

MIP280A4 FINAL PROJECT

Tyler Sherman

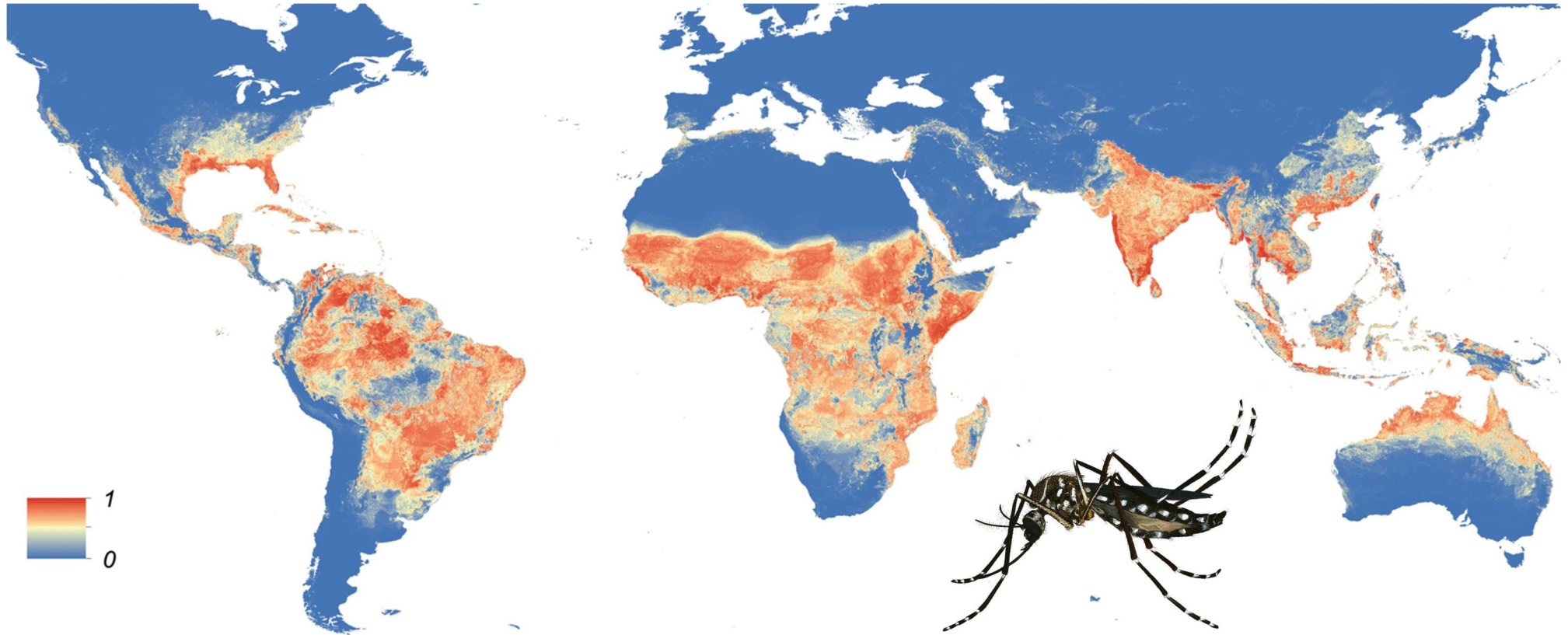
Fall 2022

A series of overlapping, irregular black lines of varying lengths and orientations, creating a complex, abstract geometric pattern on the left side of the slide. The lines intersect to form various shapes, including triangles and polygons, and extend across the top and middle of the page.

PRIMARY GOALS

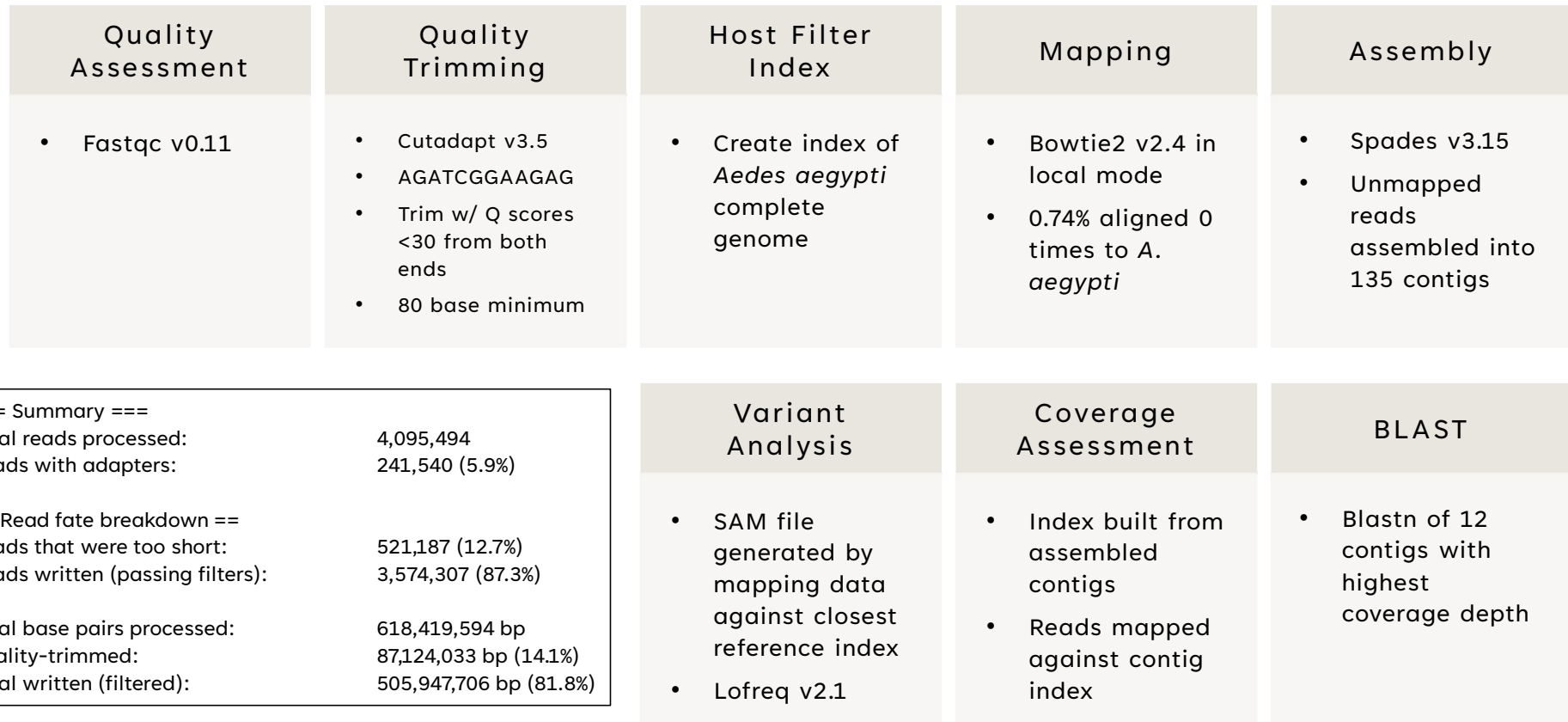
- Perform bioinformatic analysis
 - Shotgun metagenomic sequencing of total RNA extracted from pools of *Aedes aegypti* captured in Recife, Brazil (now in established colony at CSU)
 - Single-end, 150 bp reads from Illumina NextSeq500
- Further characterized sequences of interest
 - Genome annotation, pairwise identity, phylogenic & variant analysis

GLOBAL MAP OF THE PREDICTED DISTRIBUTION OF *Aedes Aegypti* IN 2015

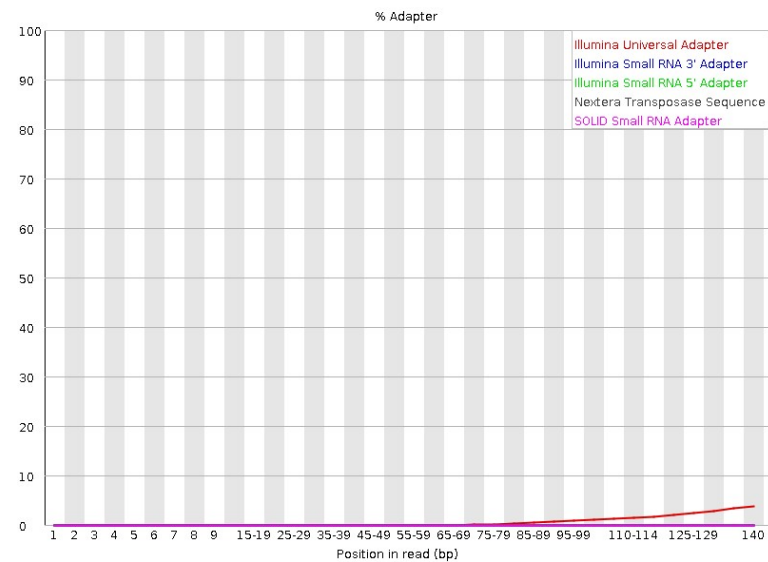
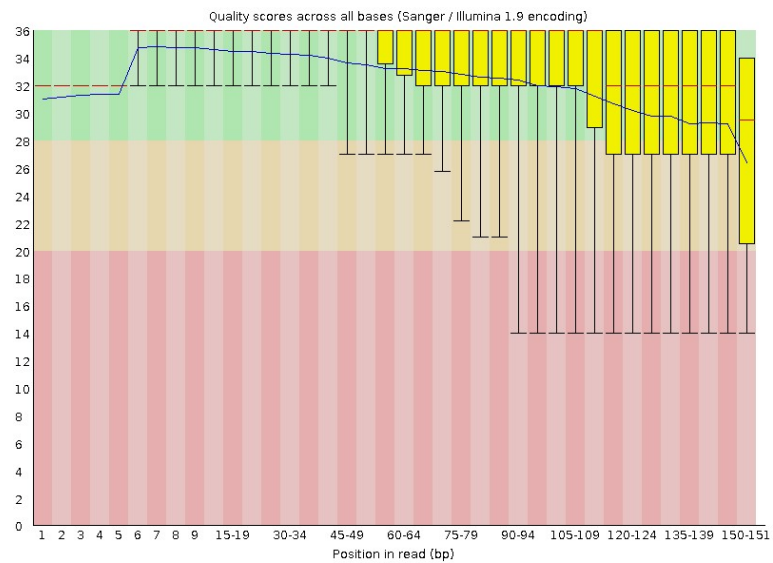


Moritz UG Kraemer, Marianne E Sinka, Kirsten A Duda, Adrian QN Mylne, Freya M Shearer, Christopher M Barker, Chester G Moore, Roberta G Carvalho, Giovanini E Coelho, Wim Van Bortel, Guy Hendrickx, Francis Schaffner, Iqbal RF Elyazar, Hwa-Jen Teng, Oliver J Brady, Jane P Messina, David M Pigott, Thomas W Scott, David L Smith, GR William Wint, Nick Golding, Simon I Hay - elifesciences.org/content/4/e08347, File:Global Aedes aegypti distribution.gif

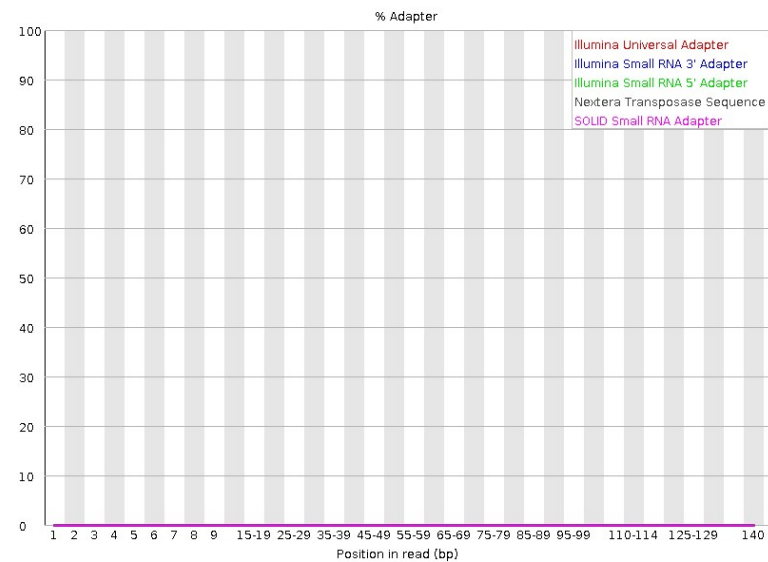
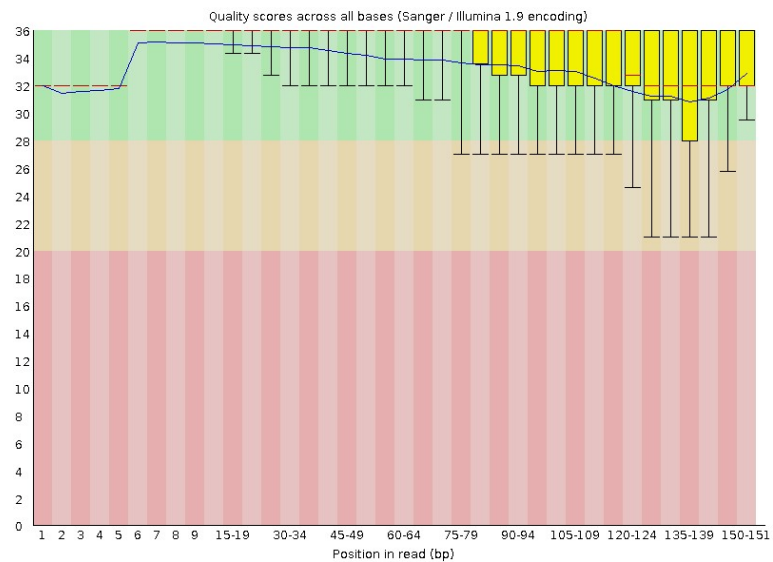
BIOINFORMATICS WORKFLOW



Pre-trim



Post-trim



BLAST RESULTS

<i>reads mapped against contigs</i>				<i>NCBI blastn of contigs</i>				
^a contig	# reads mapped	sequence length	mean coverage	top BLAST hit	query cover	percent identity	accession	pathogen family
2	3451	4695	103	Yeltsovka tombus-like_virus putative capsid	90%	80%	MW251332.1	<i>Tombusviridae</i>
3	3367	3837	127	PCLV isolate Rio segment M	99%	100%	NC_038261.1	<i>Bunyavirales</i>
1	2613	6781	55	PCLV isolate Rio segment L	99%	100%	NC_038262.1	<i>Bunyavirales</i>
4	2503	3089	115	Guadeloupe mosquito virus segment RNA1	100%	100%	MW434816.1	unclassified
11	1877	1341	202	PCLV isolate Rio segment S	100%	100%	NC_038263.1	<i>Bunyavirales</i>
5	1037	1632	85	Guadeloupe mosquito virus segment RNA2	100%	99%	MW434807.1	unclassified
13	779	1278	88	n.d.	-	-	-	-
9	344	1423	35	Chap-like virus isolate CLv.PozaRica20 ORF gene	99%	100%	MT742176.1	<i>Partitiviridae</i>
10	311	1348	33	<i>Aedes aegypti</i> leucine-rich repeat transmembrane neuronal protein 3	4%	95%	XM_001659114.2	-
6	251	1585	22	<i>Elizabethkingia anophelis</i> strain 2-8 chromosome	99%	100%	CP071530.1	<i>Weeksellaceae</i>
8	197	1454	19	Verdadero virus isolate Vv.PozaRica20 putative capsid	99%	100%	MT742175.1	<i>Partitiviridae</i>
7	144	1455	13	<i>Elizabethkingia anophelis</i> JUNP 353 DNA	100%	100%	AP022313.1	<i>Weeksellaceae</i>

^acontigs derived from Spades assembly of remaining reads when filtered against *Aedes aegypti* genome (GCA_002204515.1)

PCLV = Phasi Charoen-like virus

n.d. = no hits returned for BLAST of contig

Yeltsovka tombus-like_virus isolate Koltsovo/YTLV/2019 putative polyprotein and putative capsid protein genes, complete cds

GenBank: MW251332.1

[FASTA](#) [Graphics](#)

Go to:

LOCUS MW251332 4317 bp RNA linear VRL 05-APR-2022

DEFINITION Yeltsovka tombus-like_virus isolate Koltsovo/YTLV/2019 putative polyprotein and putative capsid protein genes, complete cds.

ACCESSION MW251332

VERSION MW251332.1

KEYWORDS .

SOURCE Yeltsovka tombus-like_virus

ORGANISM [Yeltsovka tombus-like_virus](#)

Viruses; Riboviria; Orthornavirae; Kitrinoviricota; Tolucaviricetes; Tolivirales; Tombusviridae.

REFERENCE 1 (bases 1 to 4317)

AUTHORS Ternovoi,V.A., Shvalov,A.N., Kartashev,M.Y., Ponomareva,E.P., Tupota,N.L., Horoshavin,Y.Y.A., Bayandin,R.B., Gladysheva,A.V., Mikryukova,T.P., Tregubchak,T.V., Ilyinykh,A.V. and Loktev,V.B.

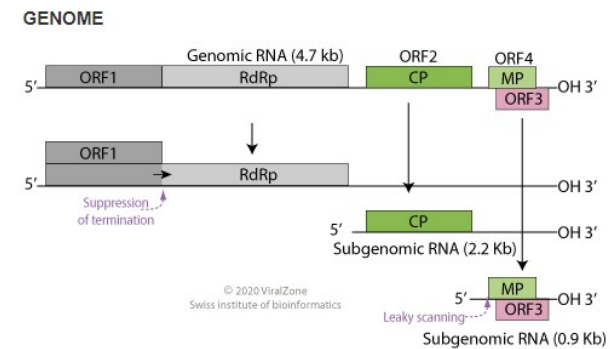
TITLE Coquillettidia richardii viruses

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 4317)

Published online 2018 Dec 18. doi: [10.1016/j.virol.2018.12.009](https://doi.org/10.1016/j.virol.2018.12.009)

Tolivirales; Tombusviridae
Tomato bushy stunt virus



Monopartite, linear, ssRNA(+) genome of 4-5.4 kb, which lacks a cap structure and a poly(A)tail.

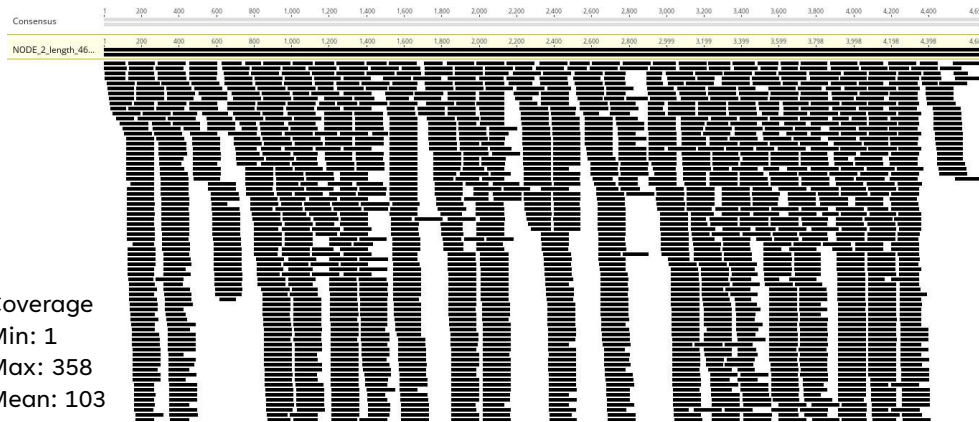
Diverse RNA viruses of arthropod origin in the blood of fruit bats suggest a link between bat and arthropod viromes

[Andrew J. Bennett](#),¹ [Trenton Bushmaker](#),² [Kenneth Cameron](#),³ [Alain Ondzie](#),³ [Fabien R. Niama](#),⁴ [Henri-Joseph Parra](#),⁴ [Jean-Vivien Mombouli](#),⁴ [Sarah H. Olson](#),³ [Vincent J Munster](#),² and [Tony L. Goldberg](#)^{1,*}

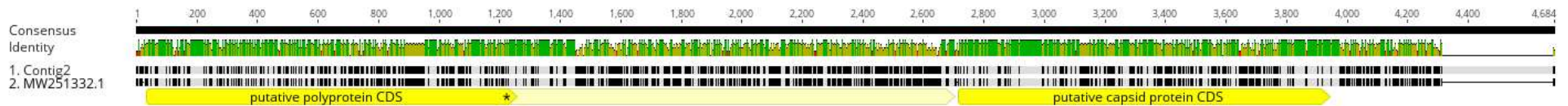
► [Author information](#) ► [Copyright and License information](#) [Disclaimer](#)

TOMBUS-LIKE VIRUS COVERAGE & ANNOTATION

Mapped against index of contig



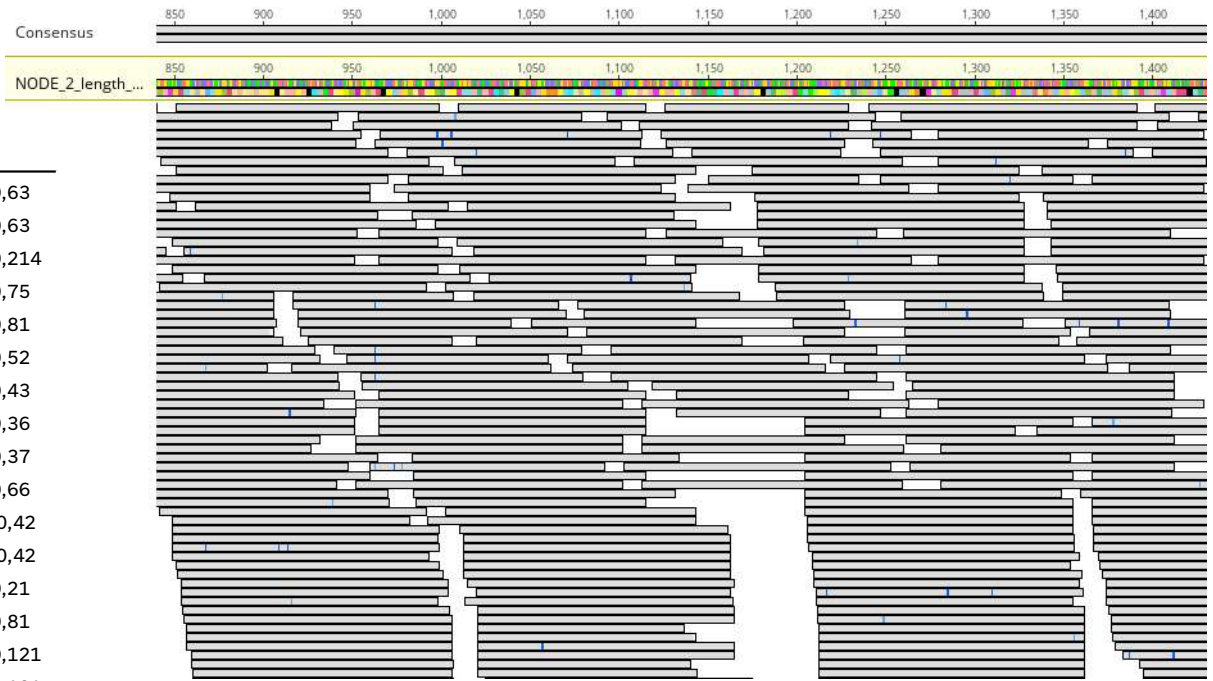
Mapped against index of YTLV



Pairwise
identity: 73%

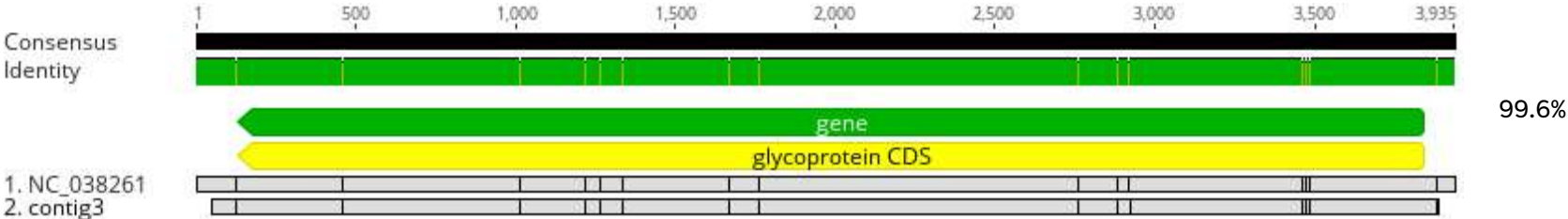
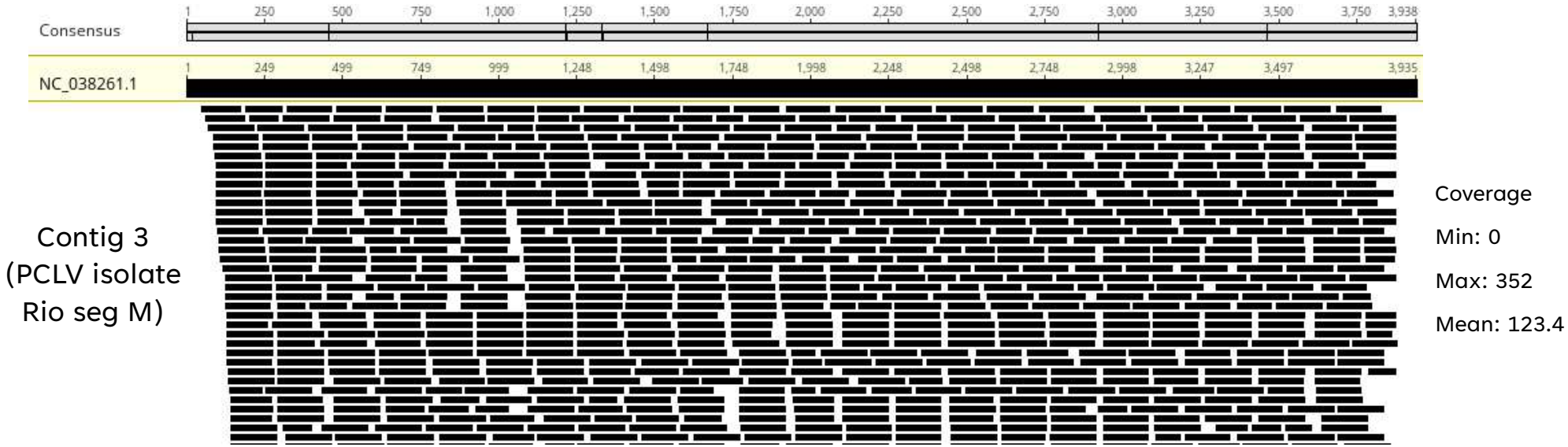
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> Yeltsovka tombus-like virus isolate Koltsovo/YTLV/2019 putative polyprotein and putative capsid protein genes...	Yeltsovka tombu...	3133	3133	90%	0.0	80.05%	4317	MW251332.1
<input checked="" type="checkbox"/> Hamarskog tombus-like virus strain SW11_partial genome	Hamarskog to...	3103	3103	88%	0.0	80.36%	4166	MN513379.1
<input checked="" type="checkbox"/> Yongsan tombus-like virus 1 strain A16_1368/ROK/2016 hypothetical protein 1_hypothetical protein 2_and hypot...	Yongsan tombus...	2252	2252	93%	0.0	76.24%	4554	NC_040725.1
<input checked="" type="checkbox"/> Mosquito nodavirus MNV-1 coat protein gene_partial cds	Mosquito nodavi...	1908	1908	24%	0.0	97.17%	1130	GU144510.1
<input checked="" type="checkbox"/> Riboviria sp. isolate long-tailedtit164con18 hypothetical protein gene_partial cds	Riboviria sp.	58.4	58.4	0%	0.012	100.00%	1095	MW239273.1

TOMBUS-LIKE VIRUS VARIANT ANALYSIS



POS	ID	REF	ALT	QUAL	FILTER	INFO
171	.	A	C	1494	PASS	DP=65;AF=0.969231;SB=0;DP4=0,2,0,63
172	.	C	T	1625	PASS	DP=65;AF=0.969231;SB=0;DP4=0,2,0,63
246	.	T	C	5973	PASS	DP=215;AF=0.995349;SB=0;DP4=0,1,0,214
306	.	C	A	1847	PASS	DP=76;AF=0.986842;SB=0;DP4=0,1,0,75
1175	.	T	G	1949	PASS	DP=83;AF=0.975904;SB=0;DP4=0,2,0,81
2845	.	A	C	1637	PASS	DP=53;AF=0.981132;SB=0;DP4=0,1,0,52
2850	.	T	G	1161	PASS	DP=45;AF=0.955556;SB=0;DP4=0,1,0,43
2865	.	T	G	1000	PASS	DP=38;AF=0.947368;SB=0;DP4=0,2,0,36
2871	.	C	T	1008	PASS	DP=38;AF=0.973684;SB=0;DP4=0,1,0,37
3213	.	T	A	1386	PASS	DP=67;AF=0.985075;SB=0;DP4=0,1,0,66
3441	.	C	T	498	PASS	DP=57;AF=0.736842;SB=0;DP4=0,15,0,42
3444	.	A	C	506	PASS	DP=57;AF=0.736842;SB=0;DP4=0,15,0,42
3561	.	A	C	436	PASS	DP=22;AF=0.954545;SB=0;DP4=0,1,0,21
3723	.	T	A	1945	PASS	DP=82;AF=0.987805;SB=0;DP4=0,1,0,81
3816	.	C	T	3222	PASS	DP=123;AF=0.983740;SB=0;DP4=0,2,0,121
3819	.	G	C	3296	PASS	DP=123;AF=0.983740;SB=0;DP4=0,2,0,121
3864	.	C	A	1154	PASS	DP=39;AF=0.974359;SB=0;DP4=0,1,0,38
3979	.	G	T	4118	PASS	DP=226;AF=0.995575;SB=0;DP4=0,1,0,225
4005	.	T	A	4837	PASS	DP=226;AF=0.995575;SB=0;DP4=0,1,0,225

PCLV SEGM COVERAGE & ANNOTATION



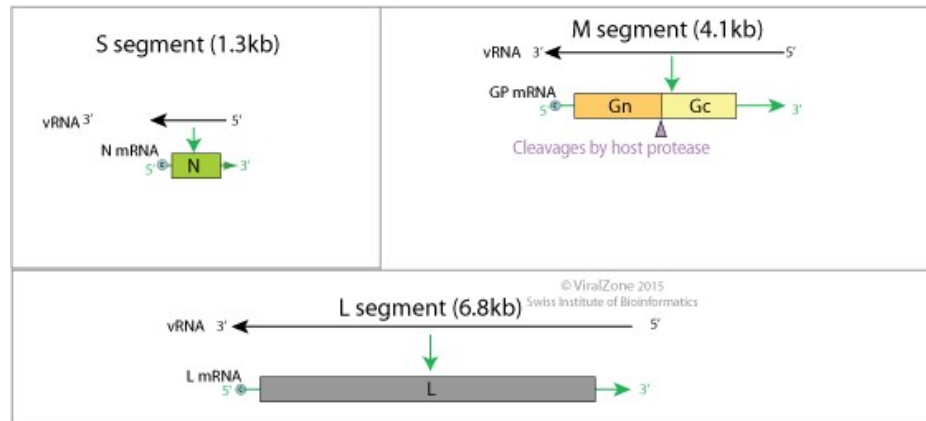
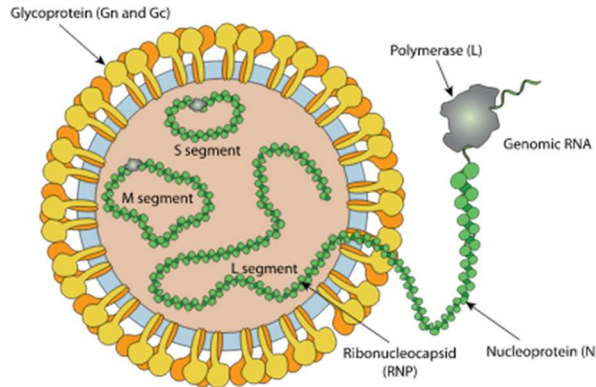
PHASIVIRUS

Journal of Parasitology and Vector Biology Vol. 3(1), pp. 19-21, January 2011
 Available online at <http://www.academicjournals.org/JPVB>
 ISSN 2141-2510 ©2011 Academic Journals

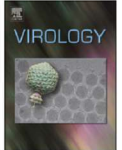
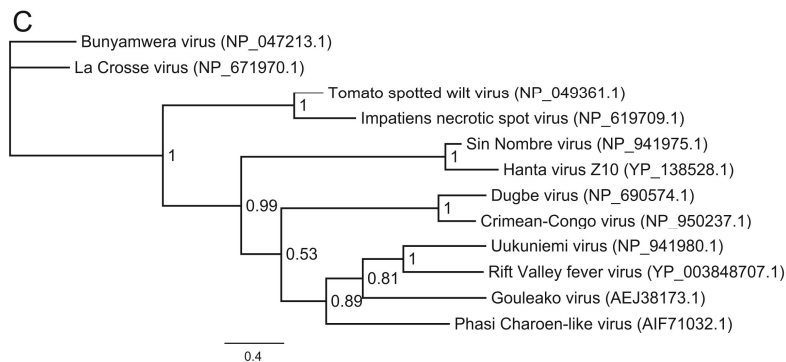
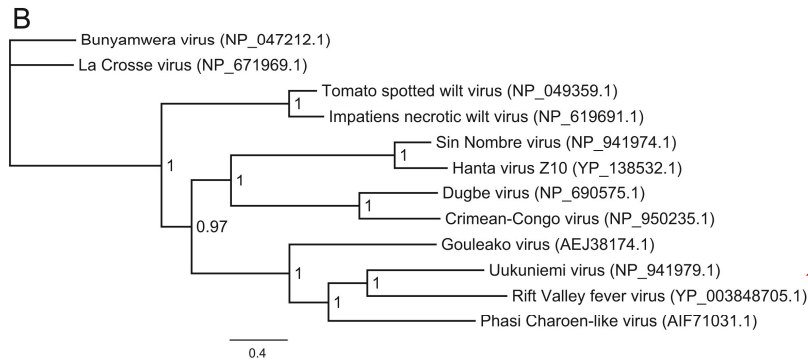
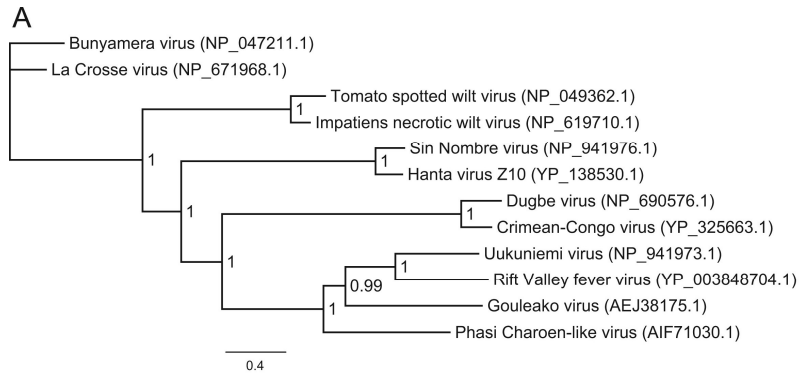
Short Communication

Prevalence of Phasi Charoen virus in female mosquitoes

Yusuke Sayama^{1,2}, Yuki Eshita³, Takuya Yamao⁴, Miho Nishimura⁴, Tomomitsu Satho⁴,
 Raweewan Srisawat⁵, Narumon Komalamisra⁵, Yupha Rongsriyam⁵, Kouji Sakai¹, Shuetsu
 Fukushi¹, Masayuki Saijo¹, Hitoshi Oshitani², Ichiro Kurane¹, Shigeru Morikawa¹ and
 Tetsuya Mizutani^{1*}



- Phasi Charoen virus initially isolated in Thailand from mosquito larvae
- ~20% of adult female mosquitos infected by PhaV



Metagenomic shotgun sequencing of a Bunyavirus in wild-caught *Aedes aegypti* from Thailand informs the evolutionary and genomic history of the Phleboviruses

James Angus Chandler^{a,*}, Panpim Thongsripong^{a,b,1}, Amy Green^c, Pattamaporn Kittayapong^d, Bruce A. Wilcox^{d,e}, Gary P. Schroth^f, Durrell D. Kapan^{g,h}, Shannon N. Bennett^{a,*}

- Phasi Chareon-like virus is basal to RVFV
- PCLV lacks a key virulence gene that is present in all other Phleboviruses

Transmission dynamics of an insect-specific flavivirus in a naturally infected *Culex pipiens* laboratory colony and effects of co-infection on vector competence for West Nile virus

Bethany G. Bolling^{a,*}, Francisco J. Olea-Popelka^b, Lars Eisen^a, Chester G. Moore^a, Carol D. Blair^a

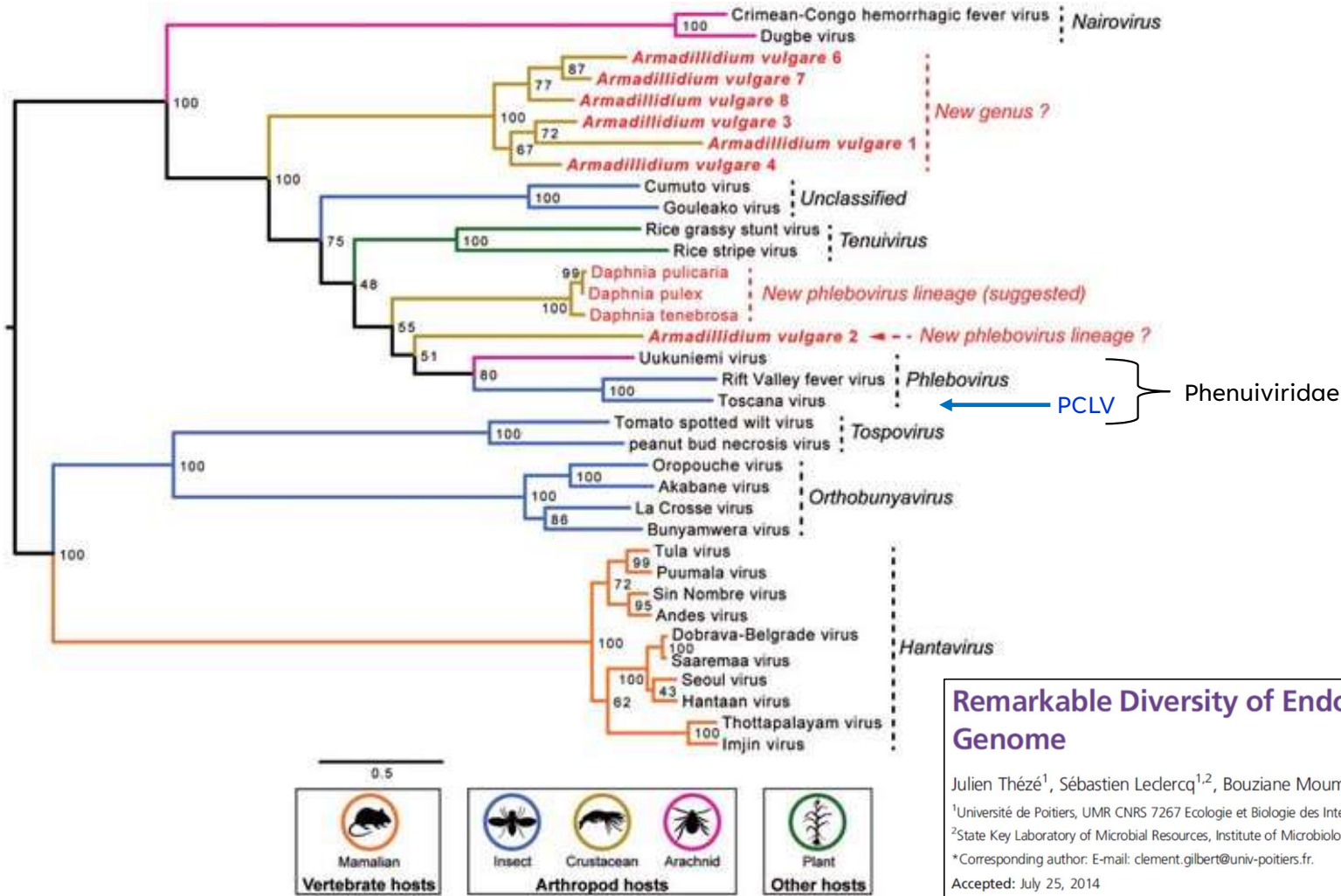
^a Arthropod-borne and Infectious Diseases Laboratory, Department of Microbiology, Immunology and Pathology, Colorado State University, Fort Collins, CO, USA

^b Veterinary Preventive Medicine, Department of Clinical Sciences, Colorado State University, Fort Collins, CO, USA

- ISVs may modulate arboviruses



Viruses; Riboviria; Orthornavirae; Negarnaviricota; Polyploviricotina; Ellioviricetes; Bunyavirales; Phenuiviridae



Remarkable Diversity of Endogenous Viruses in a Crustacean Genome

Julien Thézé¹, Sébastien Lederqcq^{1,2}, Bouziane Moumen¹, Richard Cordaux¹, and Clément Gilbert^{1,*}

¹Université de Poitiers, UMR CNRS 7267 Ecologie et Biologie des Interactions, Equipe Ecologie Evolution Symbiose, Poitiers, France

²State Key Laboratory of Microbial Resources, Institute of Microbiology, Chinese Academy of Sciences, Beijing, China

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Accepted: July 25, 2014



THANK YOU!