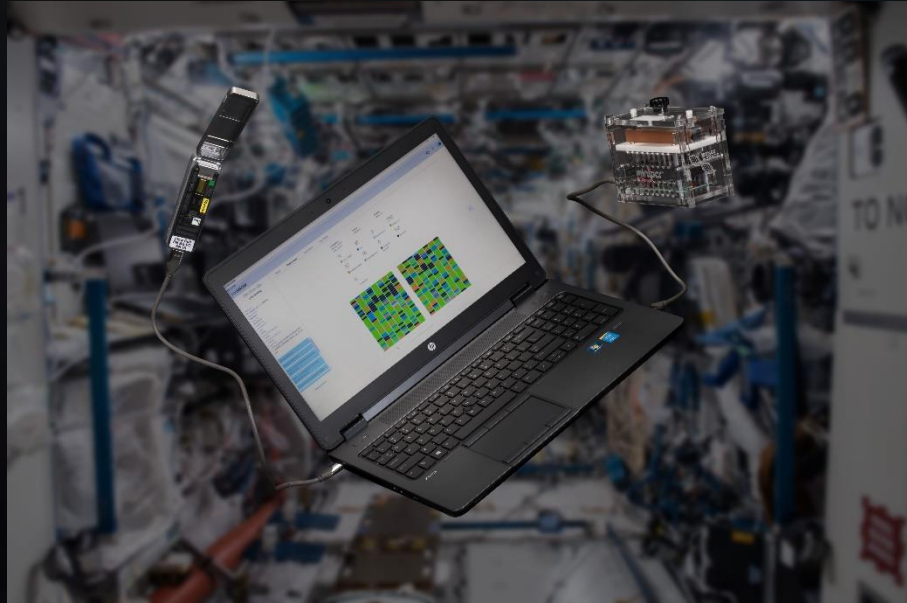
- Operational environmental monitoring
 - Identification of contaminating microbes
 - Infectious disease diagnosis
 - Reduce down mass (sample return for environmental monitoring, crew health, etc.)
- Research
 - Human
 - Animal
 - Microbes/Cell lines
 - Plants
- Med Ops
 - Response to countermeasures
 - Radiation
 - Real-time analysis can influence medical intervention
- Support astrobiology science investigations
 - Technology superiorly suited to *in situ* nucleic acid-based life detection
 - Functional testing for integration into robotics for extra-planetary exploration mission



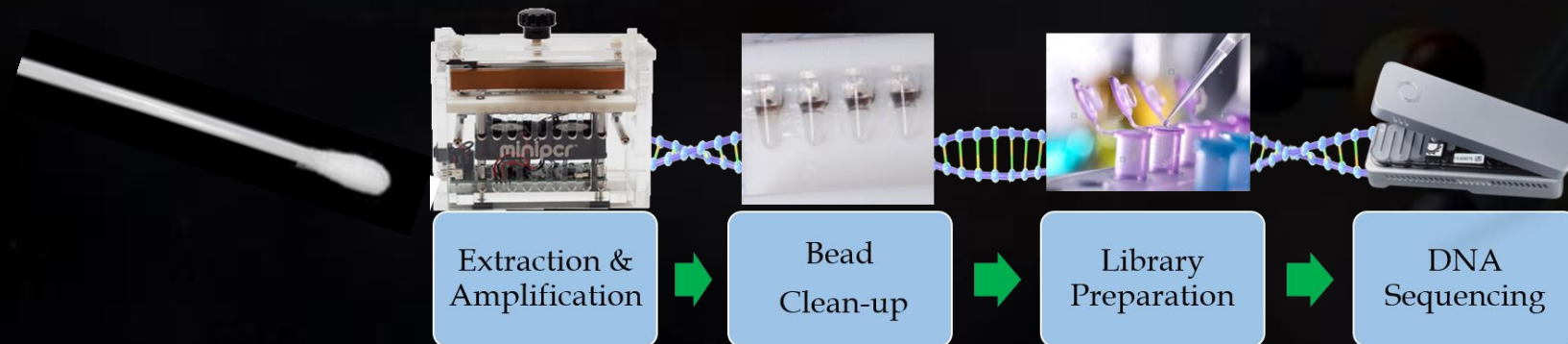
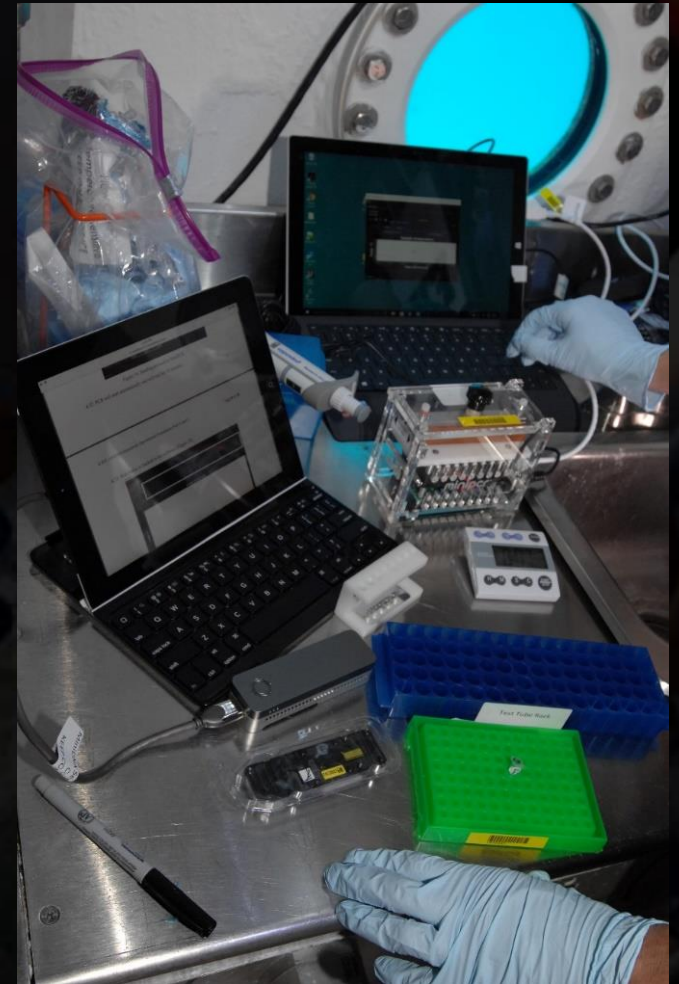
Changes in the genome? Changes in gene expression?



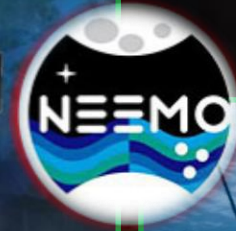
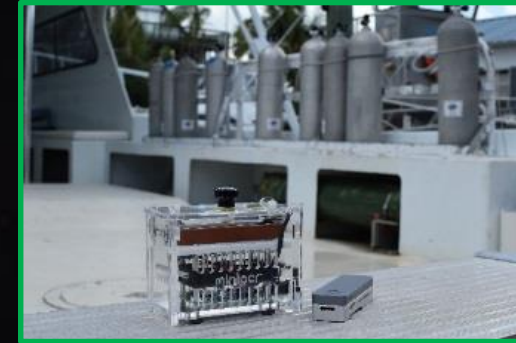
Merging the Technology: Swab-to-Sequencer



- Sample preparation methods are needed to enable use of the technology for research and medical operations.
- Method development began concurrently with the flight certification of the Biomolecule Sequencer.



Merging the Technology: Swab-to-Sequencer

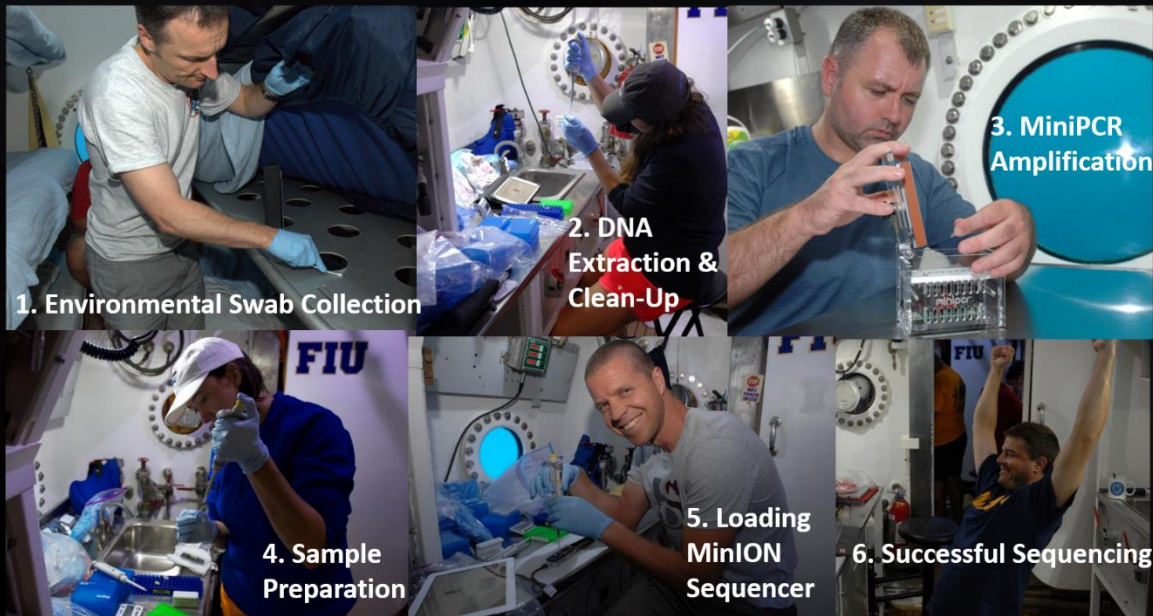


NASA Extreme Environments Mission Operations
(NEEMO)

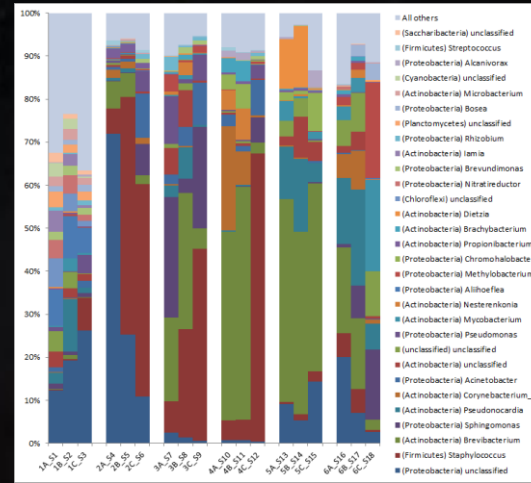
Merging the Technology: Swab-to-Sequencer



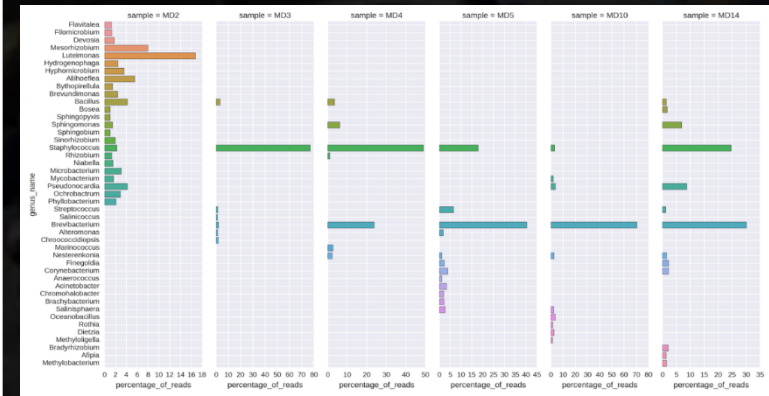
Culture-independent microbial profiling: NEEMO 21 & 22

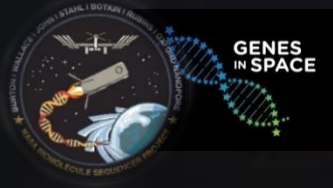


Illumina MiSeq



Oxford Nanopore Technologies MinION





Transitioning Sample Preparation to Space



- Genes in Space-3 built upon the NEEMO 21 demonstration of the joint operations between miniPCR and the MinION, as it transitioned the DNA sample preparation process and sequencing to the spaceflight environment
- Enhanced capabilities available to the Genes in Space student contestants (certified reagents, consumables, and crew procedures)
- Increasing the scientific capacity of the ISS
- A series of controlled experiments testing key steps of the DNA preparation process
- Culminated in the sequencing of unknown environmental samples from the ISS
- Genes in Space-3 launched: April 18, 2017 on OA-7



The successful implementation of this process resulted in, for the first time, the ability to identify contaminating microbes in-flight.



Genes in Space-3

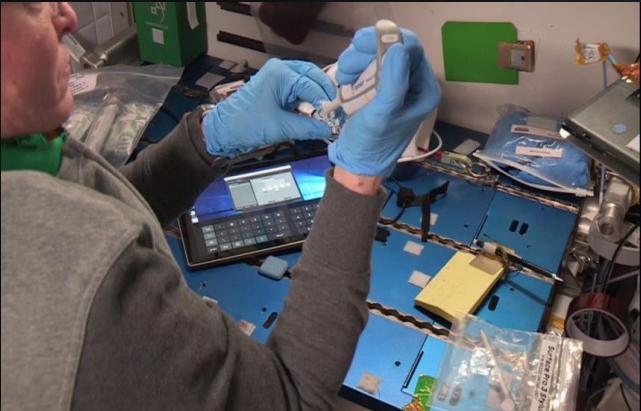


Increasing the scientific capacity of the ISS by facilitating state-of-the-art molecular biology research for both current and next generation ISS researchers.

Demonstrating the first identification of ISS-derived unknown microbes in space.

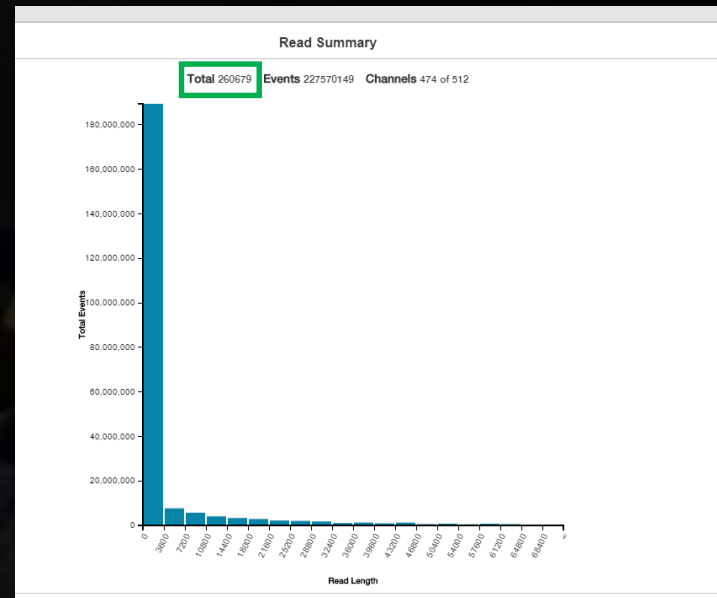
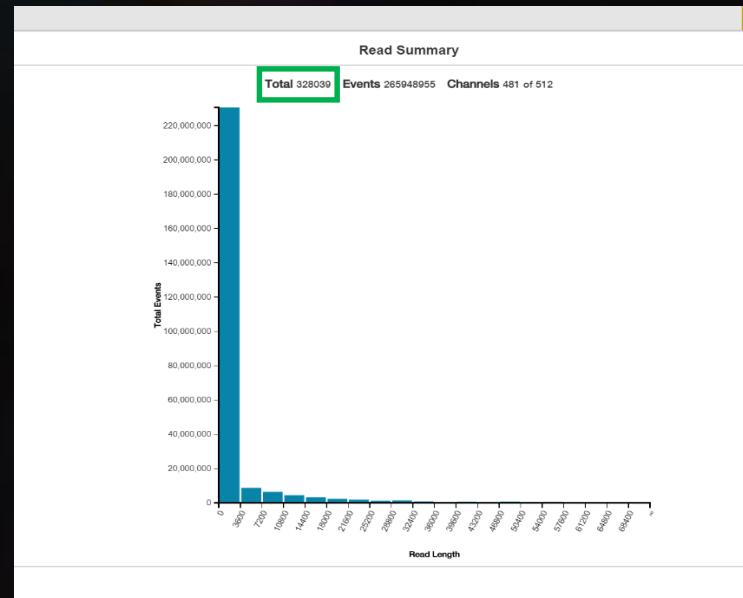


Genes in Space-3



ISS

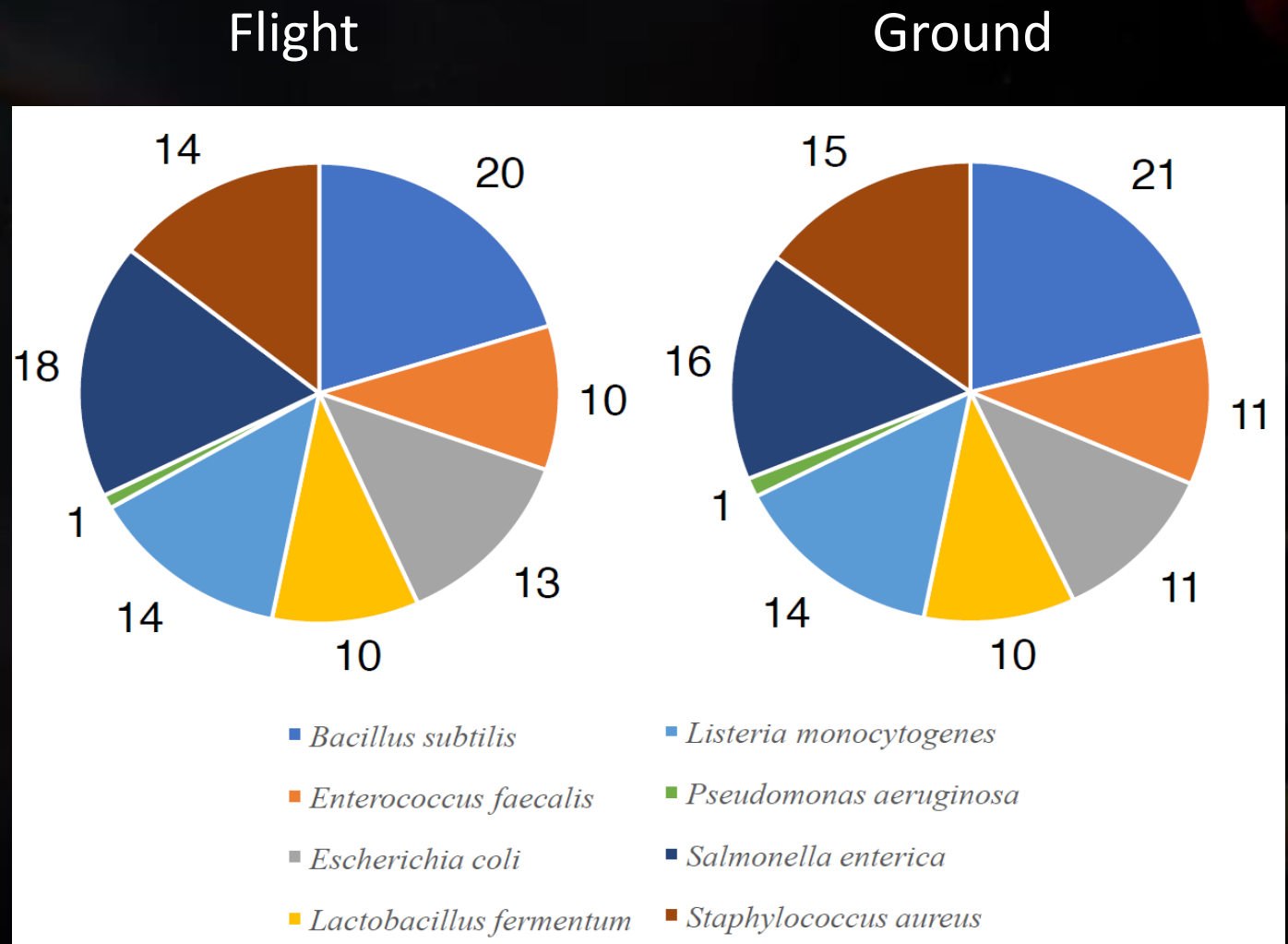
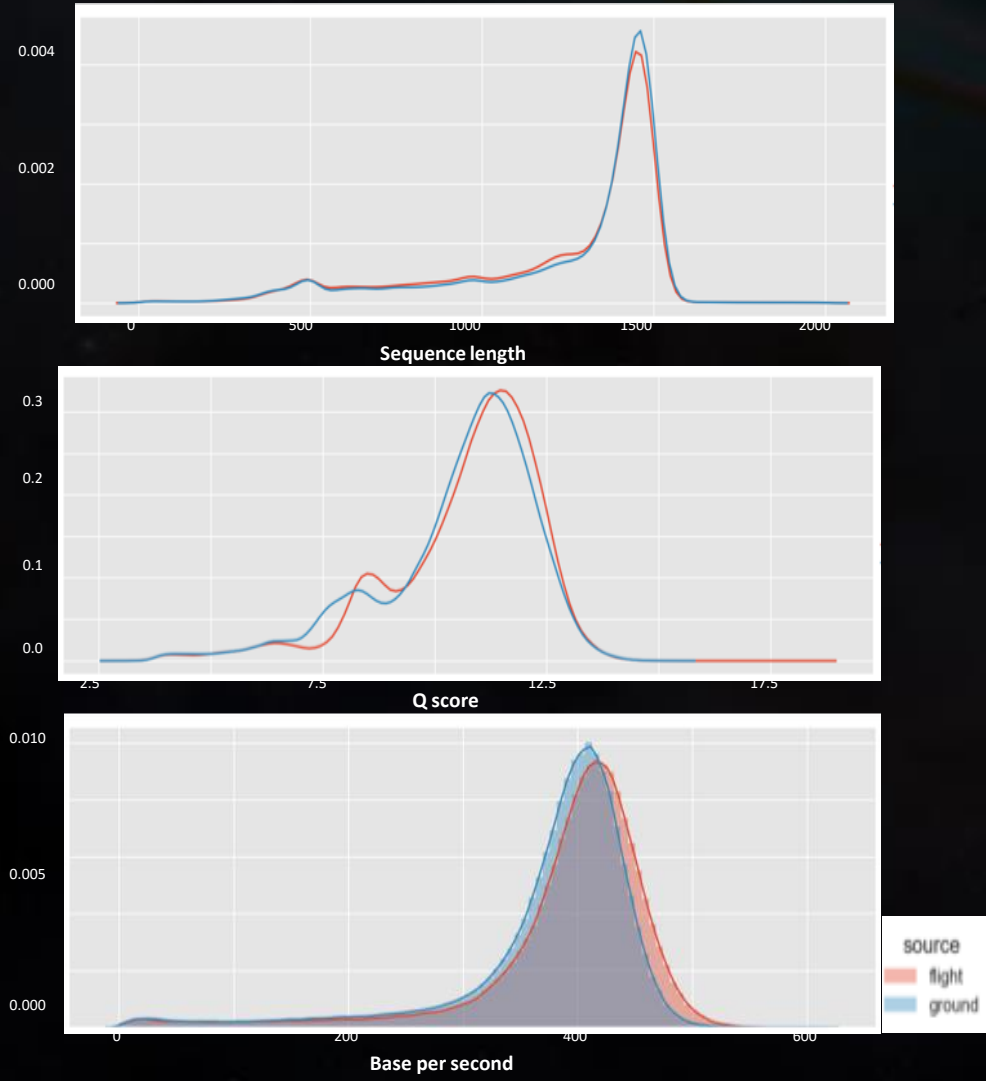
Ground



DNA sample to sequencer process successfully implemented – as it would be done on the ground – on the ISS!
Successful: pipetting, DNA amplification, DNA clean up, library preparation, flow cell preparation, and sequencing

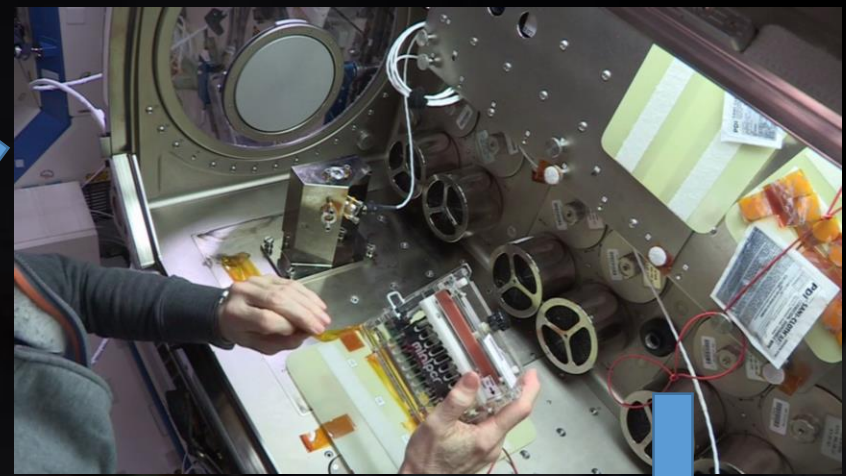
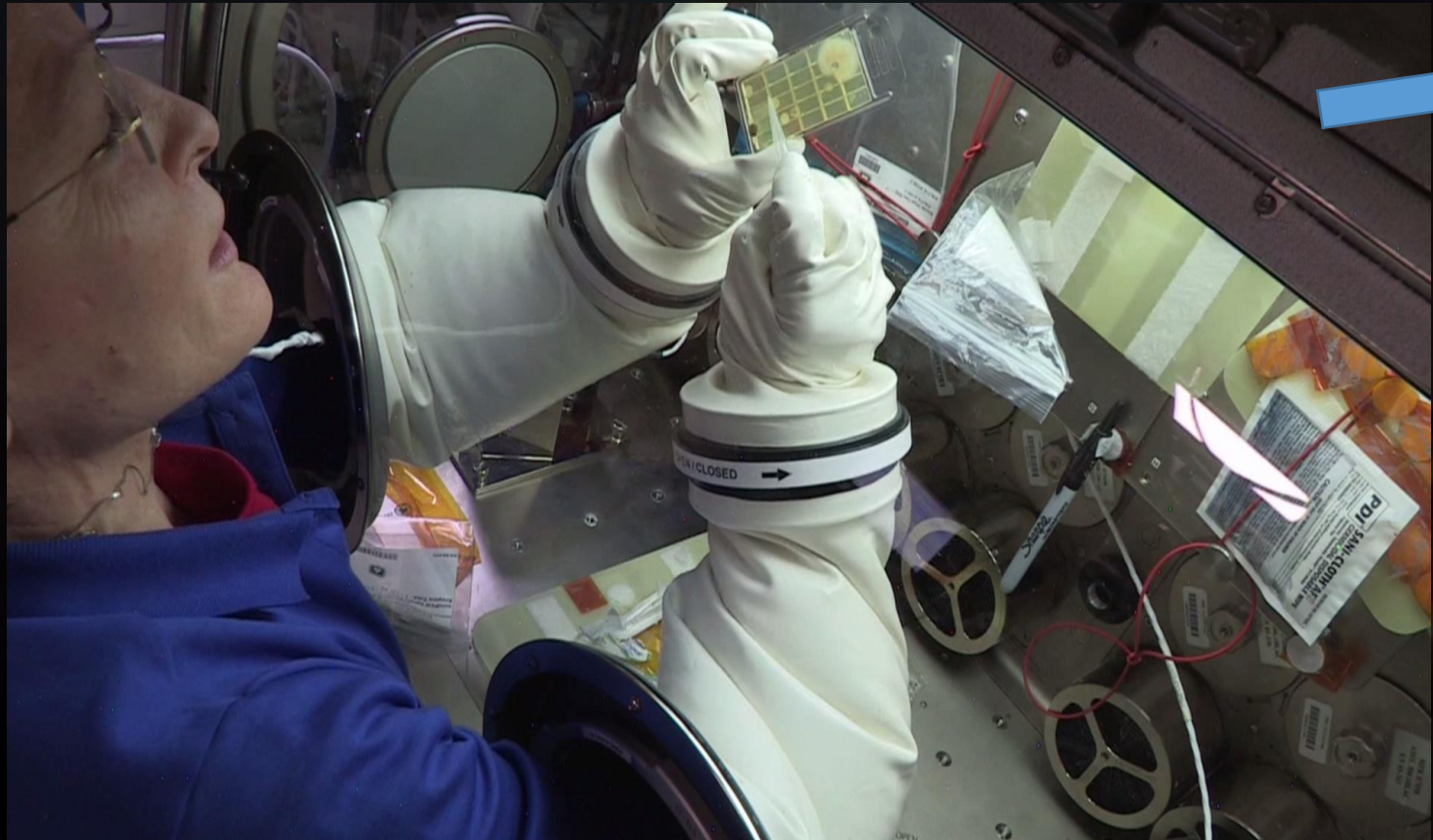


Genes in Space-3





Genes in Space-3



Astronaut Peggy Whitson collecting microbial cells from an Environmental Health Systems (EHS) Surface Sample Kit (SSK) Slide.

Microbial Identifications

Genes in Space-3



VITEK (biochemical)

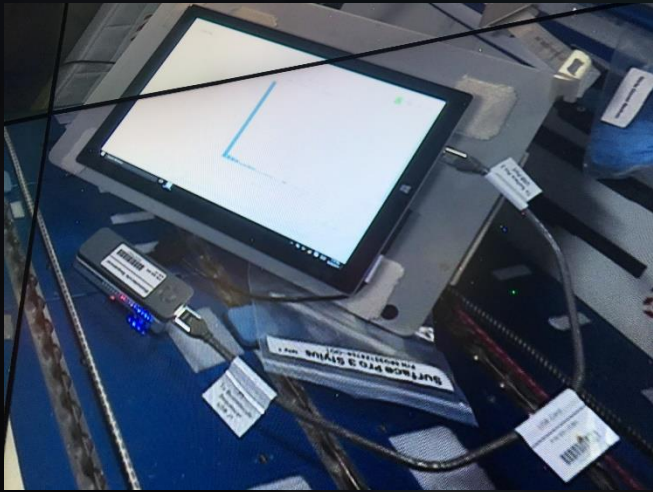


ABI 3500 (Sanger sequencing)

NASA JSC
Microbiology
Laboratory's
standard
methods for
microbial
identification

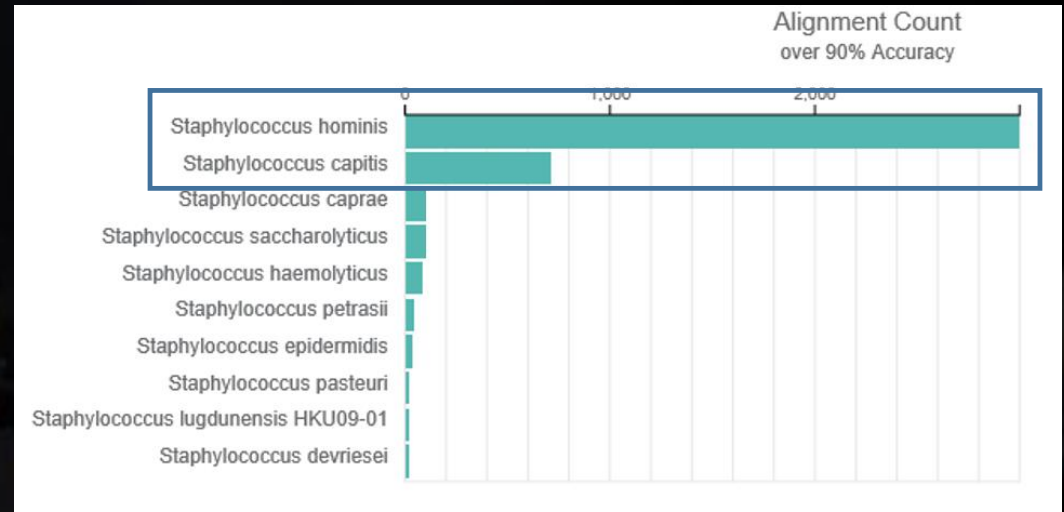
Genes in Space-3

Data obtained in flight downlinked to the ground for analysis:



```

agtcgatcgata
gctagagcatcg
atcgagggaggt
accgattagggt
attaccccgata
gggtaagatagc
agggacatttac
ggattacggaga
cttcgatacgat
actgtgaccagt
    
```



Return sample processed through normal procedures in the Microbiology Lab:



Colony	Detection Method	Sample ID	%ID
1	Biochemical	<i>Staphylococcus hominis hominis</i>	97.0
2	Biochemical	<i>Staphylococcus hominis hominis</i>	97.0
3	Biochemical	<i>Staphylococcus capitis</i>	94.0
1	Sanger Sequencing	<i>Staphylococcus hominis hominis</i> (ATCC=27844)	99.9
2	Sanger Sequencing	<i>Staphylococcus hominis hominis</i> (ATCC=27844)	100.0
3	Sanger Sequencing	<i>Staphylococcus capitis capitis</i> (ATCC=27840)	99.9

Success! The sequence data from Station matched the identifications obtained on the ground. History made!



Increasing Molecular Capabilities on Station



- ✓ Biomolecule Sequencer → Sequencing in space is possible!
- ✓ Genes in Space-3 → miniPCR and the Biomolecule Sequencer can be used for an end-to-end, culture-based microbial identification method!
- What about a rapid means of microbial identification?
- What about whole genome and epigenome analysis of cells / model organisms?
- What about transcriptomic analysis (direct RNA sequencing) of cells / model organisms?



The BEST is yet to come...



BEST



Biomolecule Extraction and Sequencing Technology

- Using hardware already on station
 - miniPCR
 - Biomolecule Sequencer
- Consumables launched on OA-9 (and SpX-16)





BEST Experiments



3 separate experiments

1. Swab-to-sequencer

- Perform culture-independent microbiome assessments through sequencing DNA directly from an environmental swab (and return additional swabs)

2. Cellular evolution

- Assess genomic changes as a function of time on the ISS in a cellular population through whole genome sequencing

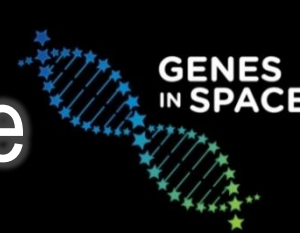
3. Direct RNA sequencing

- Demonstrate transcriptomic evaluations with the MinION through the sequencing of cDNA and RNA





BEST Experiments Progress to Date



- 3 sessions of the swab-to-sequencer run
- RNA and cDNA sequencing
- RNA sample prep and sequencing





BEST: Swab-to-Sequencer on Station



Non-culture based-microbial identification method



Swab

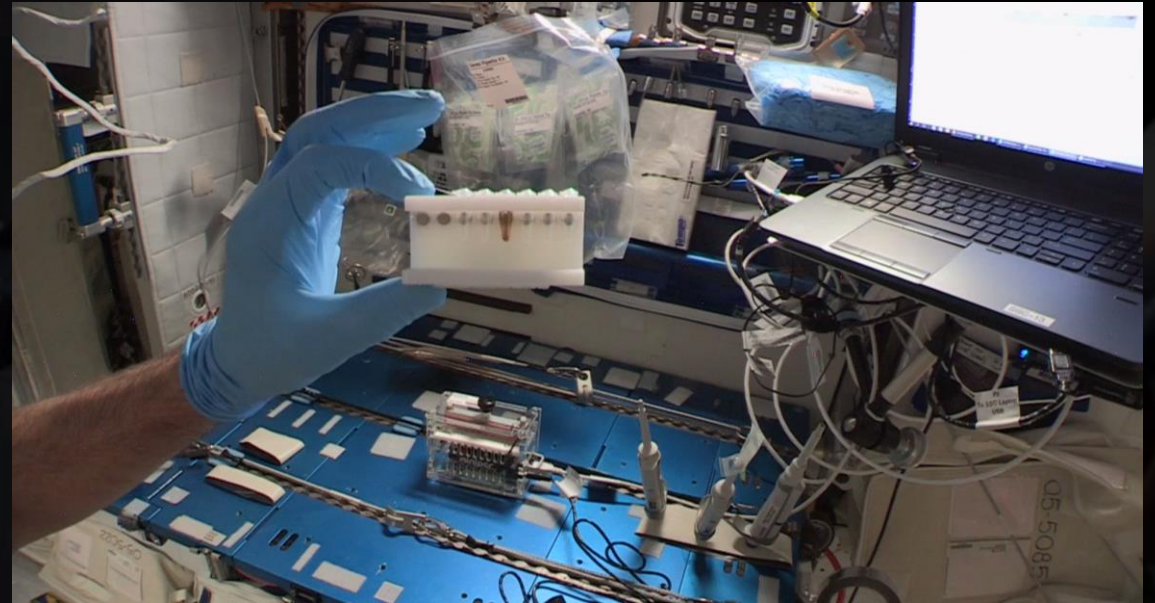
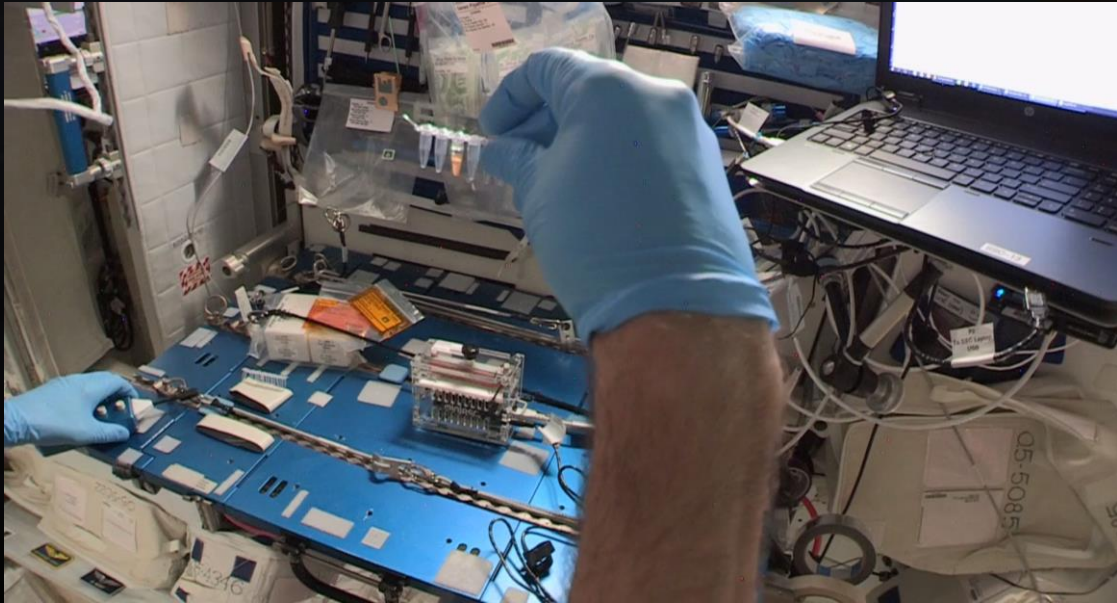


Extract

July 19, 2018



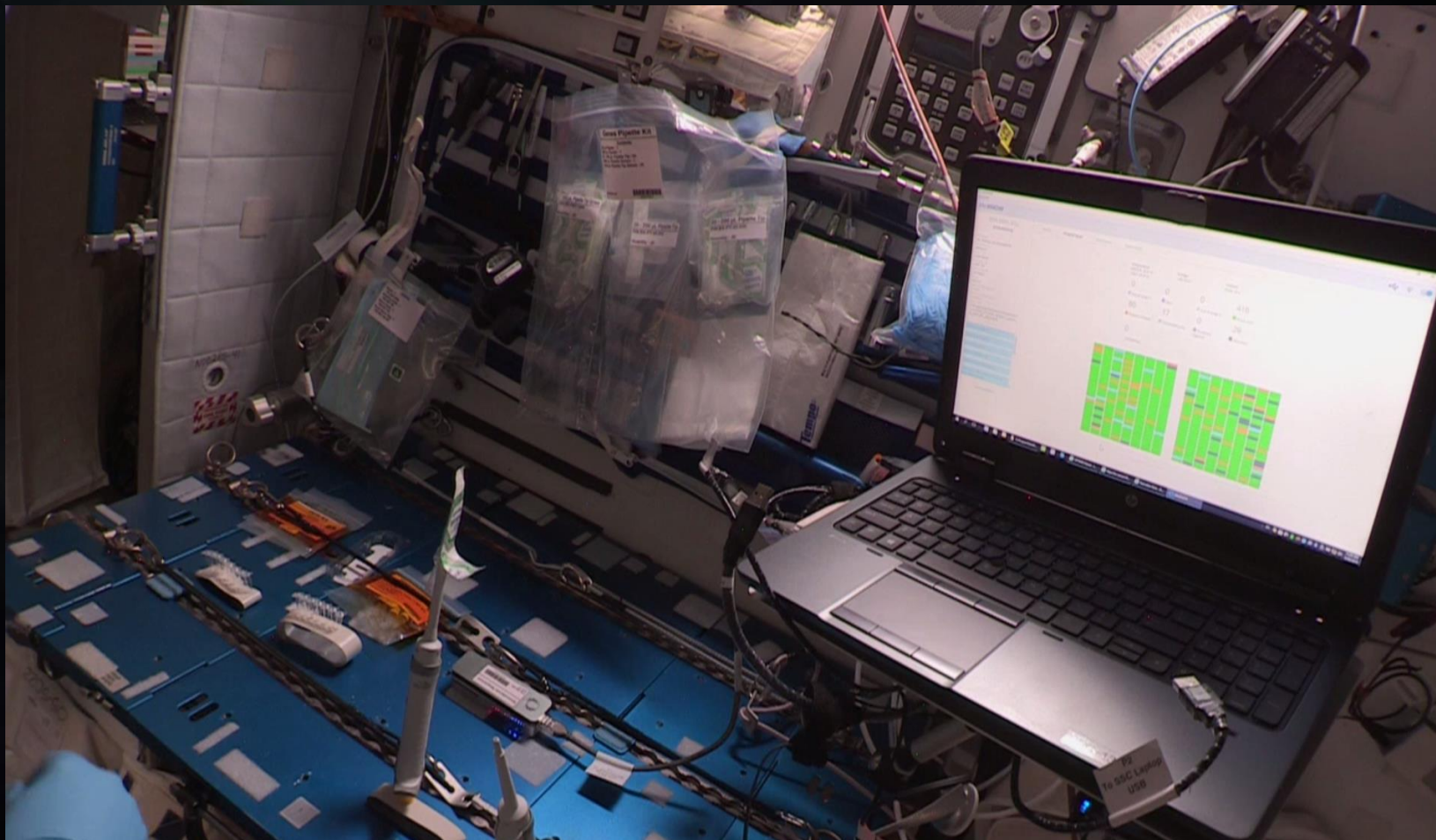
BEST: Swab-to-Sequencer on Station



A magnetic stand and magnetic beads were used to purify and concentrate DNA.



BEST: Swab-to-Sequencer on Station



Preparing libraries for sequencing

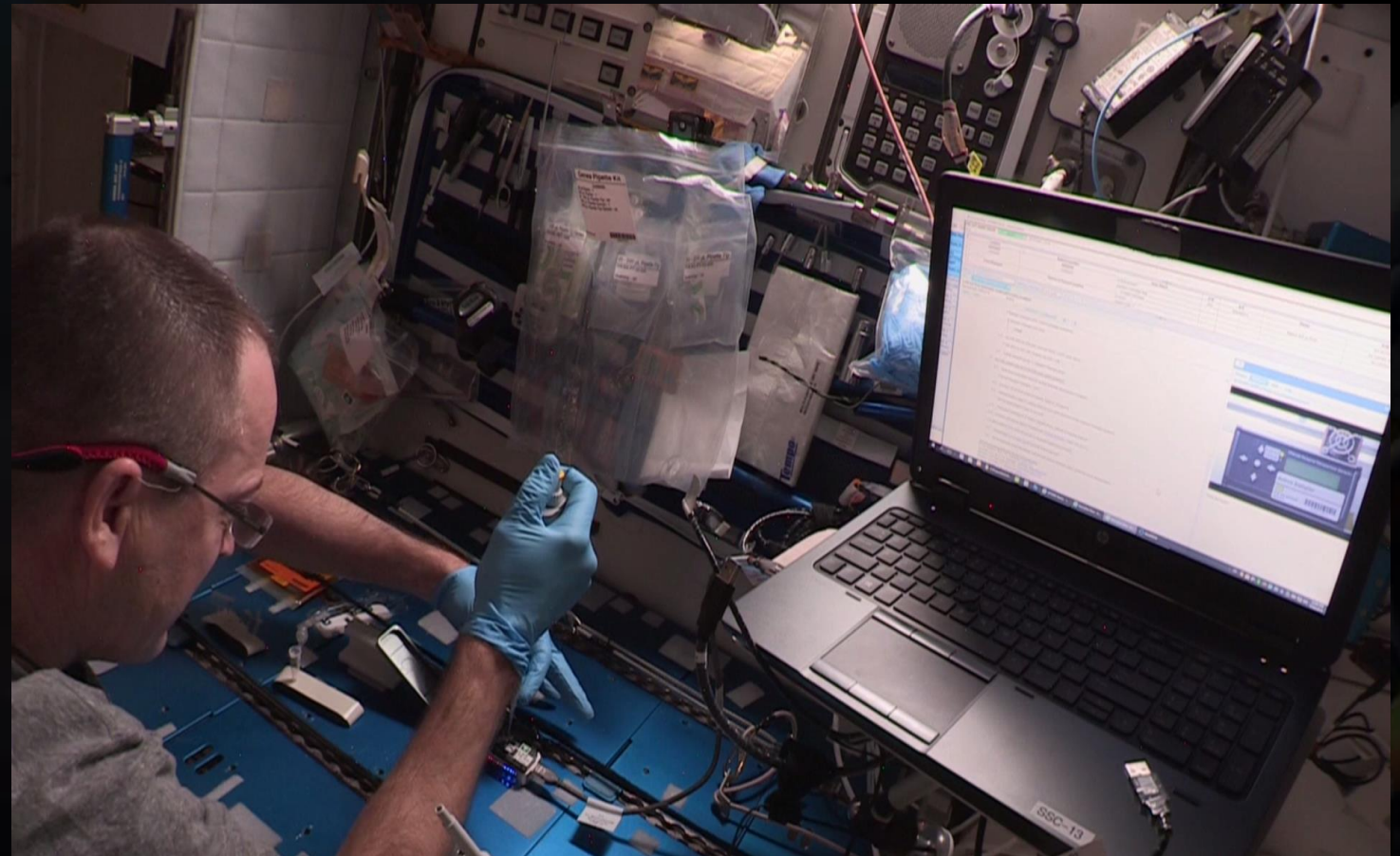


BEST: Swab-to-Sequencer on Station



Loading the flow cell of the Biomolecule Sequencer.

July 20, 2018

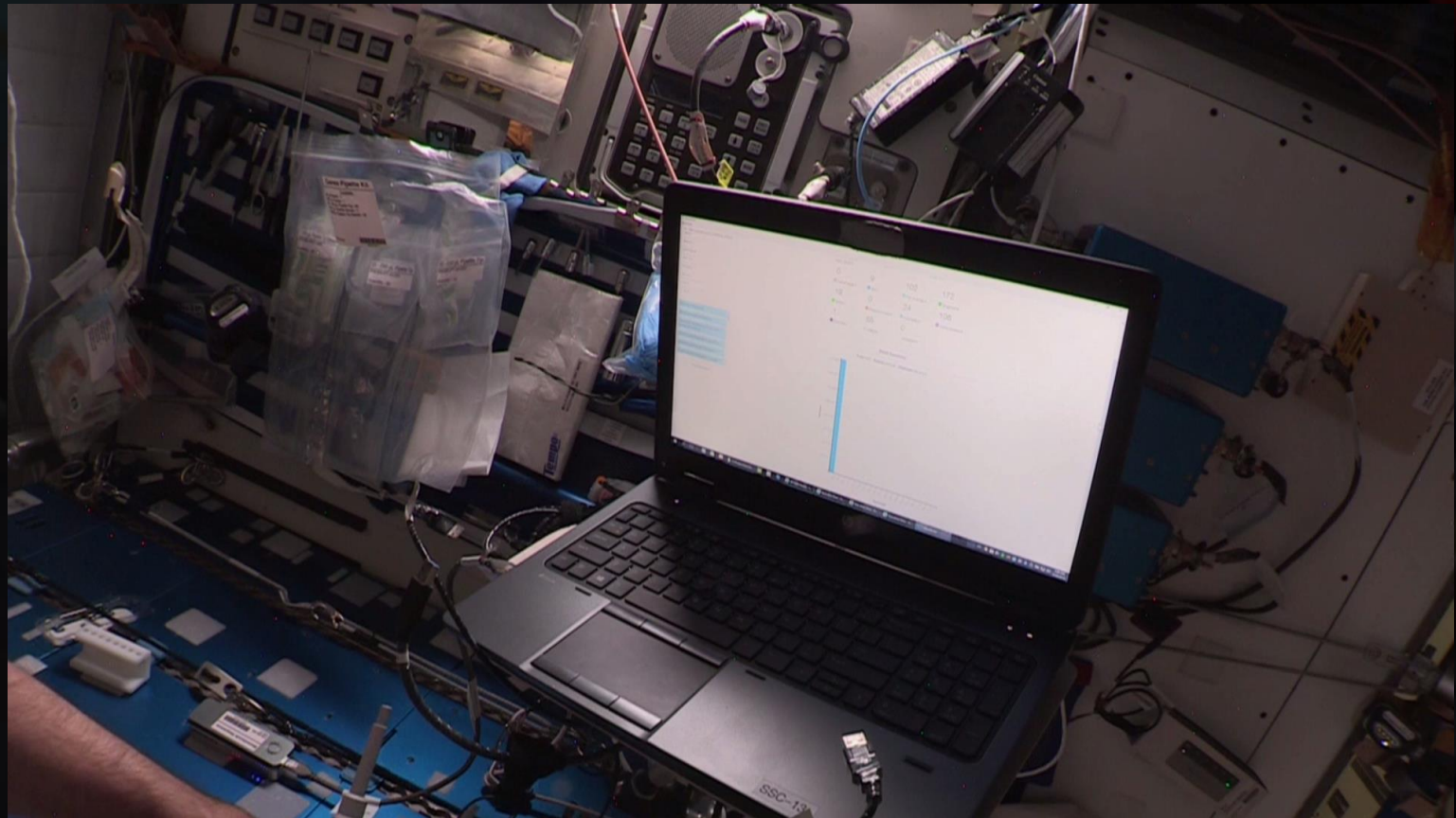




BEST: Swab-to-Sequencer on Station



- Ricky provided confirmation of success, as ~4,000 reads were sequenced within the first few minutes of the run
- A peak corresponding to the length of the 16S amplicon was immediately apparent
- Data was downlinked days to the ground days later.





BEST: First Ever RNA Sequencing in Space!



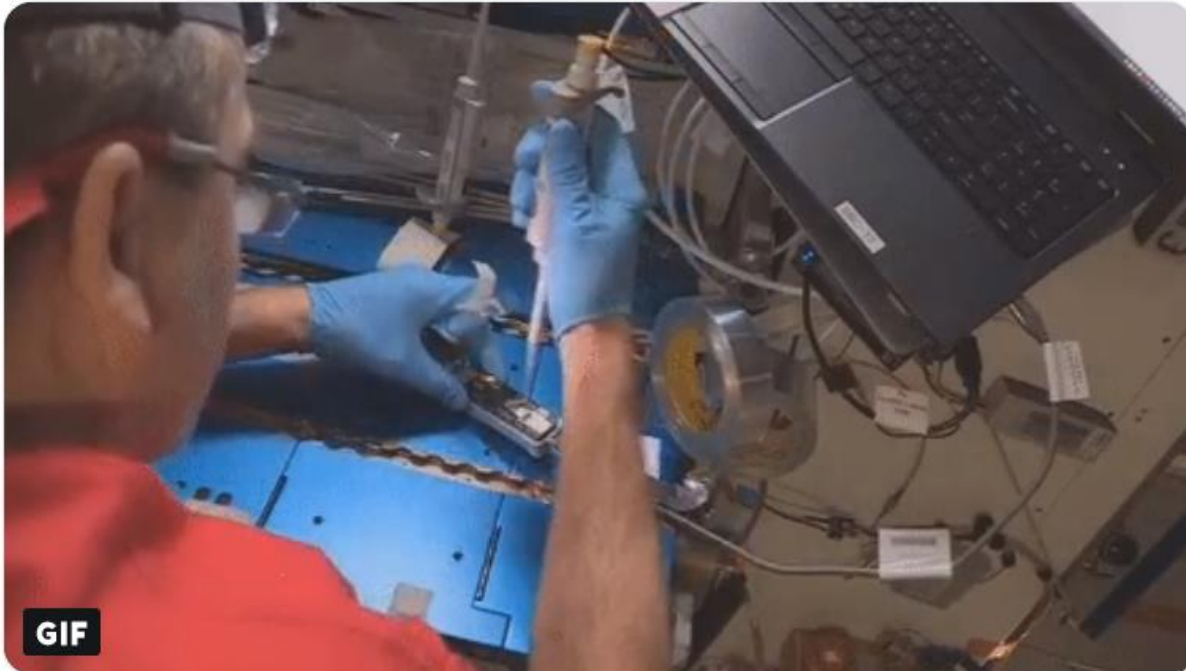
Demonstrating the direct sequencing of RNA (sample prepped on Earth) and demonstrating the preparation of RNA for direct sequencing on station.





ISS Research  @ISS_Research · Aug 29

Today, [@Astro_Ricky](#) became the first person to sequence RNA in space aboard the [@Space_Station](#)! "There is so much to be gained from that real-time snapshot of gene expression." -Dr. Sarah Wallace go.nasa.gov/2tNntKu



GIF

29 666 2.3K



ISS National Lab 
@ISS_CASIS

Following

An important milestone was achieved on [@Space_Station](#) this week -- [@Astro_Ricky](#) successfully sequenced RNA in space! Watch latest episode of [#SpaceToGround](#) for more details.

 Intl. Space Station



Space to Ground: Potential Game Changer: 08/31/2018

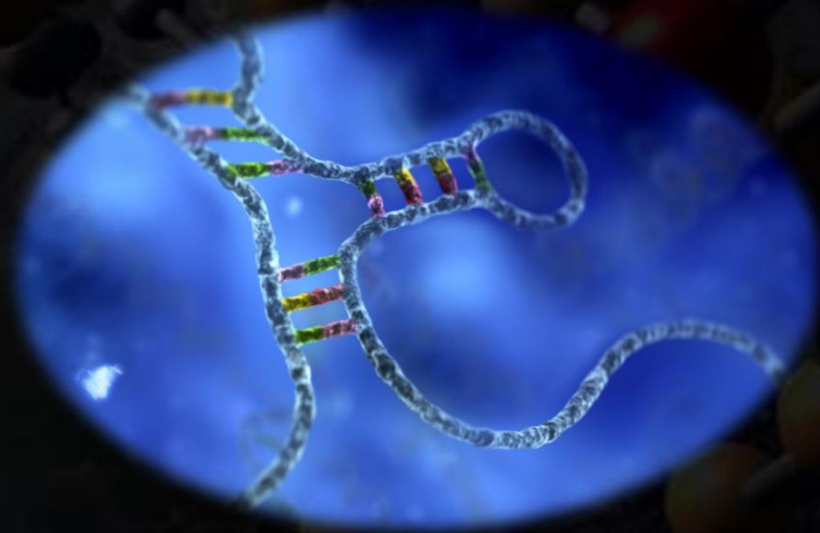
The BEST experiment is a potential game changer studying how life adapts in space . Meanwhile, pressure is holding steady on the station after the crew patched up a small hole on a Soyuz spaceship.



BEST: What's Next?



Assessing microbial mutation rates in space through long-term culture and periodic whole genome sequencing on station. Genetic and epigenetic changes will be compared against parallel cultures on the ground.

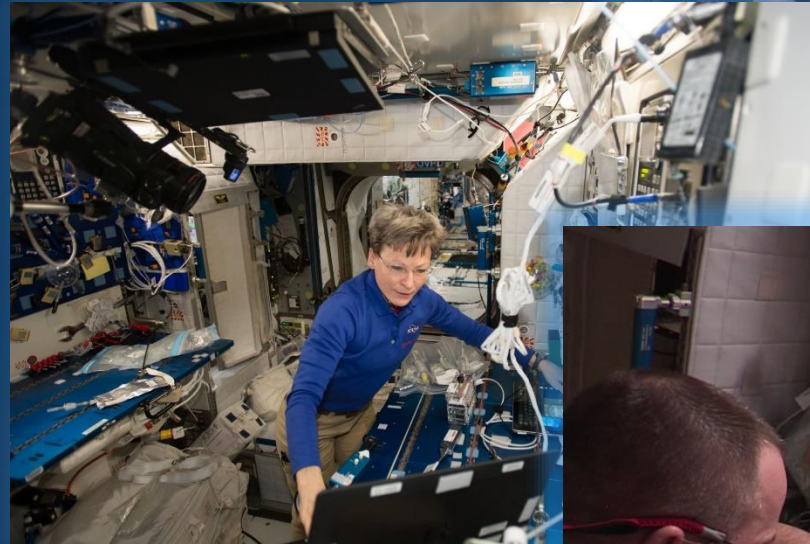
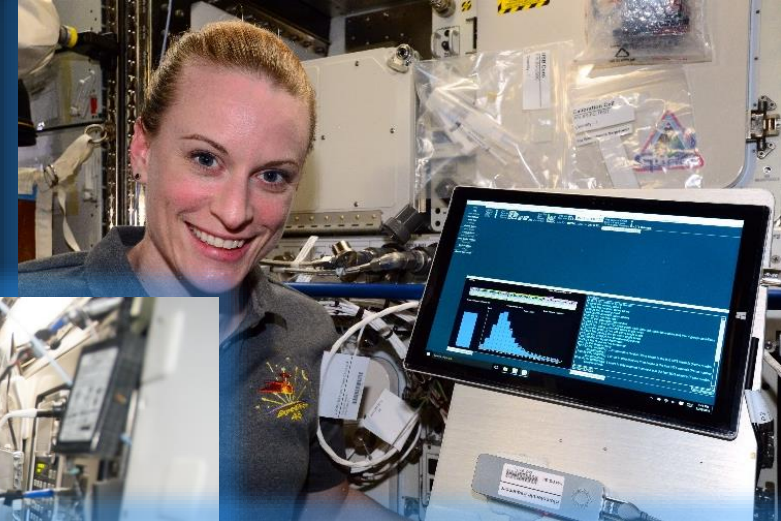
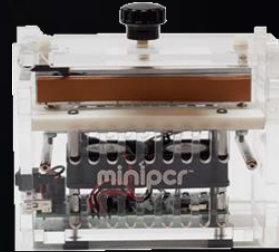




Conclusions



- We have a molecular lab on station!
 - COTS technology has transformed the science that can be accomplished on station
 - Microbes identified in space for the first time!
- Astronauts are amazing molecular biologists
 - Through the optimization of techniques and methods, basic laboratory protocols can be rapidly (and inexpensively) transitioned to ISS
 - Alteration of reagents to Tox 0 solutions allow for open cabin operations
 - Creative use of common laboratory tools alleviates the need for engineering to develop spaceflight-compatible hardware
- If put to the correct use, significant and impactful science can be accomplished during the remaining lifetime of ISS
 - More research to come!





Acknowledgments

Extreme Environment Molecular Biologists



Astronauts



Kate Rubins, Ph.D.



Ricky Arnold



NEEMO 21 Team
Reid Wiseman, NASA
Megan McArthur, NASA
Marc O Griofa
Matthias Maurer, ESA
Noel Du Toit
Dawn Kernagis



Peggy Whitson, Ph.D.



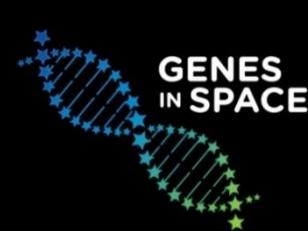
Serena Auñón-Chancellor, M.D.



NEEMO 22 Team
Kjell Lindgren, NASA
Trevor Graff
Pedro Duque, ESA
Dom D'Agnostion
Mark Hulsbeck
Sean Moore



Acknowledgments Ground Support Team



Genes in Space-3 Collaborators

Scott Copeland, Sebastian Kraves, Ph.D.,
and Ezequiel (Zeke) Alvarez Saavedra,
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Integration Team:

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PIRE: Katrina Whitlock

PARC: Lauren Catoe (Schuler)

Safety Engineer: John Nader

Ground Data Services:

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Stowage PIM: Virginia Spaniel

Manifest: Cleo Bay

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Melissa Boyer

Landon Sommer

Melanie Smith



BEST PIM

Melissa Boyer

BEST Ops Lead

Linda Gibson



Oxford Nanopore Technologies

James Brayer

Sissel Juul, Ph.D.

Dan Turner, Ph.D.

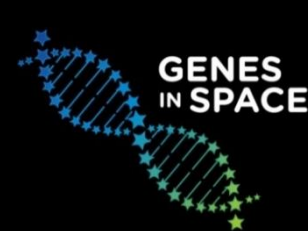
David Stoddart, Ph.D.

Michael Micorescu, Ph.D.





Acknowledgments



The Biomolecule Sequencer, Genes in Space-3, and BEST Payload Development Team: Sarah Wallace, Ph.D., Sarah Stahl, Aaron Burton, Ph.D. and Kristen John, Ph.D.

BEST Co-Investigators



Mark Akeson, Ph.D., Miten Jain, Ph.D., and Benedict Paten, Ph.D.
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BEST PD
Christian Castro,
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