

(RNA-) Structuredness in Viruses

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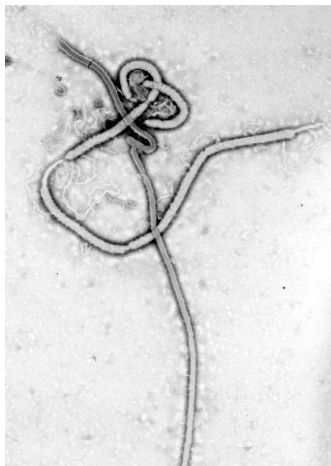
TBI Wien
University of Vienna

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Viruses I

Minimal Life Forms

- Obligate intracellular parasites
- No organelles
- (Very) small size
- DNA/RNA genomes



Electron micrograph of an Ebola Virion, size: 1000 nm
(image source: wikipedia)

Viruses II

Minimal Life Forms

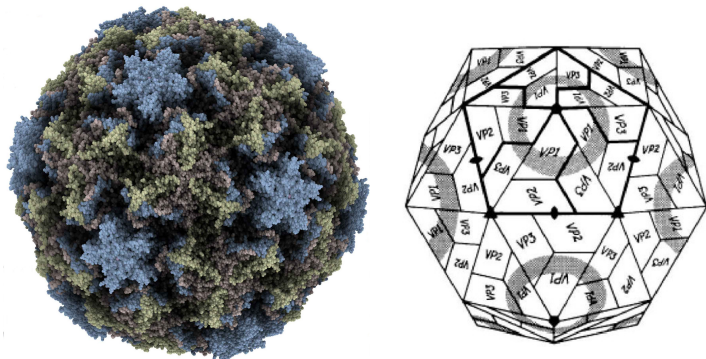


Figure: Crystal Structure and Schematic of Rhinovirus A ¹

Genome size (nt): Human: 3.2×10^9 Rhinovirus: 7×10^3

¹Zhao et al. 1996

Viruses and RNA Structure

- Viruses have tightly packed genomes
- Specific Functions are often provided by RNA Structures

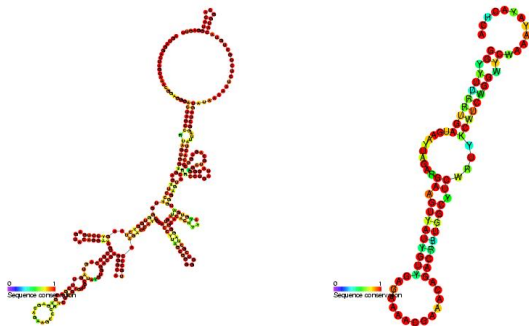
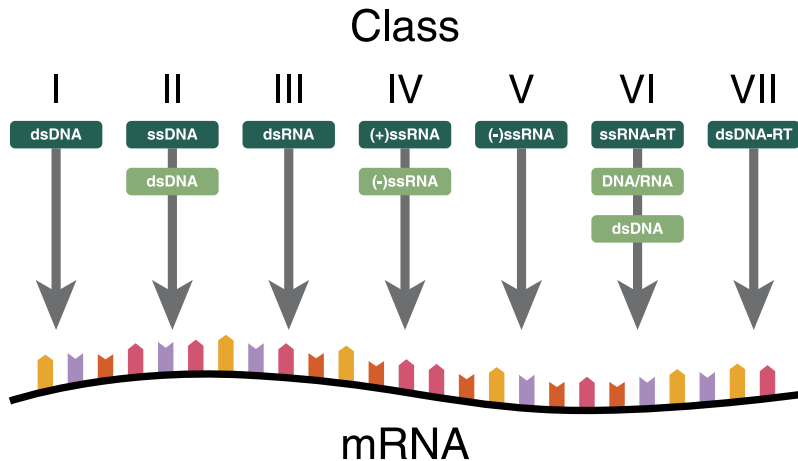


Figure: Pestivirus IRES¹, Rhinovirus CRE-Element

¹Rfam IDs: RF00209, RF00220

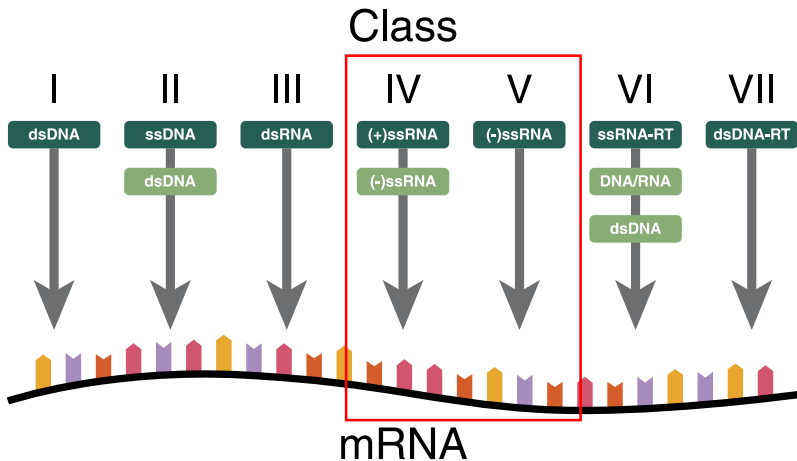
Viral Diversity

Baltimore Classification



Viral Diversity

Baltimore Classification



Viral Diversity

Viral Phylogeny

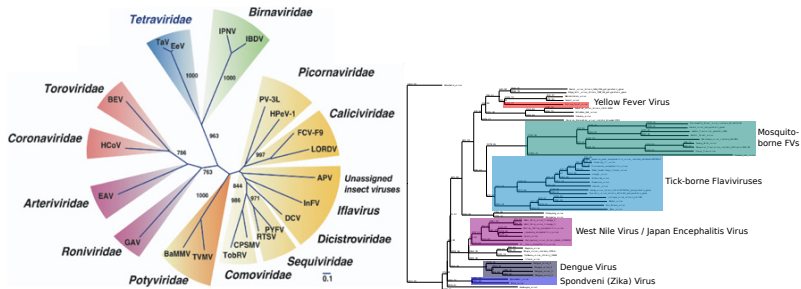


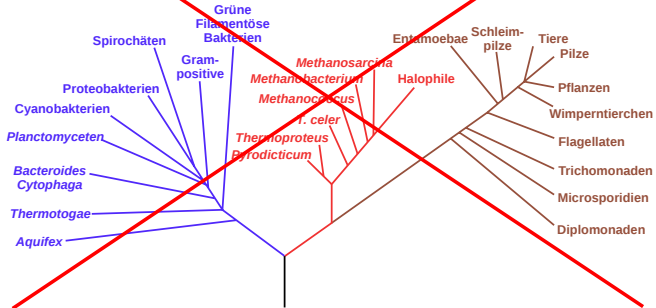
Figure: Picorna-like Viruses (left)¹, Flavivirus (right)

¹Fauquet, Schrock; 2006

Viral Diversity

Viral Phylogeny

Phylogenetic Tree of Viruses

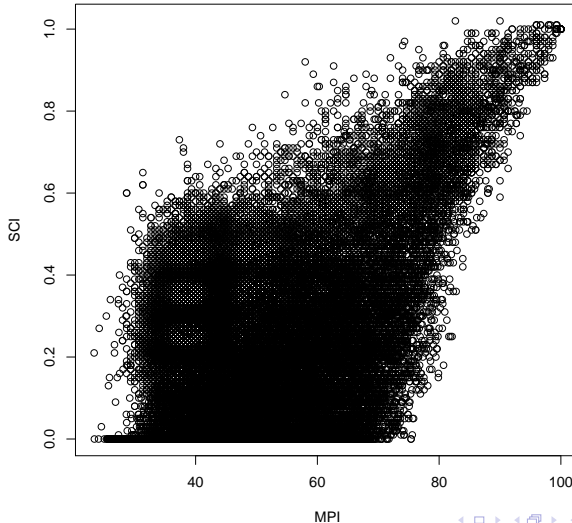


Viral Clusters of Ortholog Groups

- Groups of Ortholog proteins
- Calculated on Protein alignments
- Based on newest RefSeq Virus Genomes
- Includes all annotated viral species

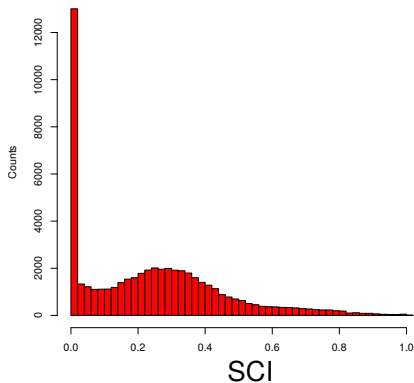
Virus Ortholog Groups

Viral Ortholog Proteins (mRNA) MPI vs SCI

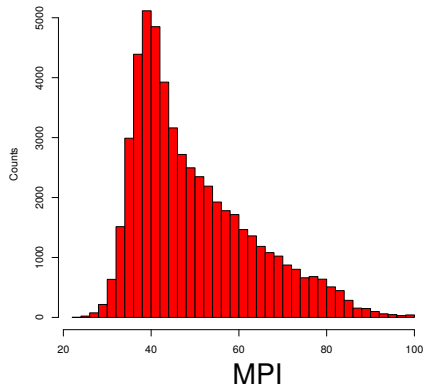


Virus Ortholog Groups

Viral Ortholog Proteins (mRNA) SCI

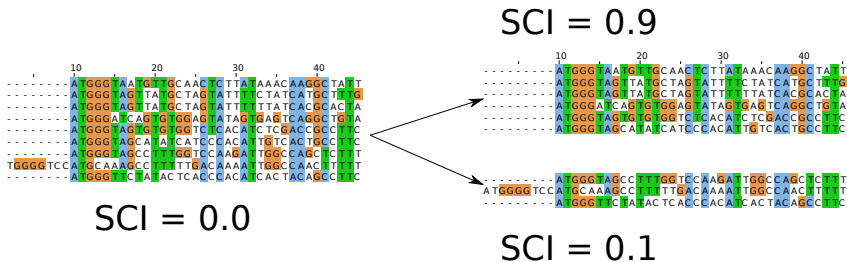


Viral Ortholog Proteins (mRNA) MPI



Viral Ortholog Proteins

Conserved sub-alignments



- No overall consensus structure but...
- Strong structure conservation in subparts of the alignment!

Viruses and structured RNAs

More than UTRs...

The Problem

- Viruses are a highly diverse group of organisms
- Just a fraction is investigated for ncRNAs
- UTRs get the most attention

Aims

- Screen all viruses for structured RNAs
- Take a close look at CDS regions

Methods

- RNAz
- R-scape

Dataset

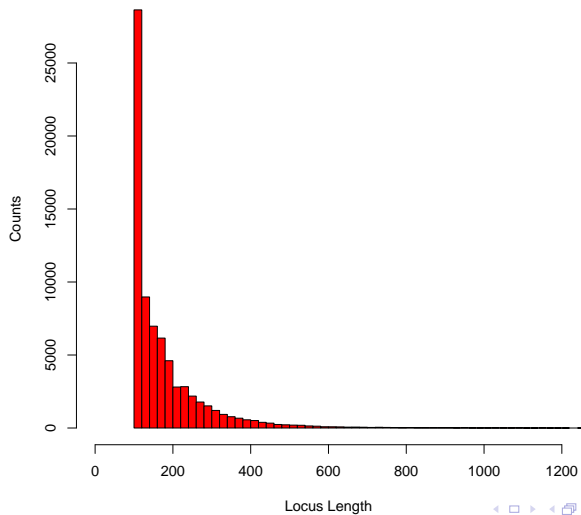
Isolation Pipeline

- 1 Fetch Species from NCBI taxonomy database
- 2 Fetch Refseq Sequences
- 3 Fetch genomes from NCBI Nucleotide Database
- 4 Align with clustal Omega
- 5 Multiple consistency checks in-between

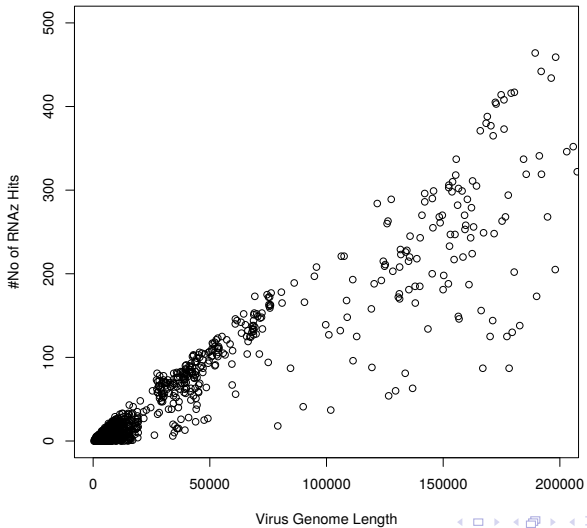
Name	#Species
NCBI Tax DB	18939
Refseq DB	8299
Consistent Species	1580

Type	#Species
dsDNA	422
ssDNA	276
dsRNA	142
ssRNA	600
RT	81
Satellites	32

Significant Hit size



#RNAz hits vs. Genome Length



Results

	#Hits	w/ Cov (G)	w/ Cov (RAF)
Total Hits	73564	4216	43554
CDS	69941	4806	41579
UTR	3664	410	1975

Summary & Outlook

Summary

- Structured Elements are widespread in Viruses
- Lots of Covariation in most elements!
- CDS and UTRs are equally affected

Outlook

- Check again with structure-based alignments
- Build covariance models for all significant loci
- Search for 'structural orthologs'

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...and you!



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Der Wissenschaftsfonds.