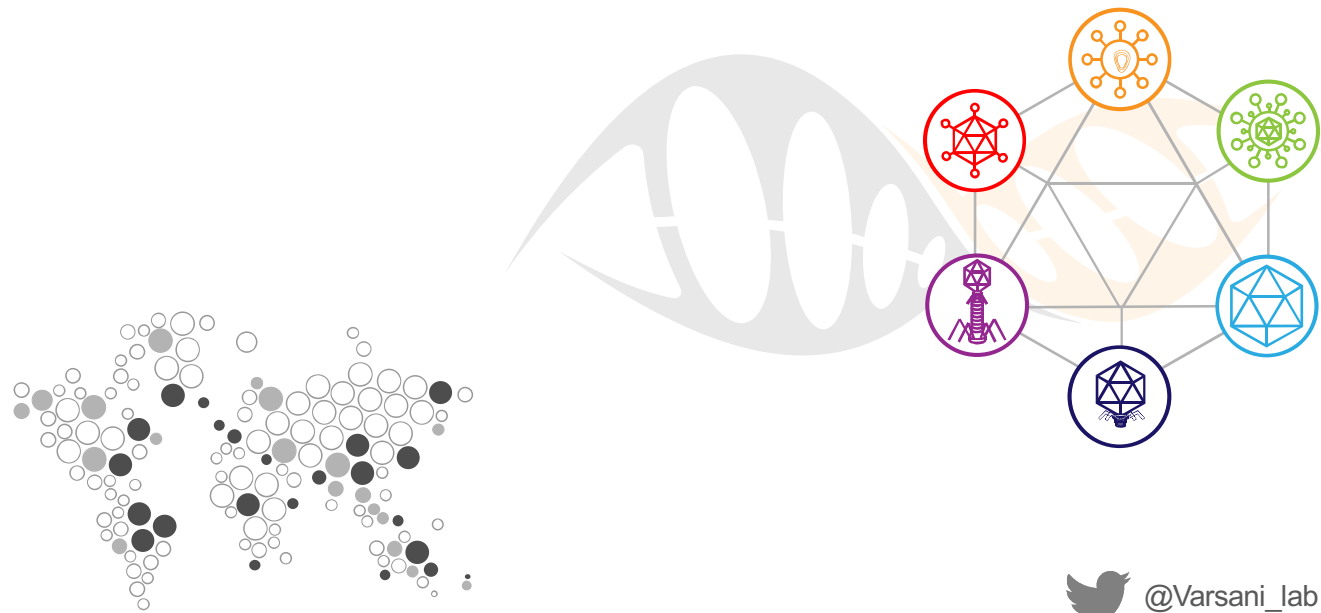


Small Circular DNA Viruses:

The muddy viral “playground” of recombinant, reassortant, and highly diverse viruses



 @Varsani_lab

Arizona State University, USA
University of Canterbury, New Zealand
University of Cape Town, South Africa

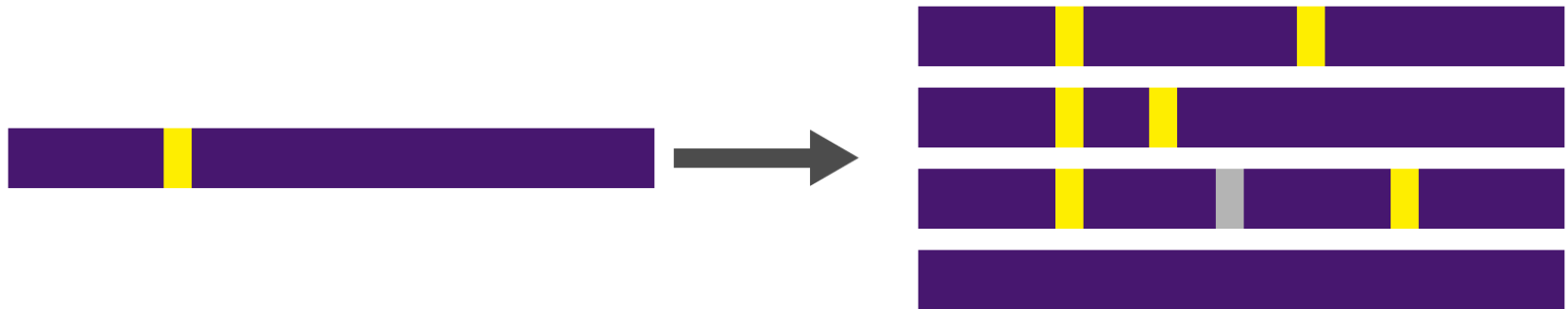
Arvind Varsani

Viral evolution

Nucleotide substitutions

Recombination

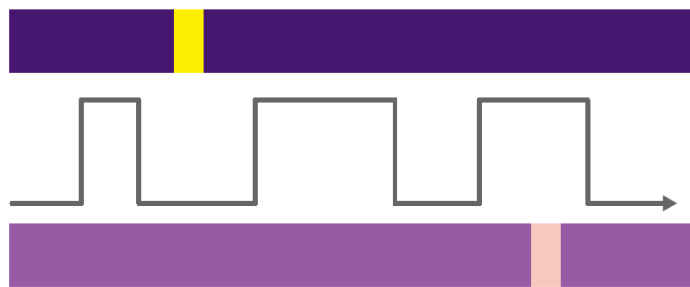
Reassortment



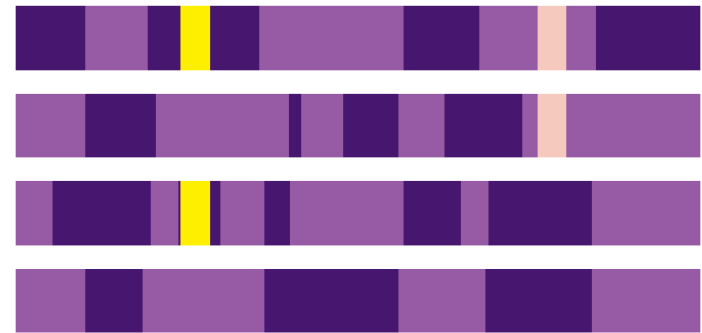
Low success rate to fix mutation
by mutation

Viral evolution

Nucleotide substitutions
Recombination
Reassortment



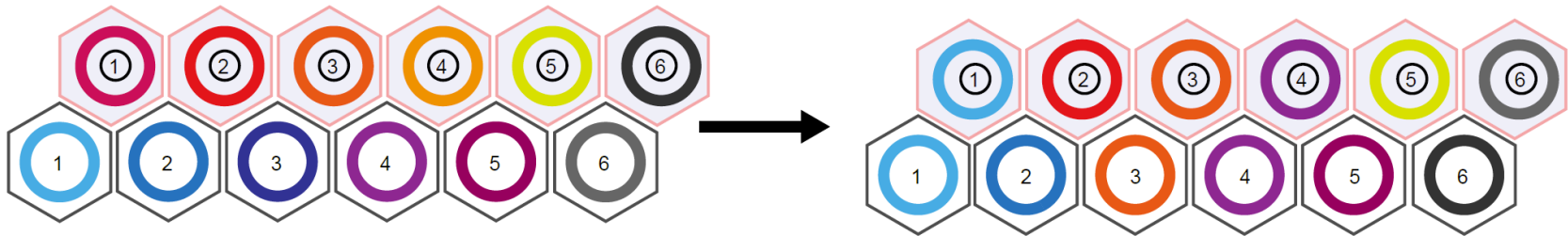
Switching between templates
during replication



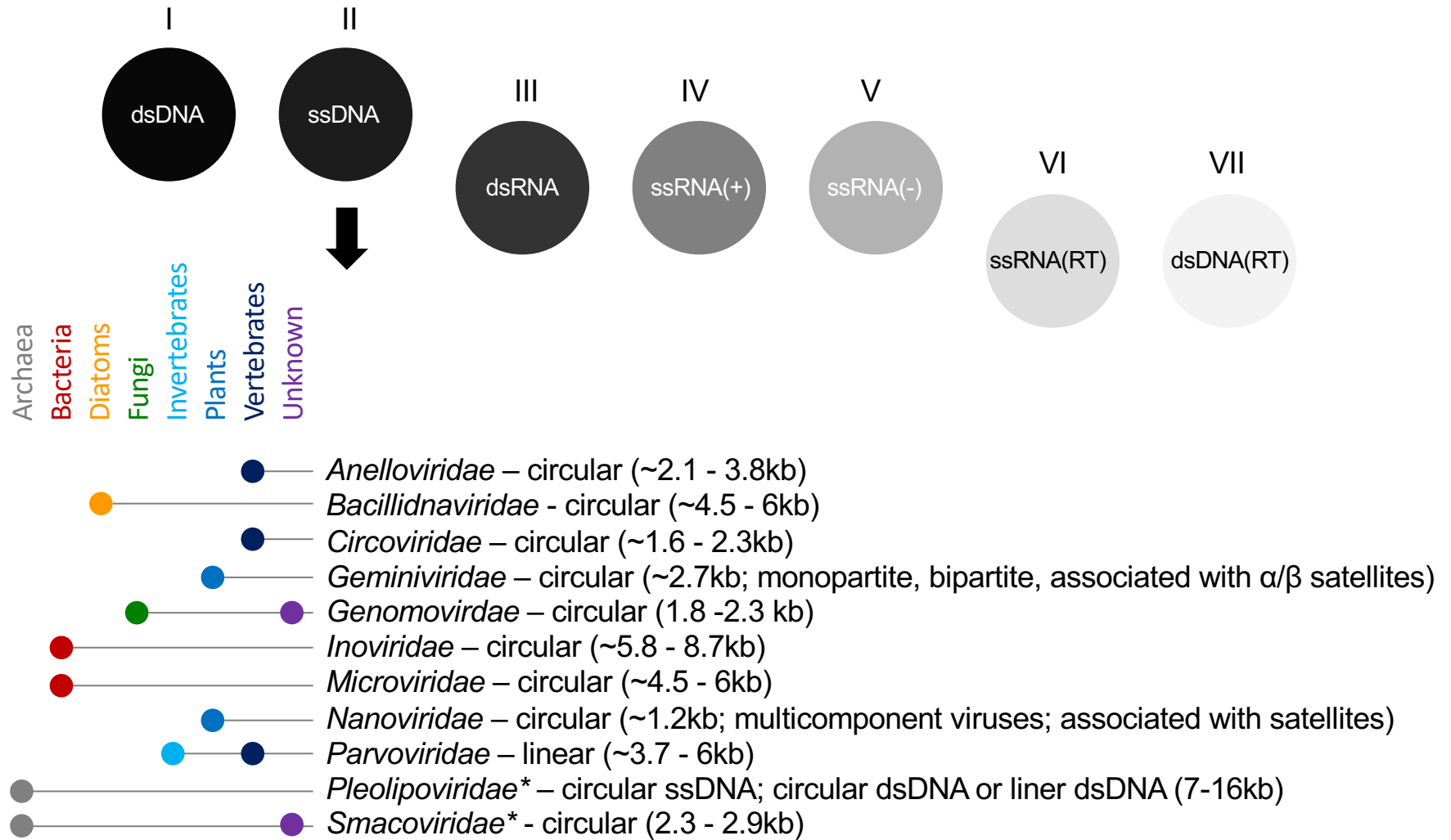
High success rate in fixing
mutation by recombination

Viral evolution

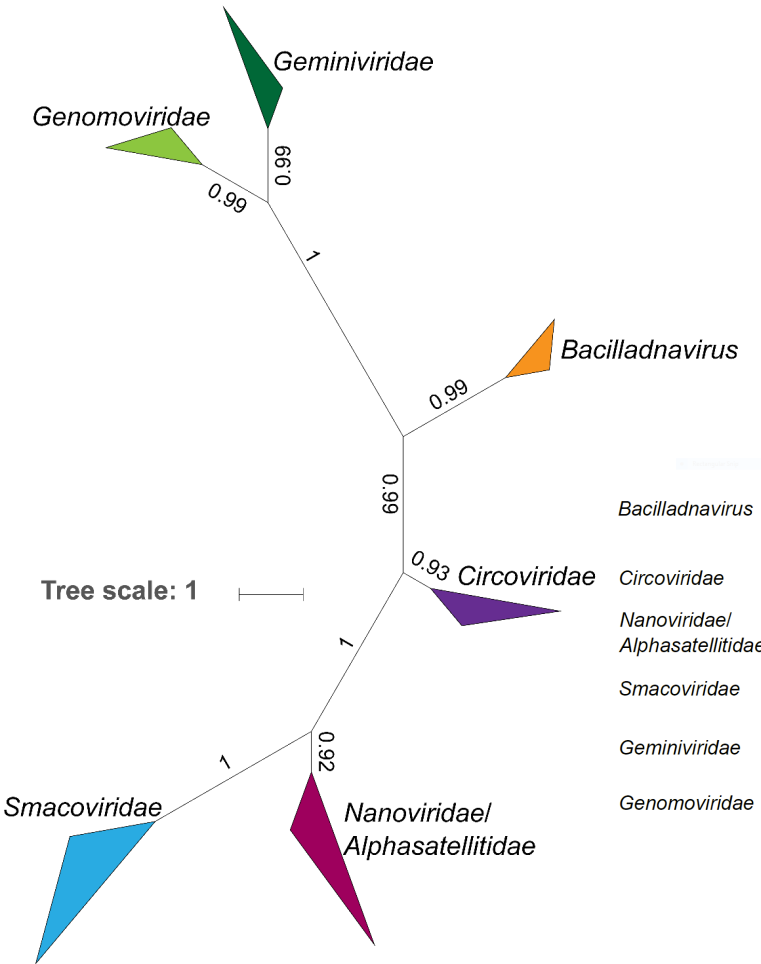
Nucleotide substitutions
Recombination
Reassortment



ssDNA viruses

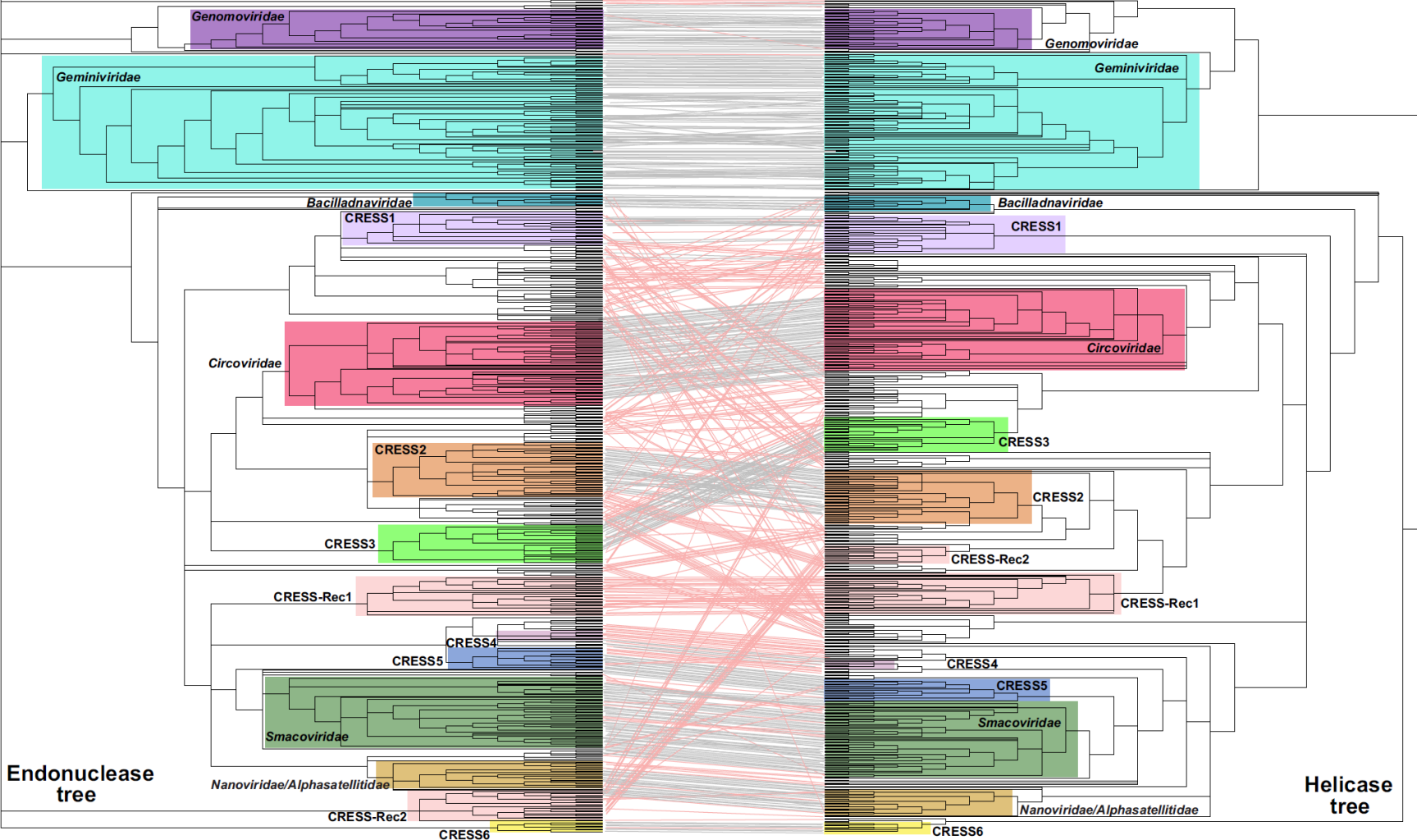


ssDNA viruses



	RC endonuclease domain			SH3 domain			
	Motif I	Motif II	Motif III	Walker A	Walker B	Motif C	Arg finger
<i>Bacilladnavirus</i>							
<i>Circoviridae</i>							
<i>Nanoviridae/Alphasatellitidae</i>							
<i>Smacoviridae</i>							
<i>Geminiviridae</i>							
<i>Genomoviridae</i>							

Chimerism in Rep



Nucleotide substitutions

Geminiviruses

MSV:	$\sim 2 \times 10^{-4}$ subs/site/year
SSRV:	$\sim 3 \times 10^{-4}$ subs/site/year
EACMV:	$\sim 1 \times 10^{-3}$ subs/site/year
TYLCV:	$\sim 3 \times 10^{-4}$ subs/site/year

Nanoviruses

FBNYV:	$\sim 1 \times 10^{-3}$ subs/site/year
BBTV:	$\sim 3 \times 10^{-4}$ subs/site/year

Circoviruses

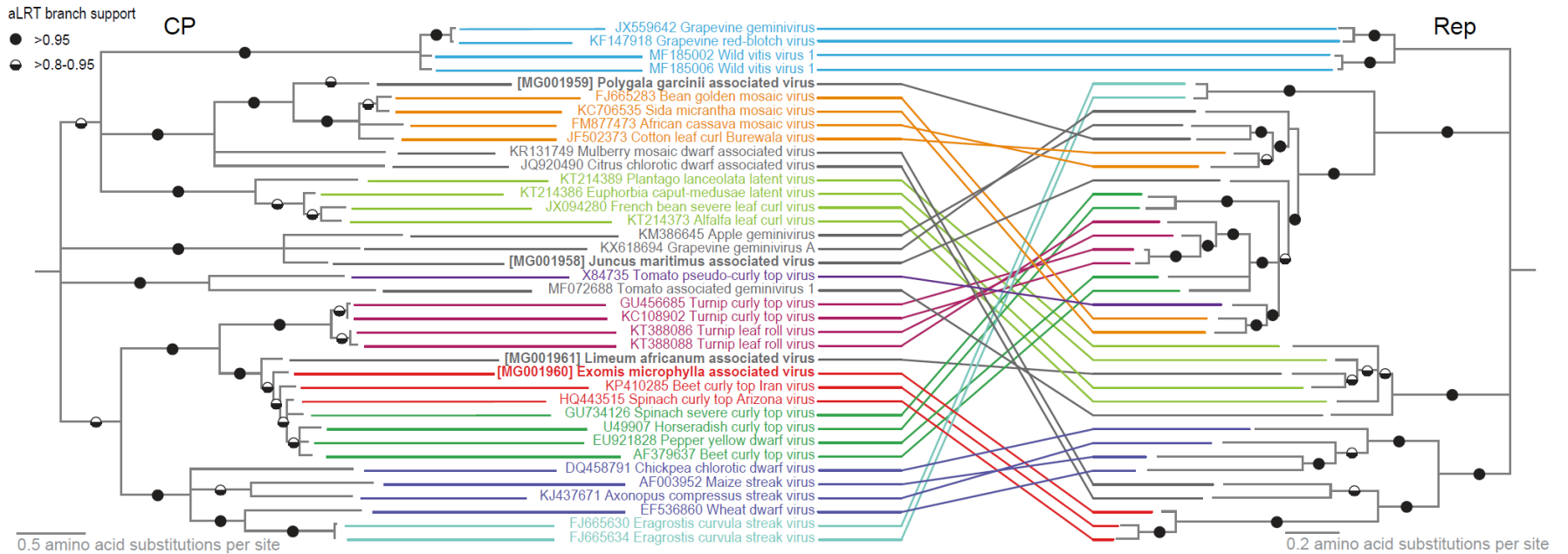
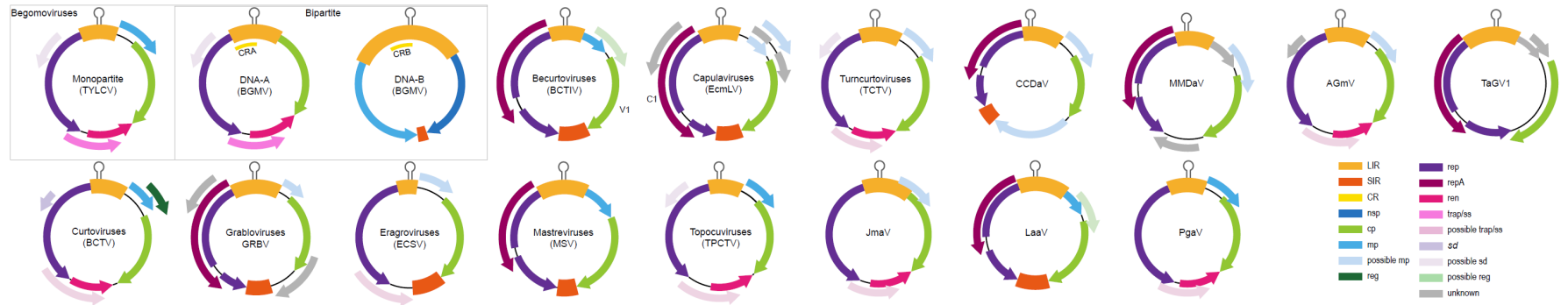
BFDV:	$\sim 2 \times 10^{-3}$ subs/site/year
PCV-2:	$\sim 1 \times 10^{-3}$ subs/site/year

Parvoviruses

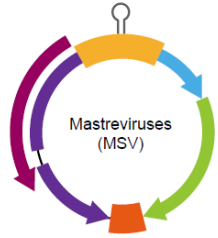
CPV:	$\sim 2 \times 10^{-4}$ - 8×10^{-5} subs/site/year (VP1; NS1)
PPV:	$\sim 3 \times 10^{-4}$ - 5×10^{-5} subs/site/year (VP1; NS1)

Recombination

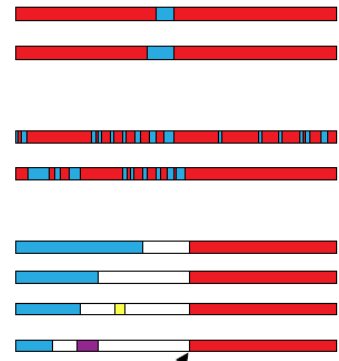
Geminiviruses



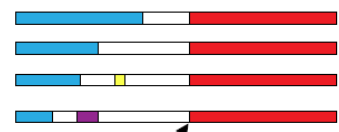
Recombination



VWV1V2Mat
MatV1V2VW



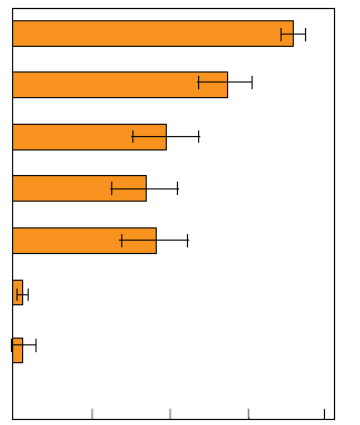
Simple recombinant
Complex recombinant



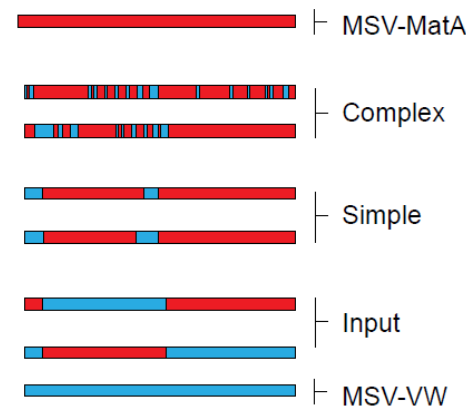
Groups of unique subgenomics
 □ Deletions
 ■ Unknown sequences
 ■ Rearrangements/inversions

c-strand ori

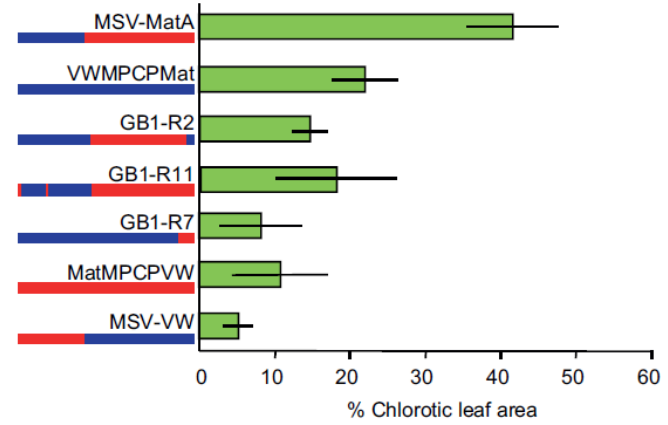
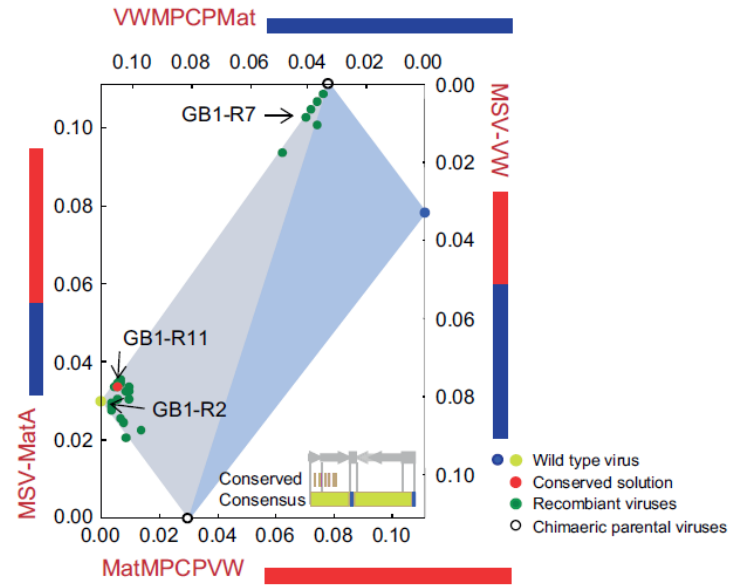
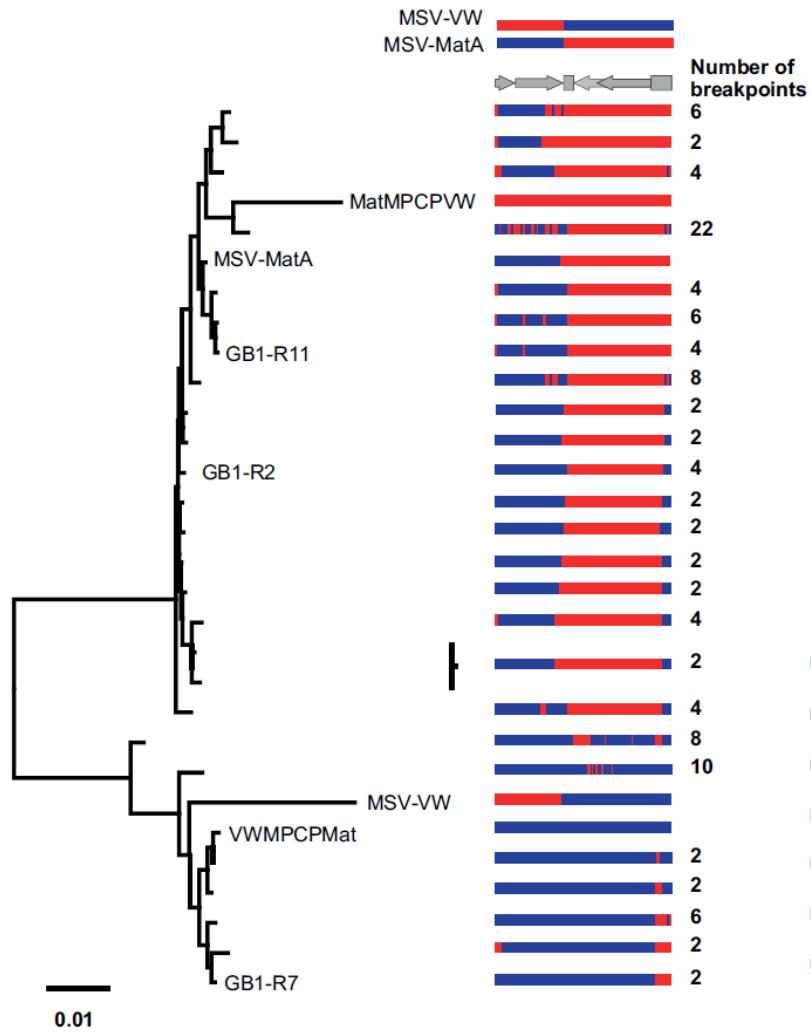
Fitness



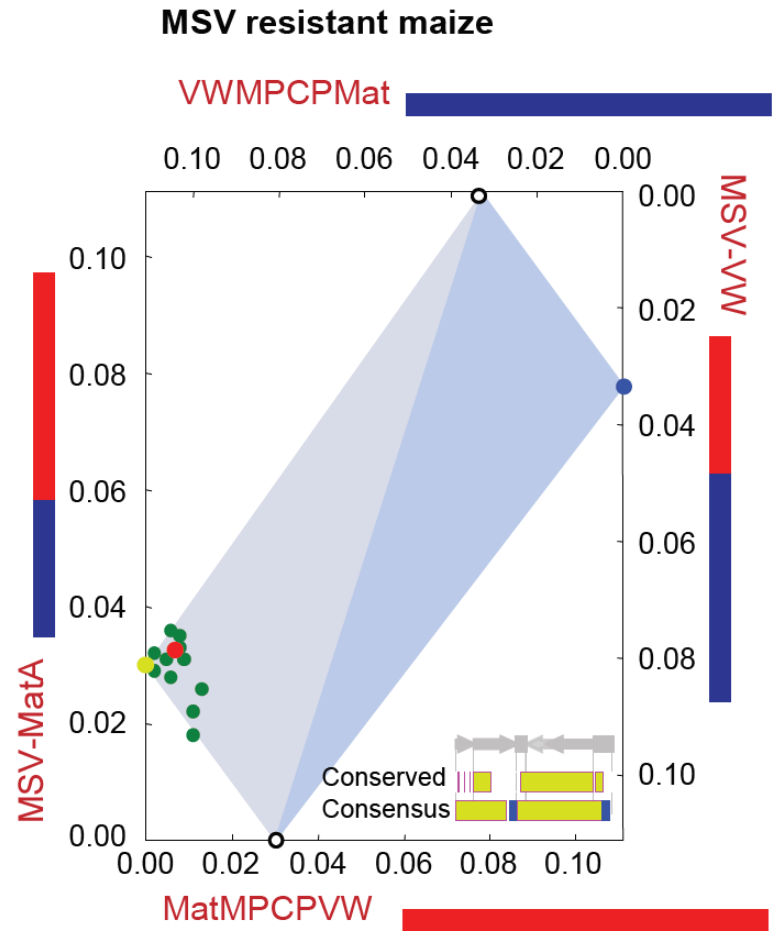
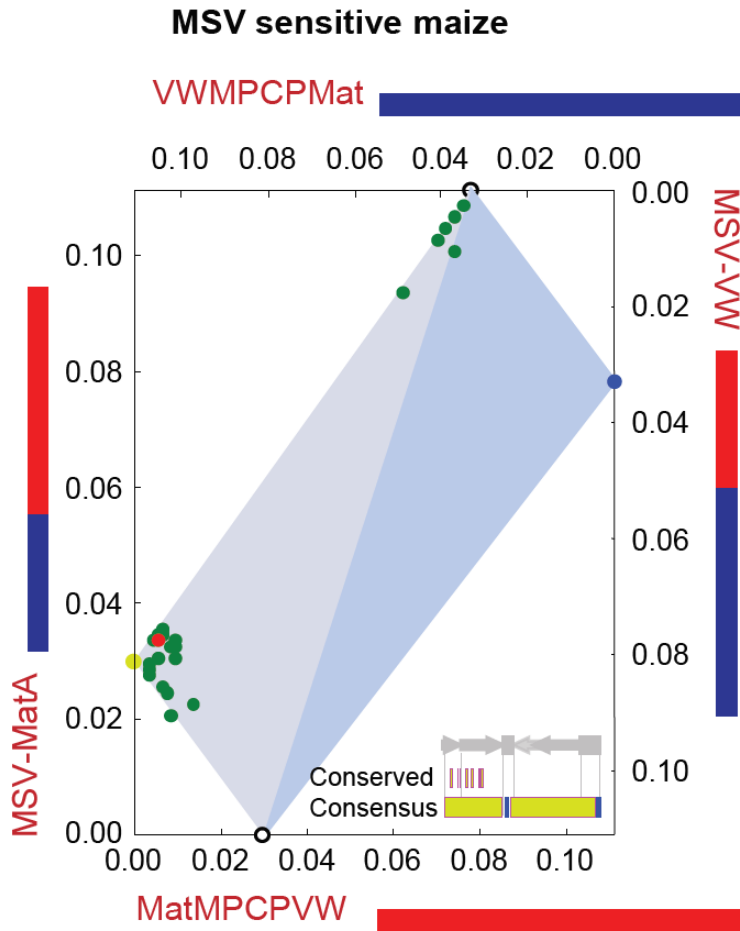
0 12 25 38 50
Chlorotic area, leaves 3-6



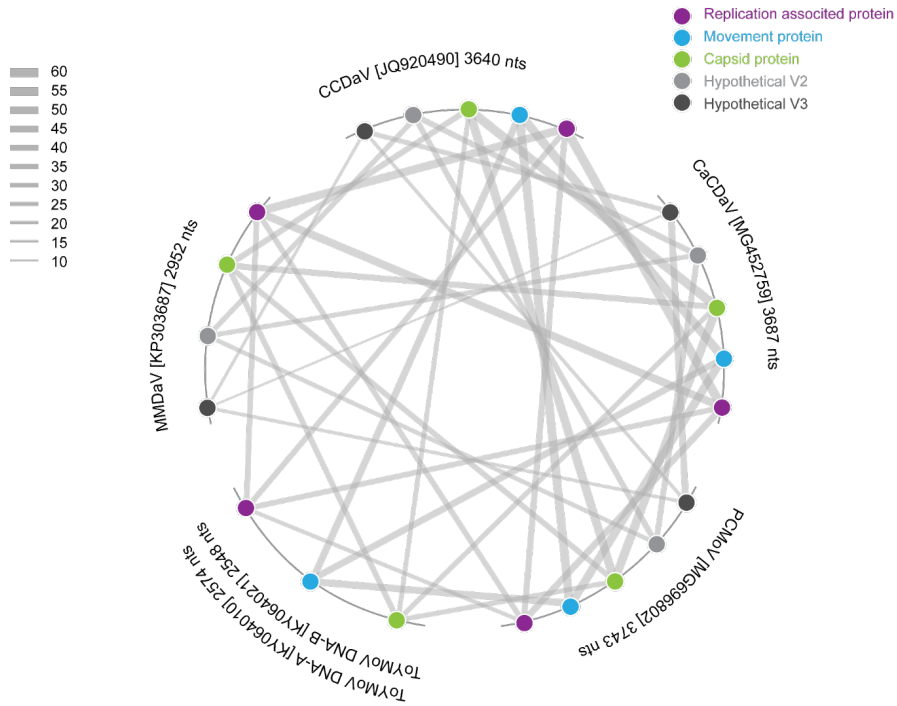
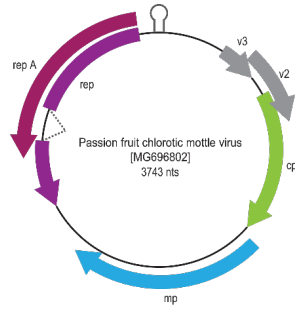
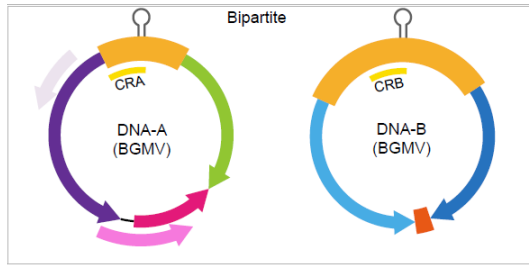
Recombination



Recombination



Genome plasticity



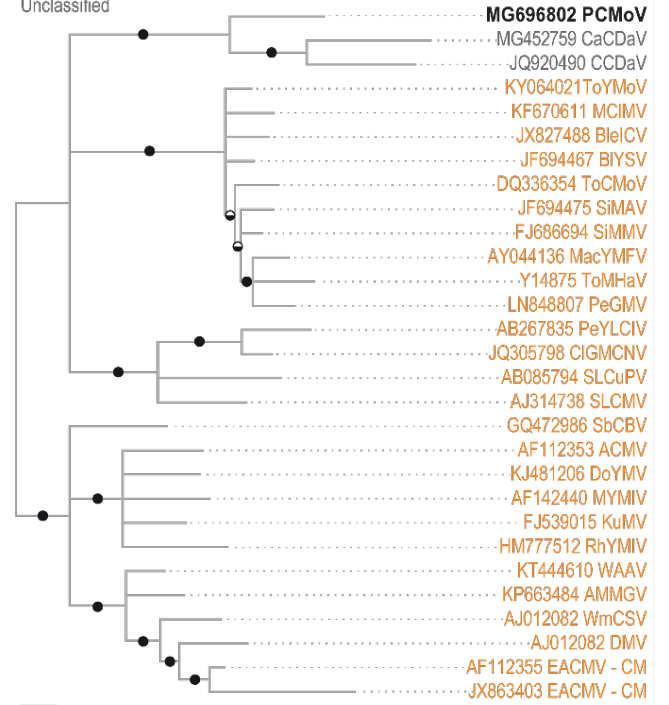
Gemimiviruses

aLRT support

- >0.9
- >0.8-0.9

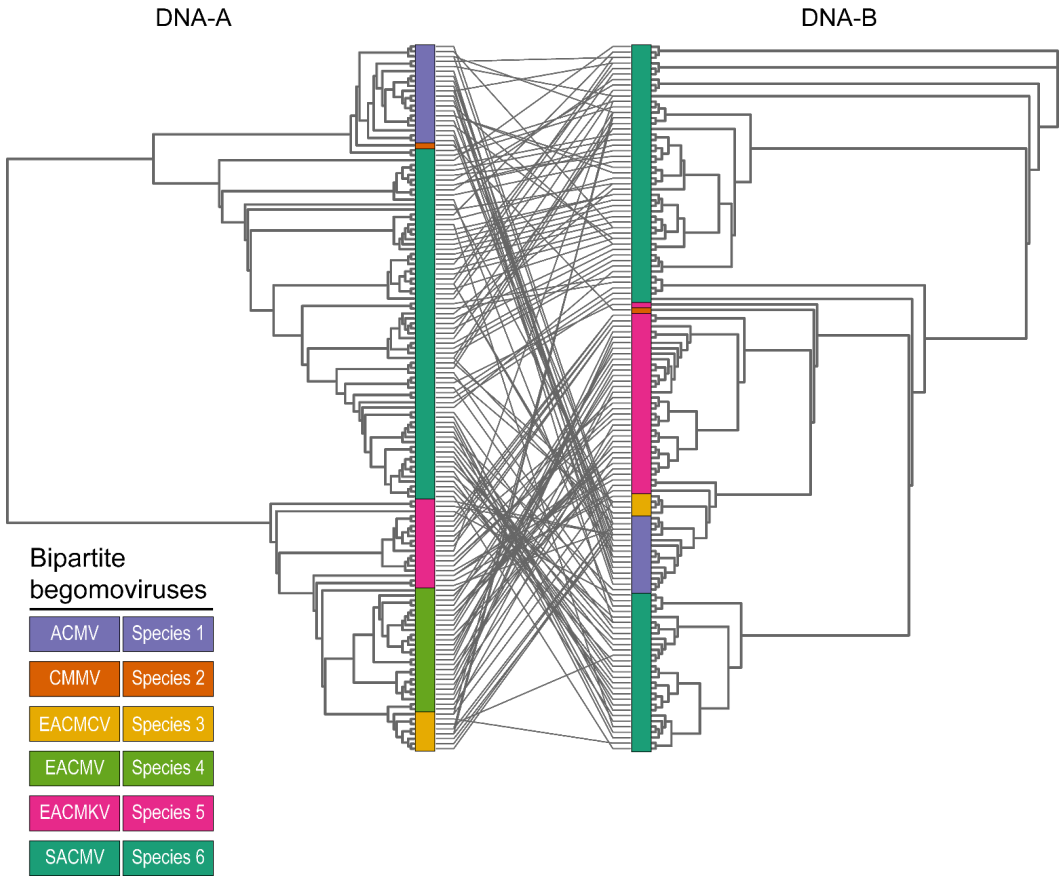
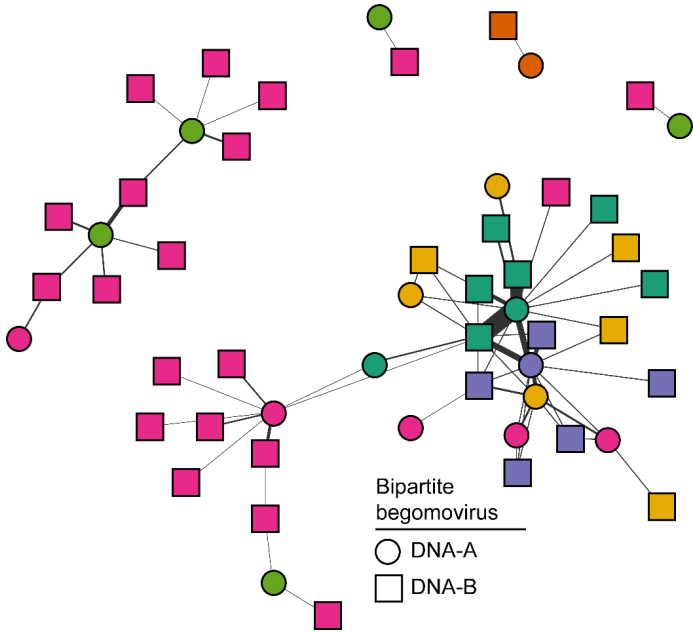
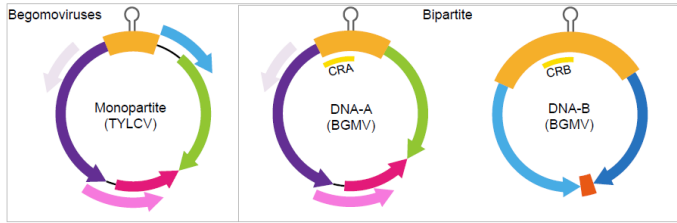
Begomovirus

Unclassified



0.2 amino acid substitutions per site

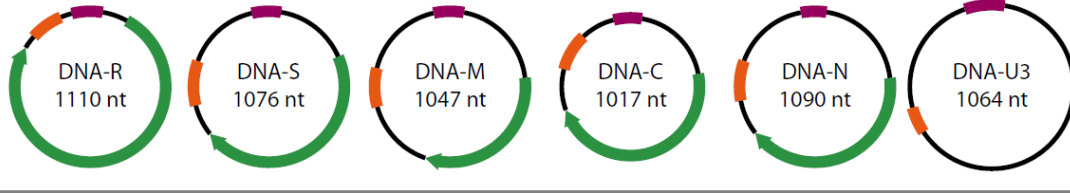
Pseudo-recombination



Reassortment

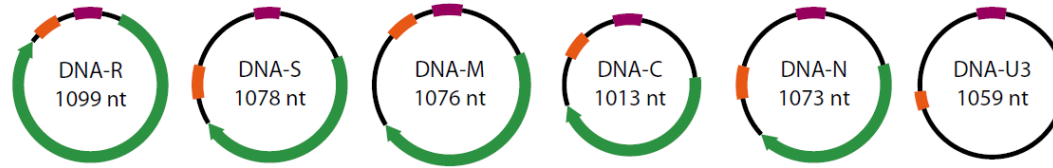
Babuvirus

Banana bunchy top virus

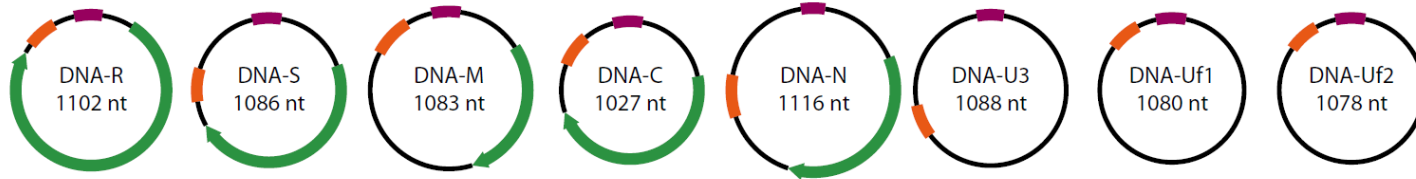


- Common region stem-loop
- Common region major
- Open reading frame
- Non coding region

Abaca bunchy top virus



Cardamum bushy dwarf virus



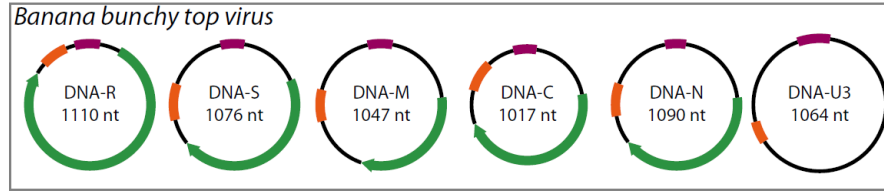
Nanovirus

Faba bean necrotic yellows virus



Reassortment

Banana bunchy top virus

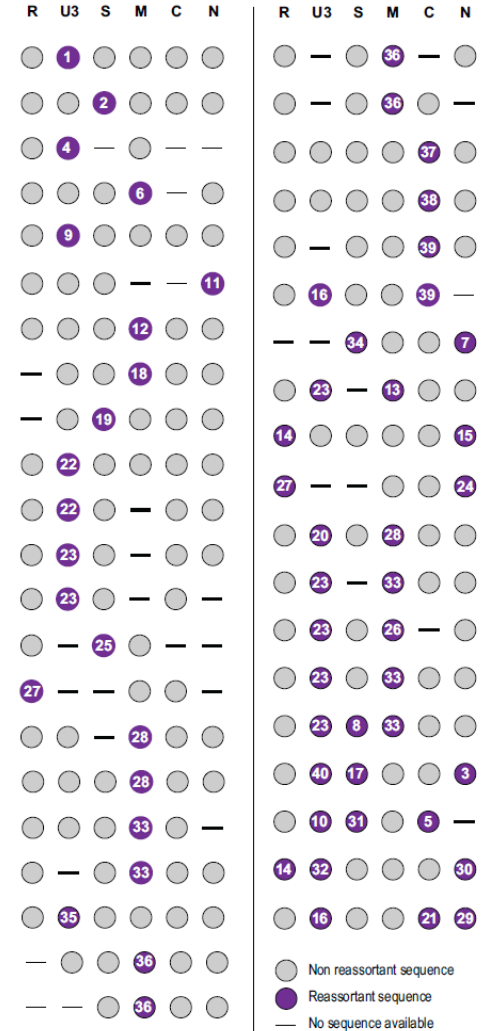


■ Common region stem-loop
■ Common region major
■ Open reading frame
■ Non coding region

Recombinant(s)			Sequence used to infer major parent(s)	Sequence used to infer minor parent(s)	Breakpoint Begin-End	Methods	P-value
<div style="display: flex; justify-content: space-around;"> <div style="text-align: center;">DNA-R</div> <div style="text-align: center;">DNA-U3</div> <div style="text-align: center;">DNA-S</div> </div>	<div style="display: flex; justify-content: space-around;"> <div style="text-align: center;">DNA-M</div> <div style="text-align: center;">DNA-C</div> <div style="text-align: center;">DNA-N</div> </div>	Tonga-Ha'apai Tonga-Vava'u	Tonga -Tonga'tapu Tonga-Ha'apai	India Pakistan	DNA-M 3393-4529	RGMCST	5.74×10^{-22}
<div style="display: flex; justify-content: space-around;"> <div style="text-align: center;">DNA-R</div> <div style="text-align: center;">DNA-U3</div> <div style="text-align: center;">DNA-S</div> </div>	<div style="display: flex; justify-content: space-around;"> <div style="text-align: center;">DNA-M</div> <div style="text-align: center;">DNA-C</div> <div style="text-align: center;">DNA-N</div> </div>	Australia	India Pakistan	Tonga -Tonga'tapu Tonga-Ha'apai	DNA-M DNA-C 3363-5388	RGBMCST	5.69×10^{-17}
<div style="display: flex; justify-content: space-around;"> <div style="text-align: center;">DNA-R</div> <div style="text-align: center;">DNA-U3</div> <div style="text-align: center;">DNA-S</div> </div>	<div style="display: flex; justify-content: space-around;"> <div style="text-align: center;">DNA-M</div> <div style="text-align: center;">DNA-C</div> <div style="text-align: center;">DNA-N</div> </div>	Tonga -Tonga'tapu	Tonga -Tonga'tapu	Tonga -Tonga'tapu	DNA-U3 1140-2346	RBST	6.94×10^{-9}

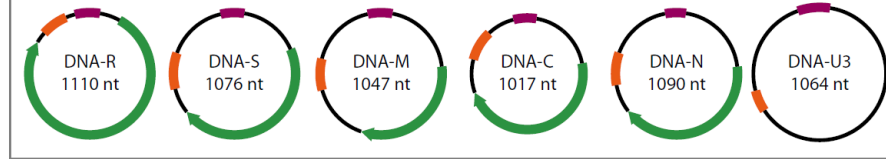
● inferred major parent
● inferred minor parent

Methods R - RDP G - GENECONV B - Bootscan M - Maxchi C - Chimaera S - SiSscan T - 3Seq

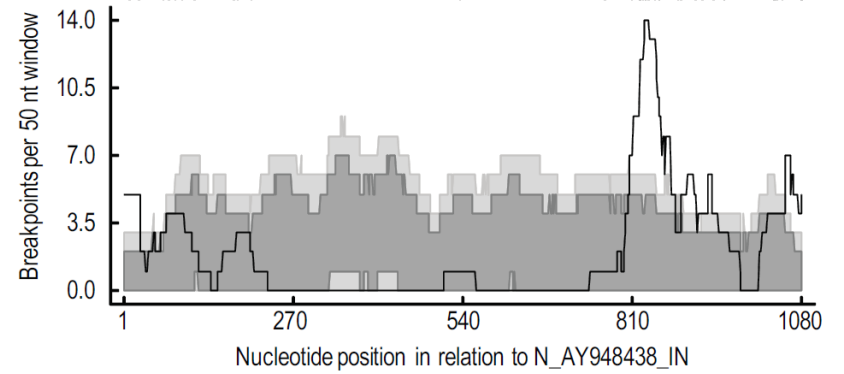
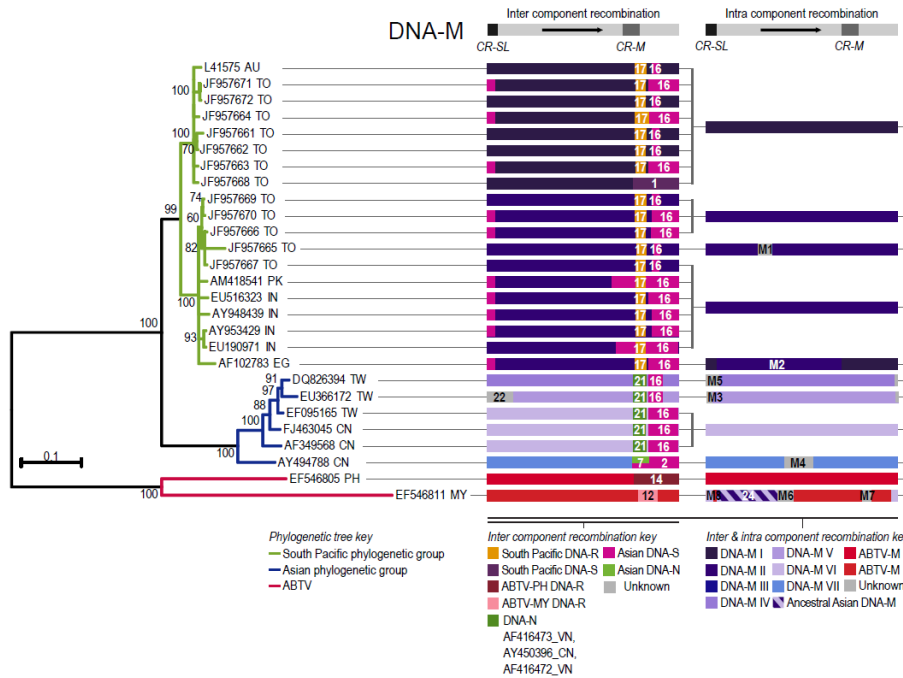


Recombination

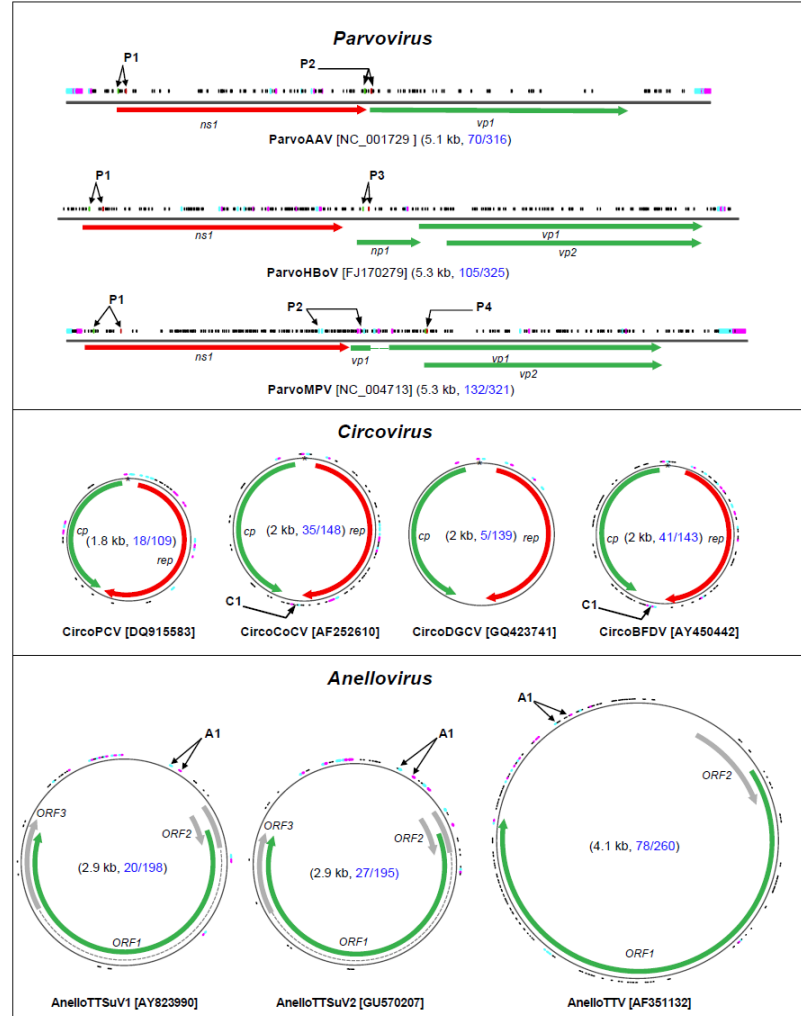
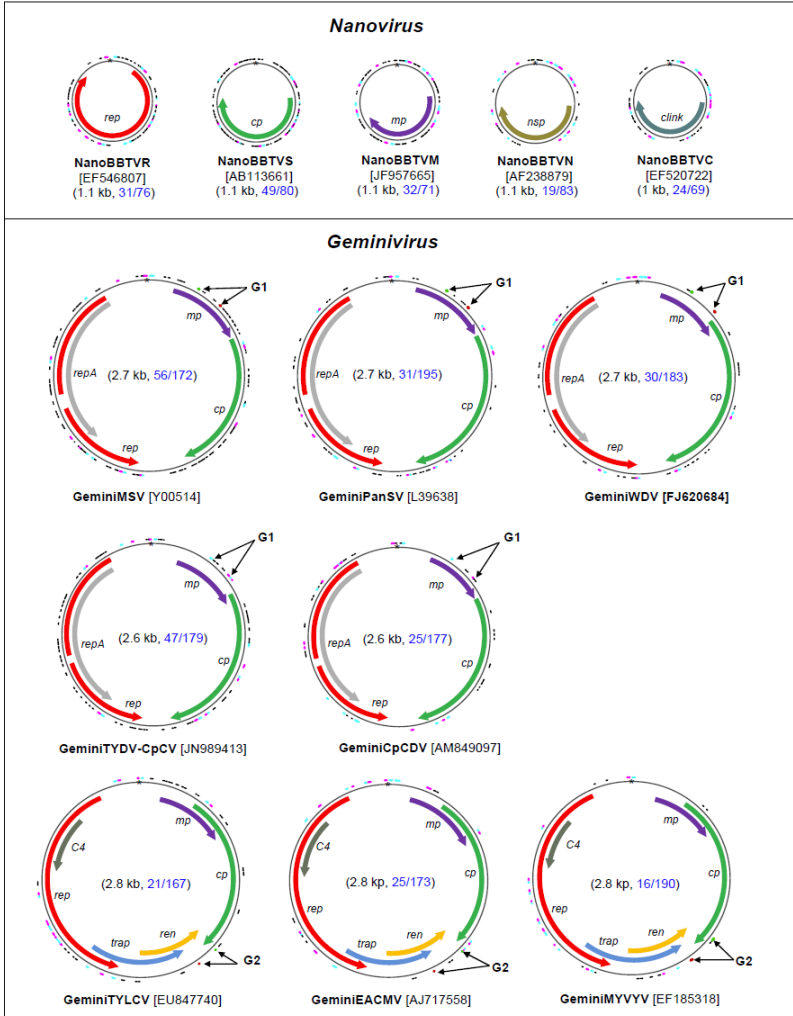
Banana bunchy top virus



- █ Common region stem-loop
- █ Common region major
- █ Open reading frame
- █ Non coding region

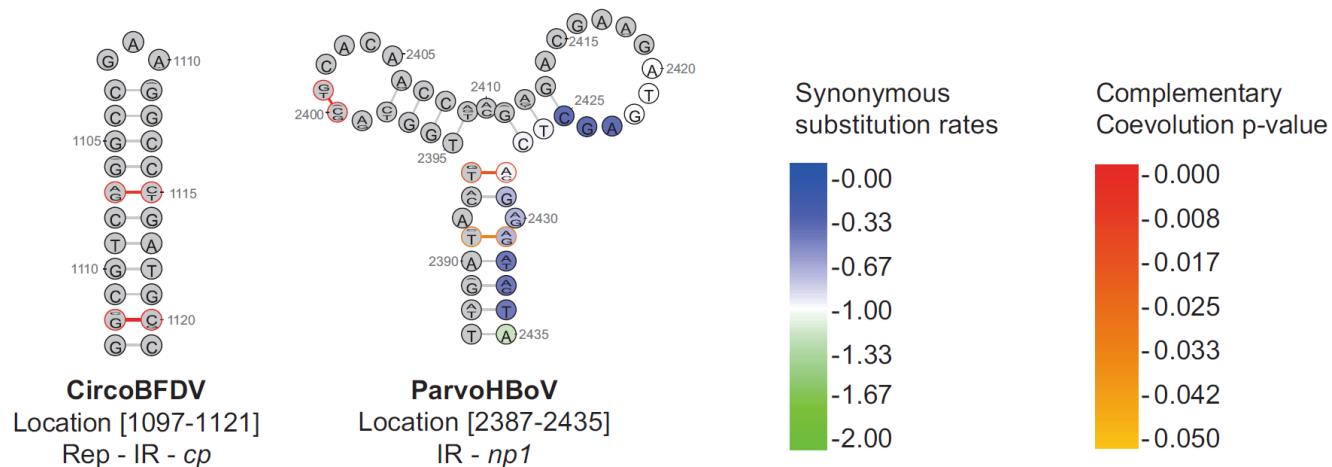


Secondary structure

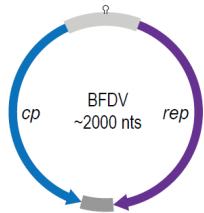


Secondary structure

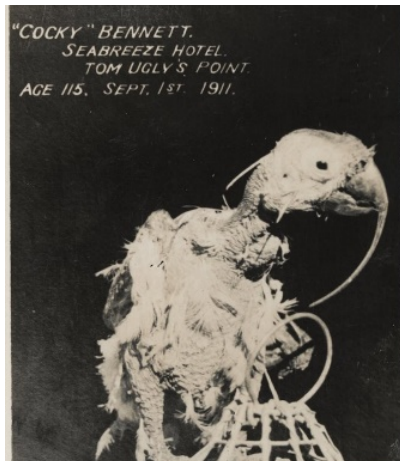
- **Purifying selection** is apparently **strongest** at paired-nucleotide sites
- **Synonymous substitution** rates are unusually **low** at paired genomic sites
- Short-term evolution experiments - **mutations** tend to **preferentially accumulate** at **unpaired sites**
- Base-paired sites tend to **complementarily coevolve**



Circoviruses

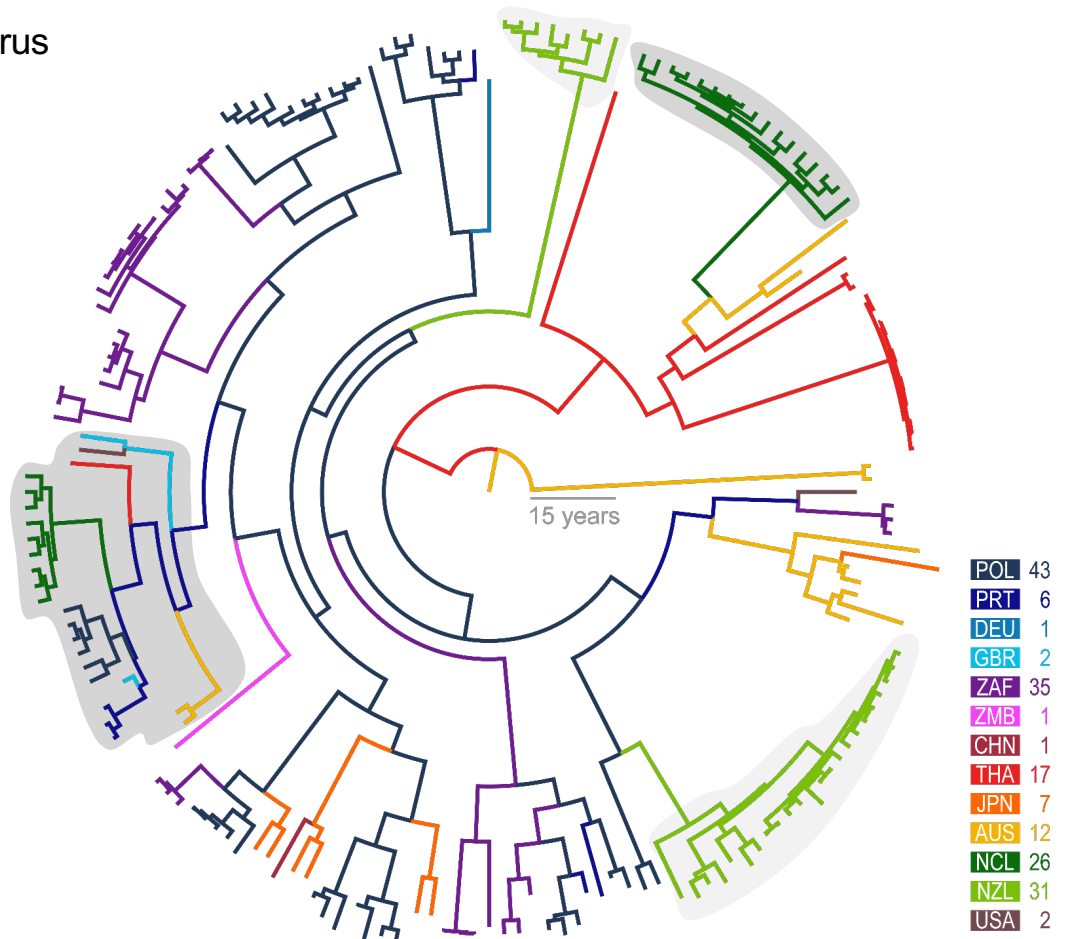


Circoviruses Beak and feather disease virus

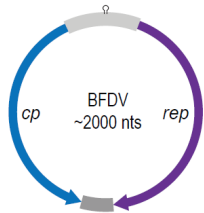


A VENERABLE COCKATOO.

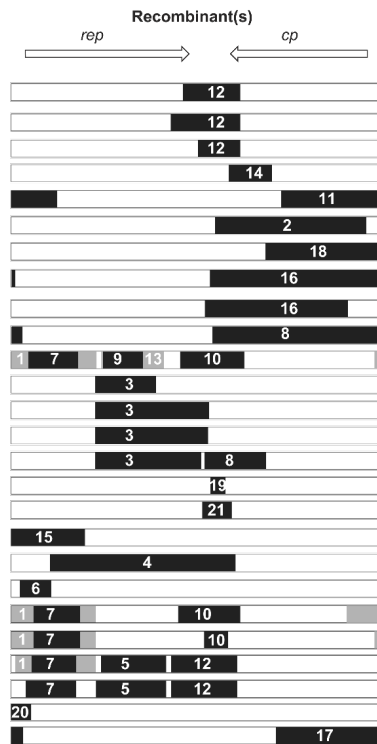
"Cocky Bennett," a sulphur-crested Australian cockatoo, died on Friday in his 120th year at Canterbury. This age is a record in longevity for an Australian parrot so far as the official records are concerned. For many years this bird was in the possession of Mrs. Sarah Bennett, the licensee of the Sea Breeze Hotel, at Tom Ugly's Point. When she left there, about 12 months ago, she transferred the parrot to her nephew, Mr. Murdoch Alexander Wagschall, at Woolpack Hotel, Canterbury. The old bird was absolutely featherless for the last 20 years, but it maintained its "patter" till the day before its death. "Cocky Bennett" was a great traveller, and is said to have journeyed seven times round the world. Mr. Wagschall has arranged to have the remains of this historic parrot preserved by a taxidermist.



Trafficking and evolution



Beak and feather disease virus



Scientific name	Common name	Number tested	Number positive	Virus strain
<i>Agapornis</i> sp.	Lovebirds	6	0	
<i>Alisterus scapularis</i>	Australian King Parrot	4	2	
<i>Amazona aestiva</i>	Blue-fronted Amazon	5	1	
<i>Amazona amazonica</i>	Orange-winged Amazon	2	1	
<i>Amazona barbadensis</i>	Yellow-shouldered Amazon	3	0	
<i>Amazona ochrocephala</i>	Yellow-fronted Amazon	2	0	
<i>Amazona</i> sp.	Amazon Parrot	2	0	
<i>Aprosmictus erythropterus</i>	Red-winged Parrot	4	2	
<i>Ara ararauna</i>	Blue and Yellow Macaw	17	0	
<i>Ara chloroptera</i>	Red and Green Macaw	8	0	
<i>Ara macao</i>	Scarlet Macaw	3	0	
<i>Aratinga acuticaudata</i>	Blue-crowned Conure	1	0	
<i>Barnardius barnardi</i>	Mallee Ring-necked Parrot	8	0	
<i>Barnardius zonarius</i>	Port Lincoln Parrot	2	0	
<i>Cacatua alba</i>	White Cockatoo	1	1	
<i>Cyanoliseus patagonus</i>	Patagonian Conure	1	0	
<i>Diopsittaca nobilis</i>	Red-shouldered Macaw	2	0	
<i>Eclectus roratus</i>	Eclectus Parrot	1	0	
<i>Elaphus roseicapillus</i>	Galah	8	0	
<i>Forpus coelestis</i>	Pacific Parrotlet	1	1	
<i>Melopsittacus undulatus</i>	Budgerigar	13	9	
<i>Pionites melanocephalus</i>	Black-headed Caique	1	0	
<i>Platyercus elegans</i>	Crimson Rosella	4	2	
<i>Platyercus eximius</i>	Eastern Rosella	2	1	
<i>Poicephalus robustus</i>	Cape Parrot	1	1	
<i>Poicephalus senegalus</i>	Senegal Parrot	6	2	
<i>Probosciger aterrimus</i>	Palm Cockatoo	1	0	
<i>Propyrrhura maracana</i>	Blue-winged Macaw	2	0	
<i>Psephenus</i> sp.	Grass Parrots	2	0	
<i>Psittacula alexandri</i>	Red-breasted Parakeet	3	0	
<i>Psittacula cyanocephala</i>	Plum-headed Parakeet	2	0	
<i>Psittacula derbiana</i>	Lord Derby's Parakeet	1	0	
<i>Psittacula eupatria</i>	Alexandrine Parakeet	3	2	
<i>Psittacula krameri</i>	Ring-necked Parakeet	32	9	
<i>Psittacus erithacus</i>	African Grey Parrot	52	9	
<i>Trichoglossus haematodus</i>	Rainbow Lorikeet	3	0	
Total		209	43	



Genomoviruses

Animal faeces

Blood

Buccal and cloacal swab

Cerebrospinal fluid

Cervical sample

Insect abdomen

Leaf material

Mosquito samples

Mycelial samples

Pharyngeal & rectal swabs

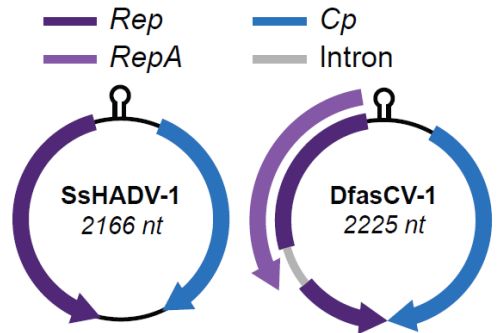
Plasma

Rectal swab

River sediments

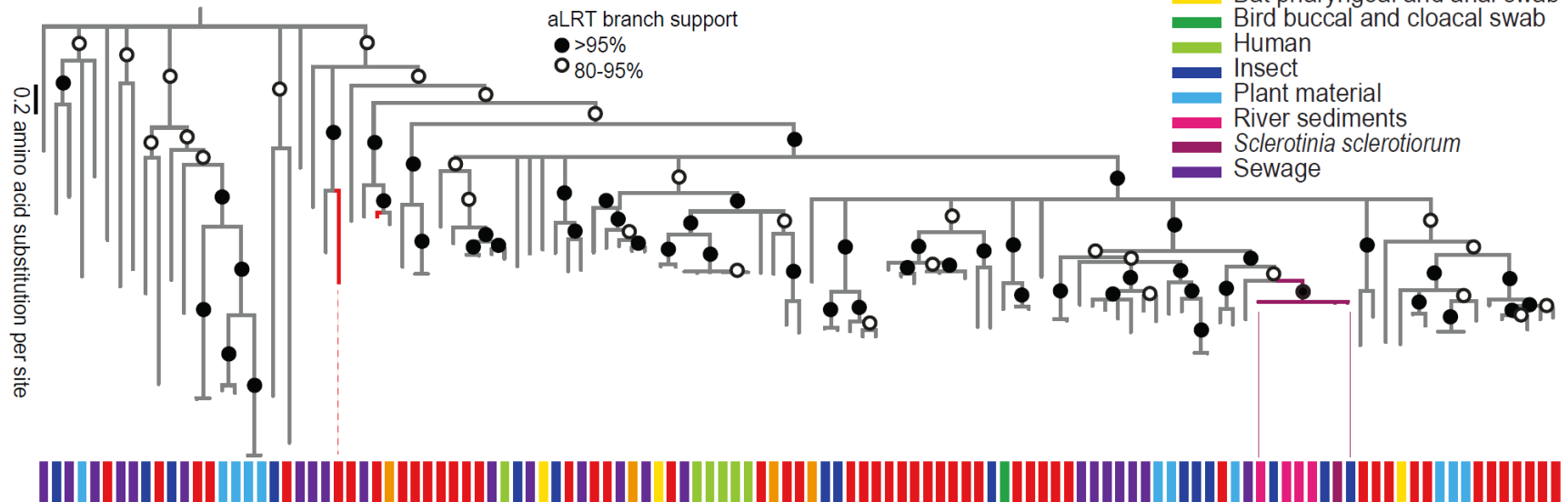
Serum

Sewage

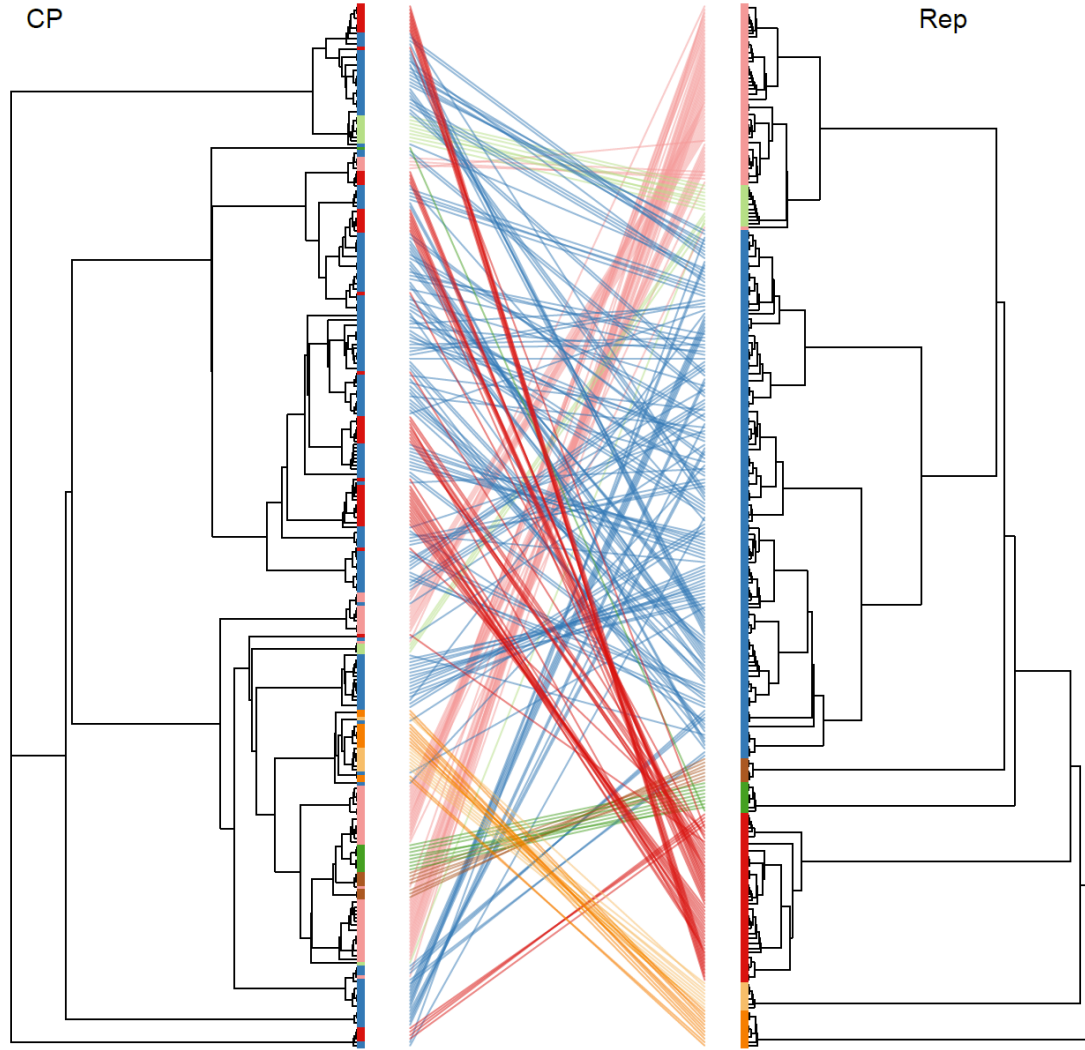
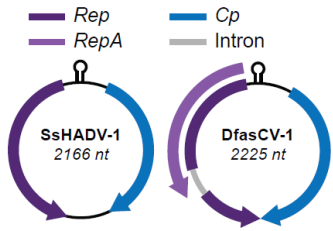


Isolation source

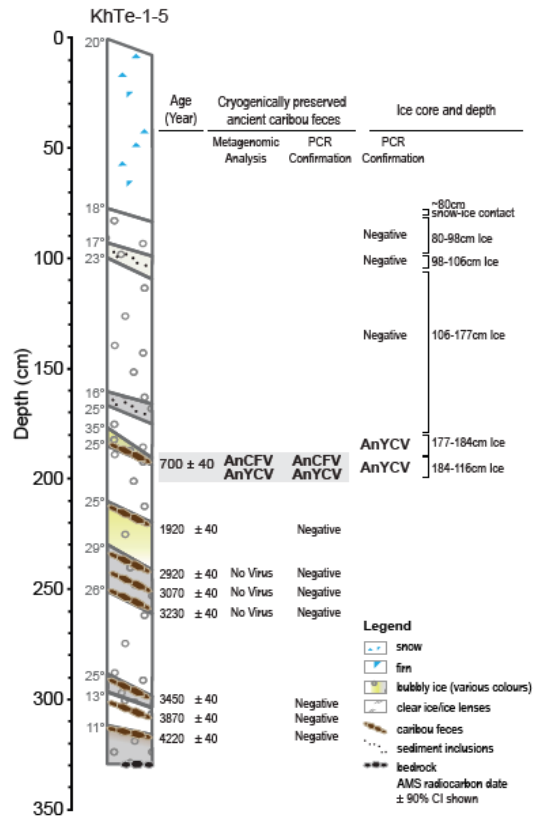
- Animal faeces
- Animal blood
- Bat pharyngeal and anal swab
- Bird buccal and cloacal swab
- Human
- Insect
- Plant material
- River sediments
- *Sclerotinia sclerotiorum*
- Sewage



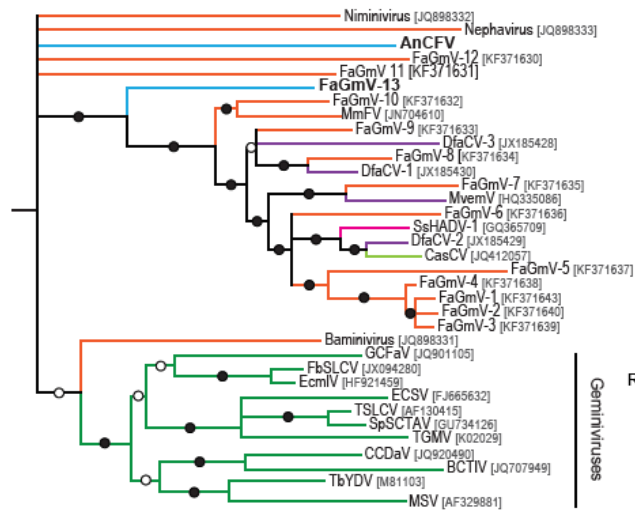
Genomoviruses



“Archived” viruses



Virome	Virus detected	Expected host	Virus type
Frozen feces - 700 yr BP	Geminivirus/Gemycircularvirus-like - AnCFV	Plant/Fungi?	DNA non-enveloped
<i>R. tarandus</i>	Cripavirus - AnYCV	Insect	RNA non-enveloped
Present-day feces - 2012	Tombusvirus	Plant	RNA non-enveloped
<i>R. tarandus</i>	Sobemovirus	Plant	RNA non-enveloped
	Gemycircularvirus - GmV-13	Plant/Fungi?	DNA non-enveloped



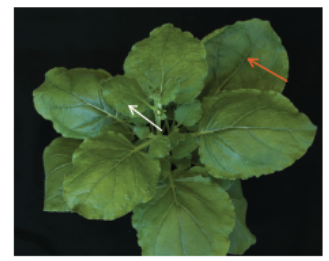
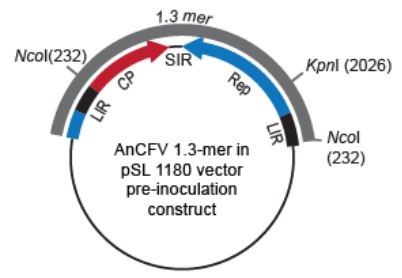
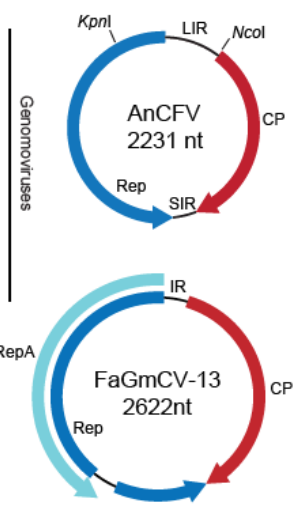
0.5 amino acid substitutions per site

aLRT branch support

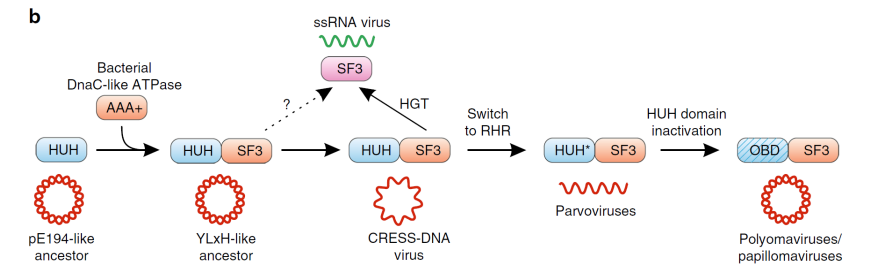
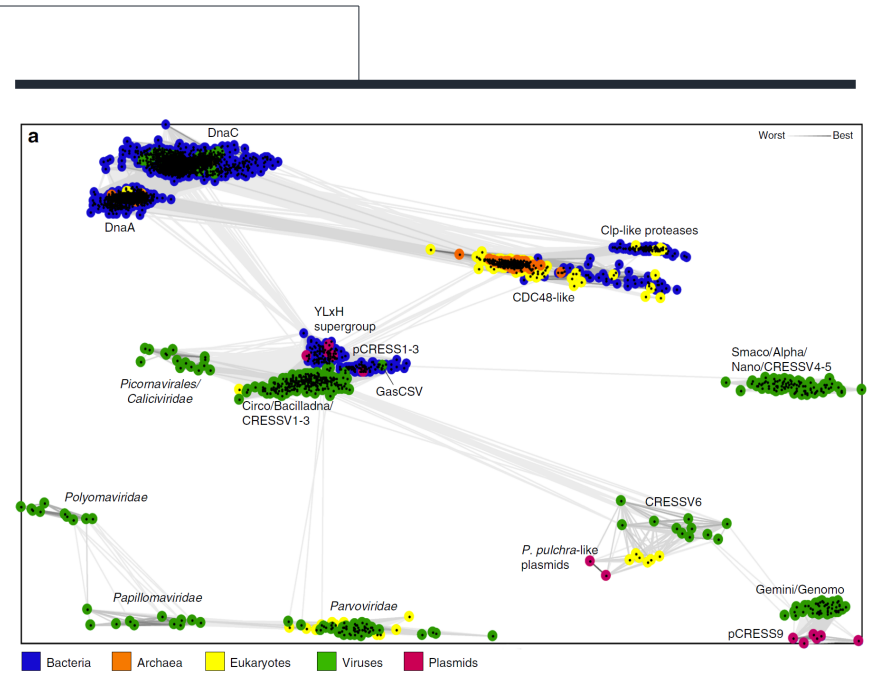
- >90%
- 80-90%

Origin

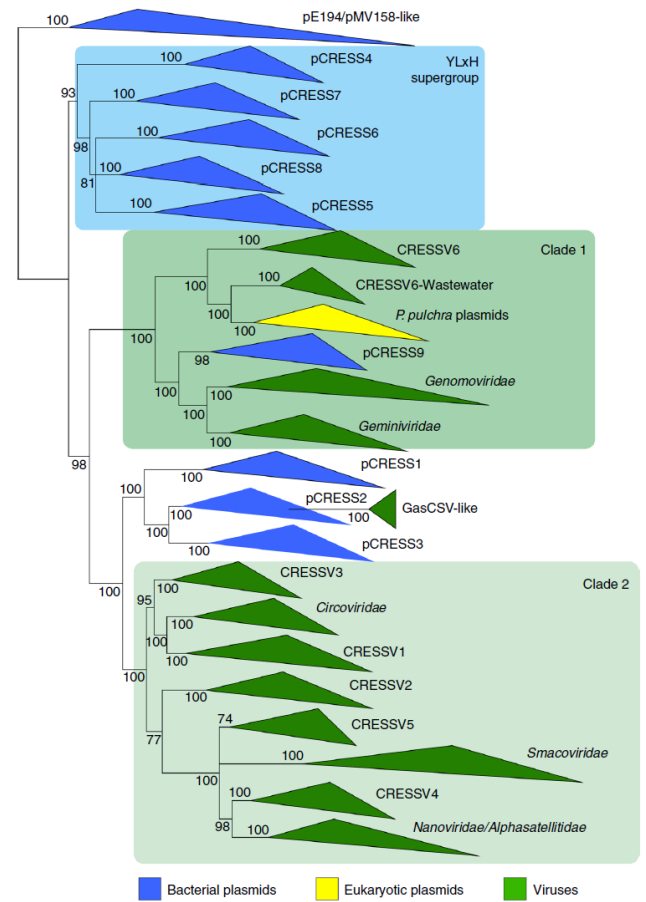
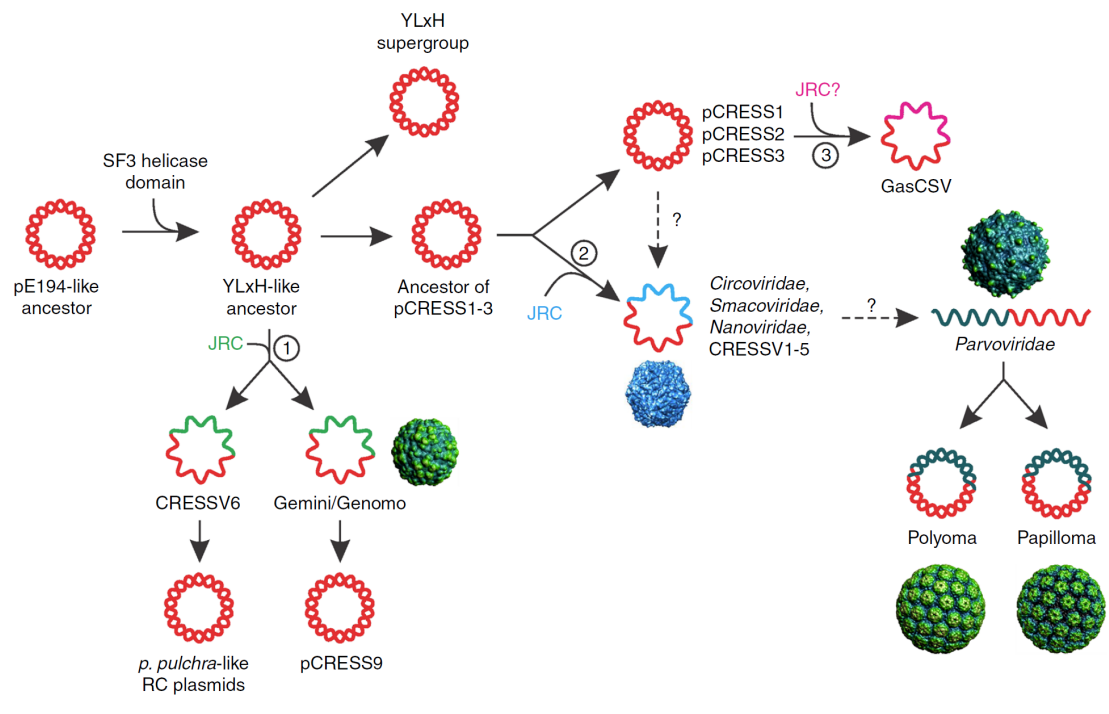
- Caribou feces
- Various feces
- Insects
- Fungi
- Possible plant / fungi
- Moccot and dicot plants



Reps of ssDNA viruses



Origin of ssDNA viruses



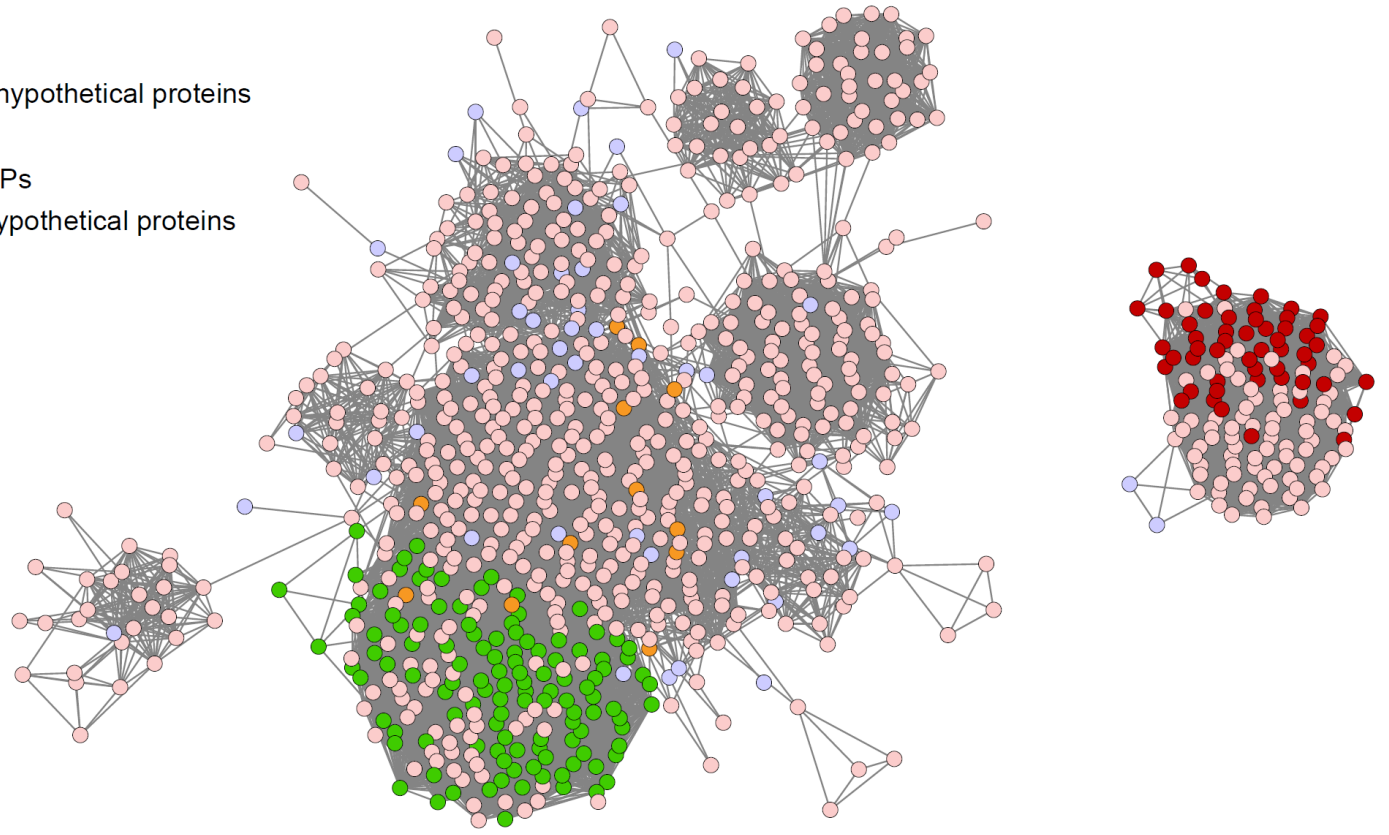
CRESS DNA virus CPs

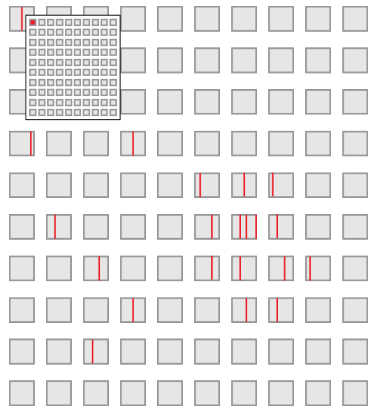
CRESS DNA virus CPs / hypothetical proteins

- Geminiviruses
- Unclassified CRESS CPs
- Unclassified CRESS hypothetical proteins

RNA virus CPs

- Tomusviruses
- Virtoviruses (STNV)



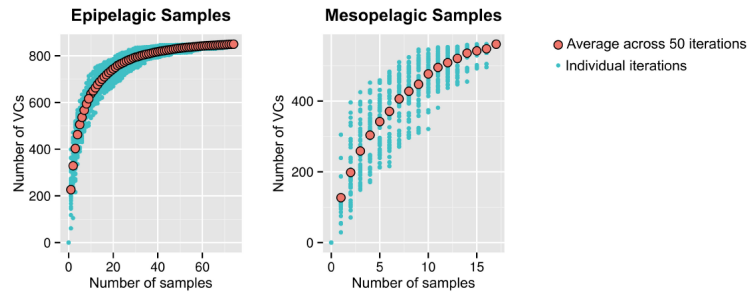


LETTER

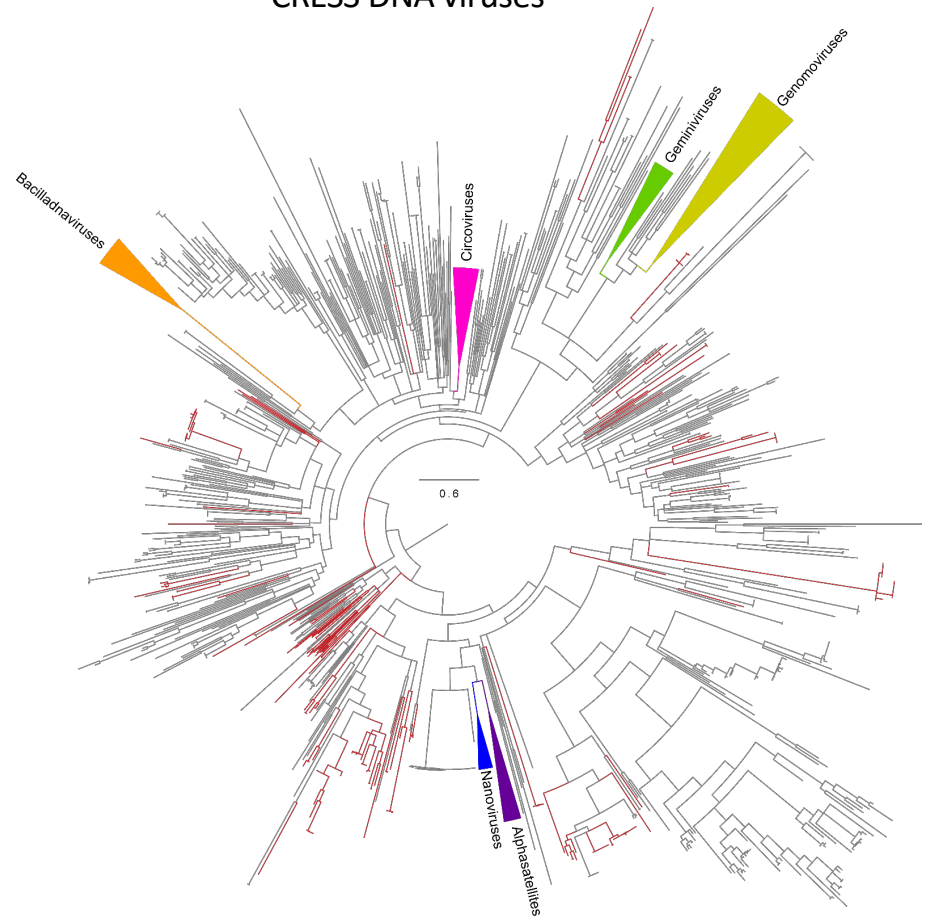
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Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses

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CRESS DNA viruses



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