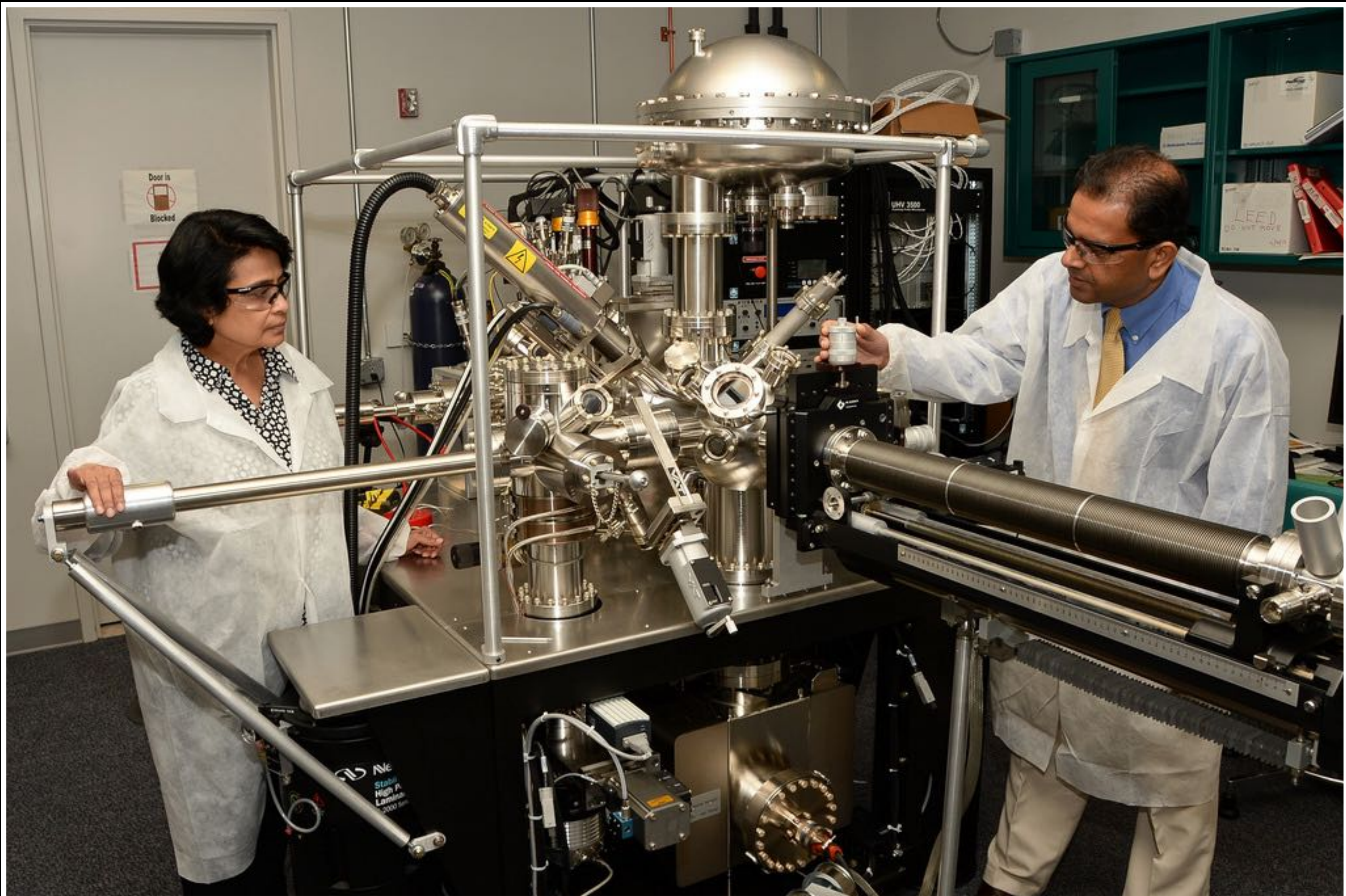
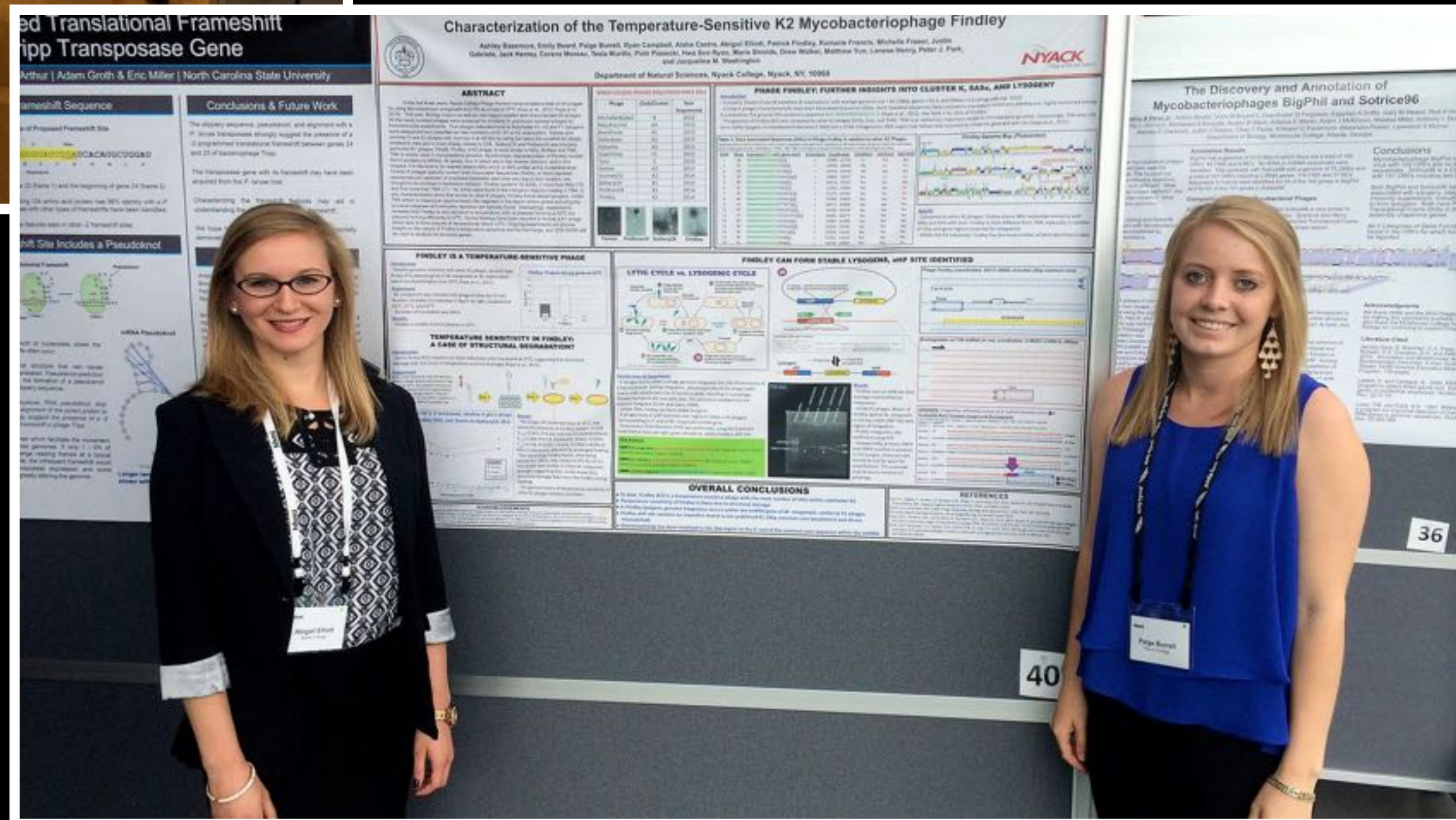
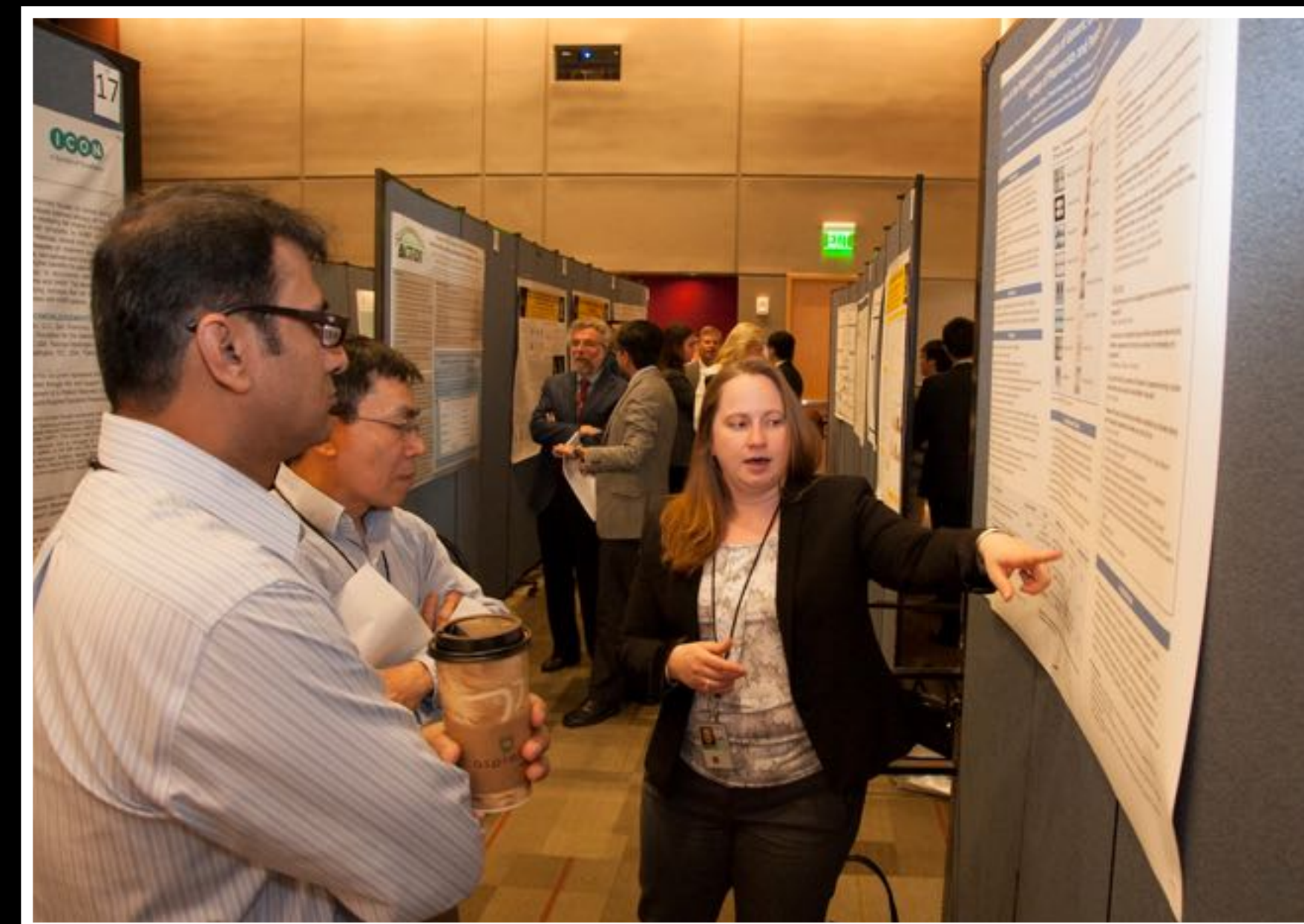


Science





Findley	K2	2014
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Fameo ProfessorX BatteryCK Findley

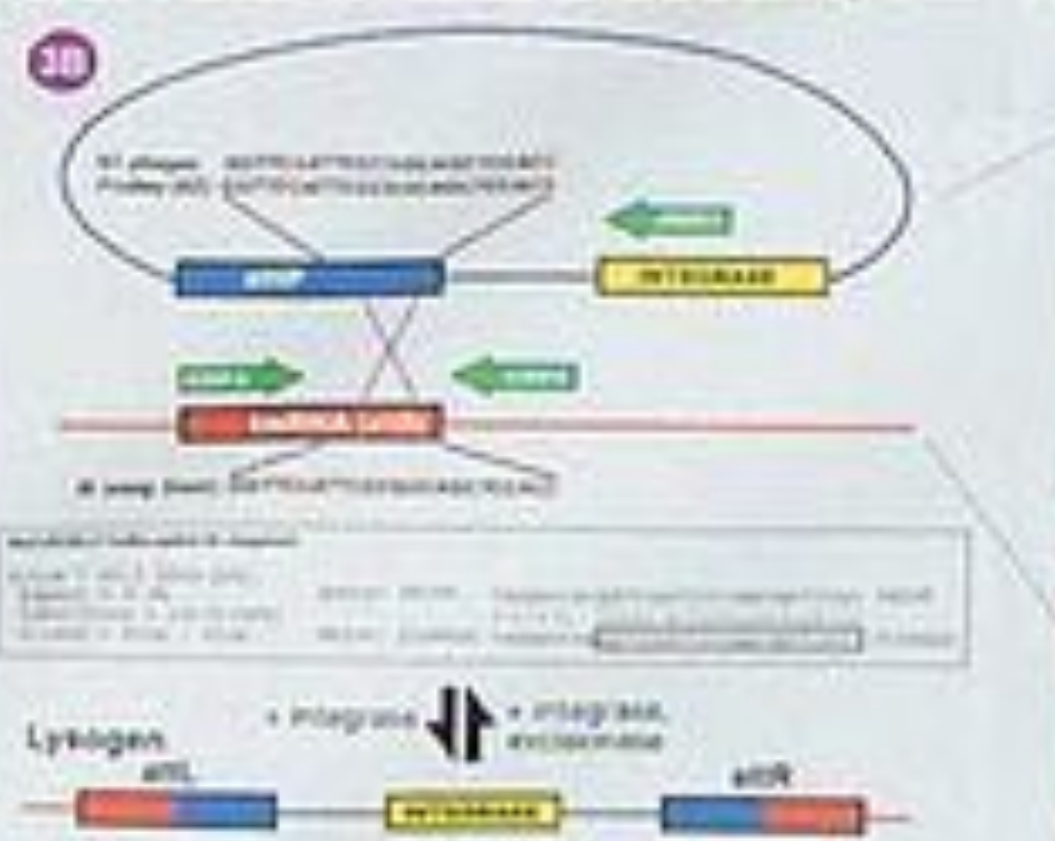
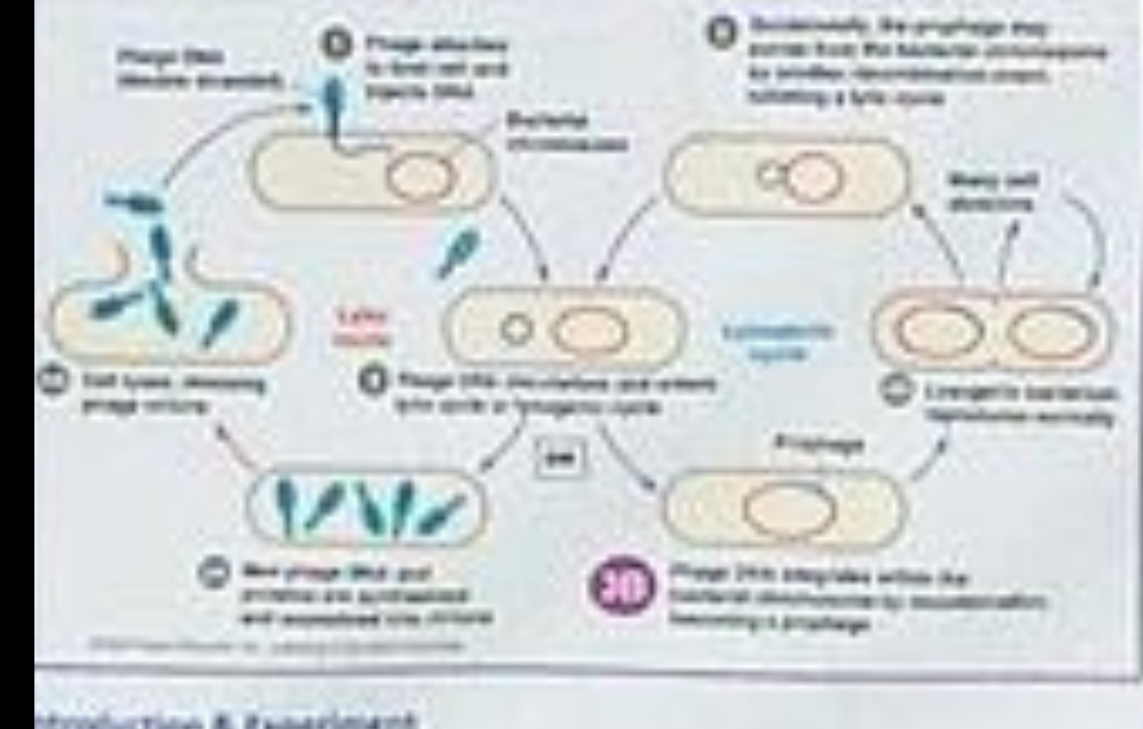
7	62	GGGATGAGAGGCTTACCGACAGG	+	81170	31183	Yes	Yes	Yes
8	44	GGGATGAGAGGCTTACCGACAGG	+	82990	31603	Yes	Yes	Yes
9	53	GGGATGAGAGGCTTACCGACAGG	+	38072	35084	Yes	Yes	Yes
10	49	GGGATGAGAGGCTTACCGACAGG	+	46030	44704	Yes	Yes	Yes
11	73	GGGATGAGAGGCTTACCGACAGG	+	43045	48077	Yes	Yes	Yes
12	82	GGGATGAGAGGCTTACCGACAGG	+	52087	52099	Yes	Yes	Yes
13	86	GGGATGAGAGGCTTACCGACAGG	+	51824	53746	Yes	Yes	Yes
14	87	GGGATGAGAGGCTTACCGACAGG	+	51834	51944	Yes	Yes	Yes
15	90	GGGATGAGAGGCTTACCGACAGG	+	51231	55243	Yes	Yes	Yes
16	93	GGGATGAGAGGCTTACCGACAGG	+	54074	54086	Yes	Yes	Yes

Results

- Compared to other K2 phages, Findley shares 98% nucleotide similarity with Mily and PHN with Zoa1. Findley is most different from TMA, especially in number of SAAs and gene regions essential for integration.
- Within the K2 subcluster, Findley has the most number of SAAs identified to date.

...viruses perform? Are...
...genomes?
...plating and *Escherichia coli*...
...with *Mycobacterium*...
...accomplished by...
...isolations.

LYTIC CYCLE vs. LYSOGENIC CYCLE



IDENTIFIED



LYSOGEN: Integration of Findley occurs at 5' end of common core (43)

Nucleotide BLAST between lysogen and M. smegmatis:

Query:	30	GGGATGAGAGGCTTACCGACAGG	+	33845	33857	Yes	Yes	Yes
Match:	1112000	GGGATGAGAGGCTTACCGACAGG	+	33845	33857	Yes	Yes	Yes
Query:	40	GGGATGAGAGGCTTACCGACAGG	+	33845	33857	Yes	Yes	Yes
Match:	2112000	GGGATGAGAGGCTTACCGACAGG	+	33845	33857	Yes	Yes	Yes
Query:	100	GGGATGAGAGGCTTACCGACAGG	+	33845	33857	Yes	Yes	Yes
Match:	8112000	GGGATGAGAGGCTTACCGACAGG	+	33845	33857	Yes	Yes	Yes
Query:	200	GGGATGAGAGGCTTACCGACAGG	+	33845	33857	Yes	Yes	Yes
Match:	5384000	GGGATGAGAGGCTTACCGACAGG	+	33845	33857	Yes	Yes	Yes

Model

...reacts with attachment site of...
...flanked by hybrid attB and attP...
...enzyme Integrase (Groth and...
...Like TMA, Findley can form...
...K phages have an attP with...
...corresponding to 5' end of attB...
...Polymerase Chain Reaction (PCR)...
...listed below (also see right, gr...
PCR Primers:

CMF4 (R1 phage attB) 5'-CGTGGAGAGGCTTACCGACAGG-3'

CMF5 (R1 phage attP) 5'-TTTCTTCTTCTTCTTCTTCTTCTT-3'

...Findley uses an attB site that...
...flanked by hybrid attB and attP...
...enzyme Integrase (Groth and...
...Like TMA, Findley can form...
...K phages have an attP with...
...corresponding to 5' end of attB...
...Polymerase Chain Reaction (PCR)...
...listed below (also see right, gr...
PCR Primers:

CMF4 (R1 phage attB) 5'-CGTGGAGAGGCTTACCGACAGG-3'

CMF5 (R1 phage attP) 5'-TTTCTTCTTCTTCTTCTTCTTCTT-3'

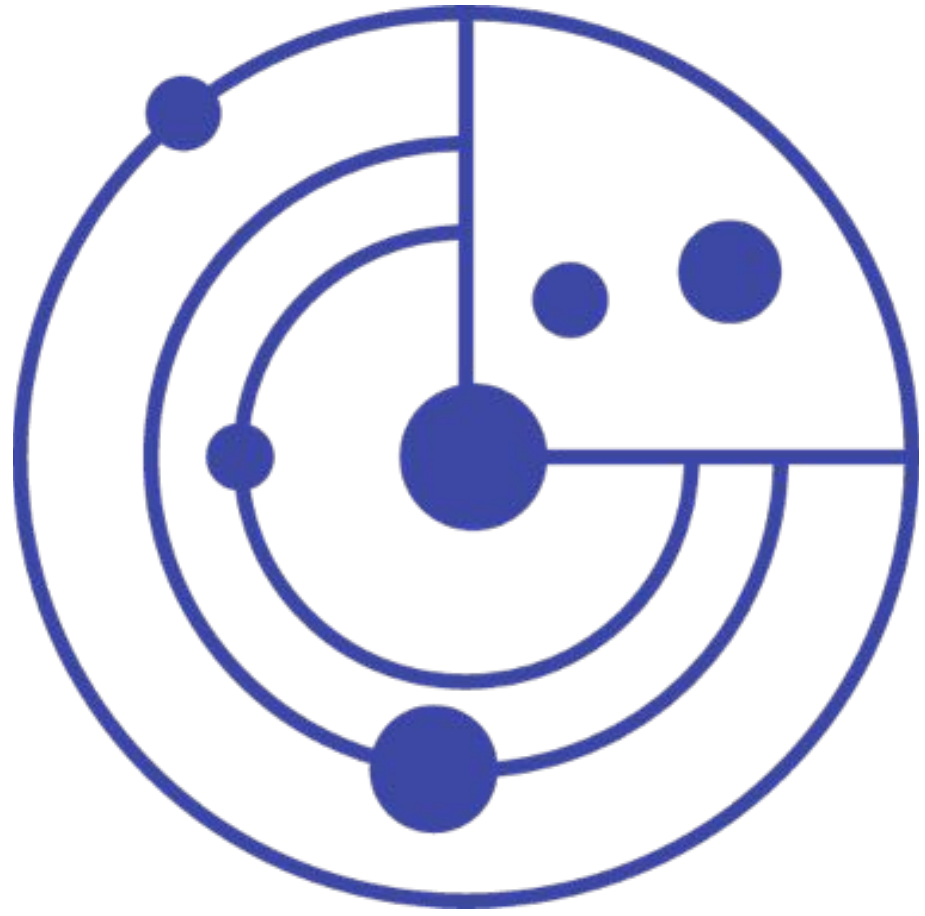
...may be due to evolution of...
...prophage.

OVERALL CONCLUSIONS

- To date, Findley (K2) is a temperature-sensitive phage with the most number of SAAs within subcluster K2.
- Temperature sensitivity of Findley is likely due to structural damage.
- In Findley lysogens, genome integration occurs within the *trnRNA* gene of *M. smegmatis*, similar to K1 phages.
- Findley attP site contains an imperfect match to the published K1 24bp common core (positions 6 and 24 are mismatched).
- Strand exchange has been localized to the 5bp region at the 5' end of the common core sequence within the *trnRNA*.

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Developing
and Using
Models



ESS3



Earth
and Human
Activity



Systems
System Models





Questions?

Habitat

Design

