

CHALLENGES FOR EMERGING VIRUS DETECTION IN CLINICAL SAMPLES BY RANDOM METAGENOMICS

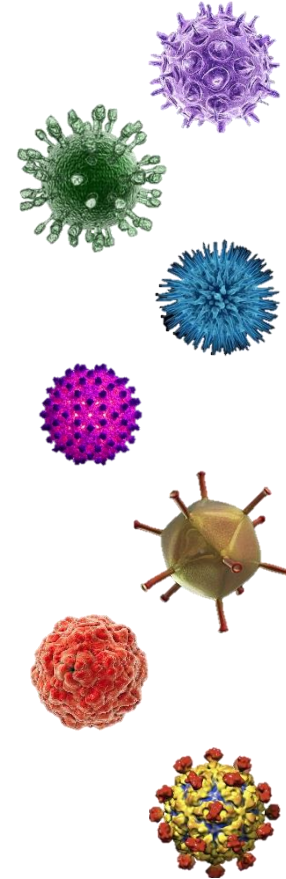
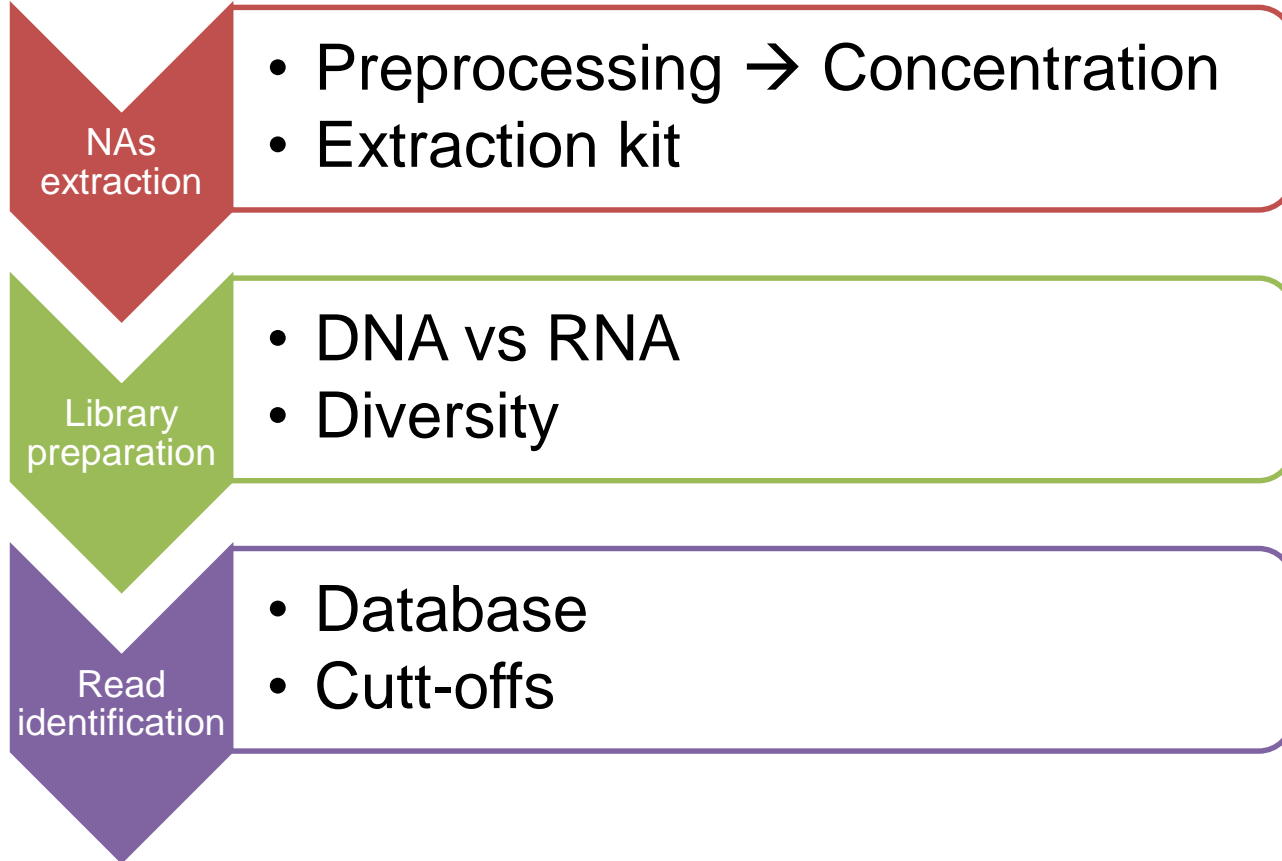
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M. Carmen Collado¹, Gloria Sánchez¹

¹*Instituto de Agroquímica y Tecnología de Alimentos, CSIC, Valencia (Spain).*

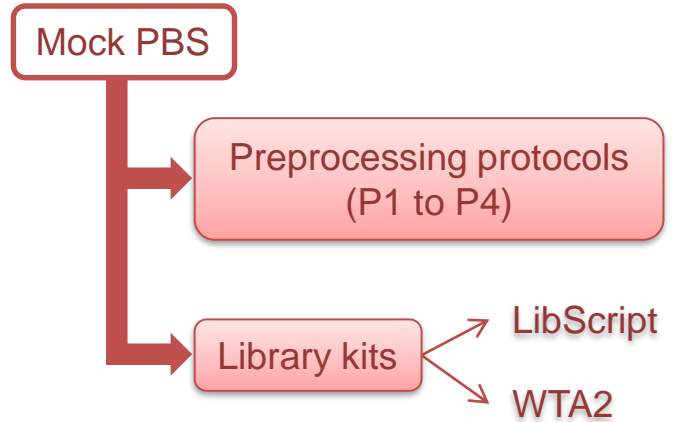
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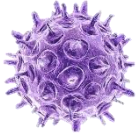
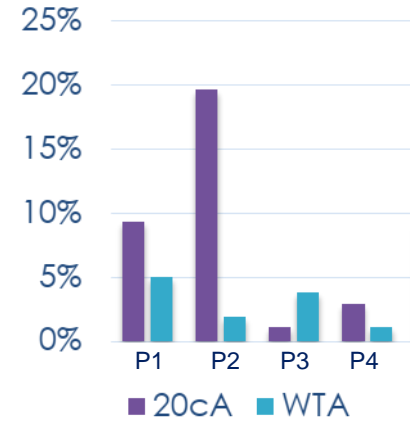
CRITICAL STEPS



LIBRARY PREPARATION



% viral reads



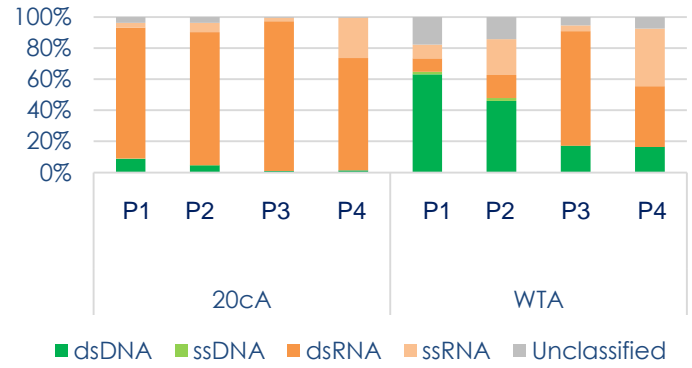
Detection

		NoV	MgV	HAV	HEV	RV	AstV
NN-AN	qPCR	Green	Red	Red	Red	Green	Green
	18c	Green	Red	Red	Red	Green	Green
	20cA	Red	Red	Red	Green	Red	Red
	WTA	Red	Green	Red	Red	Red	Green
NN-AY	qPCR	Green	Red	Red	Red	Green	Green
	18c	Green	Red	Red	Red	Green	Green
	20cA	Red	Red	Red	Red	Red	Red
	WTA	Red	Green	Red	Red	Red	Green
NY-AN	qPCR	Red	Red	Red	Red	Green	Green
	18c	Green	Red	Red	Red	Green	Green
	20cA	Red	Green	Red	Green	Red	Red
	WTA	Red	Green	Red	Red	Red	Green
NY-AY	qPCR	Green	Red	Red	Red	Green	Green
	18c	Red	Red	Red	Red	Green	Green
	20cA	Red	Red	Red	Red	Red	Red
	WTA	Red	Green	Red	Red	Red	Green

Diversity



Genomic groups



READ IDENTIFICATION

Options

nt

How To

Nucleotide viruses[Organism]

Create alert Advanced

Summary ▾ 20 per page ▾ Sort by Sequence Length ▾

Send to: ▾

Items: 1 to 20 of 3224439

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[Saccharopolyspora erythraea NRRL2338 complete genome](#)
 1. 8,212,805 bp circular DNA
 Accession: AM420293.1 GI: 133909243
[Assembly](#) [BioProject](#) [BioSample](#) [Protein](#) [PubMed](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

[Saccharopolyspora erythraea NRRL 2338, complete sequence](#)
 2. 8,212,805 bp circular DNA
 Accession: NC_009142.1 GI: 134096620
[Assembly](#) [BioProject](#) [BioSample](#) [Protein](#) [PubMed](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

[Pseudomonas aeruginosa strain K34-7 chromosome, complete genome](#)
 3. 7,038,012 bp circular DNA
 Accession: CP029707.1 GI: 1399187661
[Assembly](#) [BioProject](#) [BioSample](#) [Protein](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

[JP 2016041065-A/1: OLIGONUCLEOTIDE ANALOG AND METHOD FOR TREATING FLAVIVIRUS INFECTIONS](#)
 618541. 8 bp linear
 Accession: HZ783553.1 GI: 1041292475
[Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

[JP 2016041065-A/3: OLIGONUCLEOTIDE ANALOG AND METHOD FOR TREATING FLAVIVIRUS INFECTIONS](#)
 618542. 8 bp linear
 Accession: HZ783555.1 GI: 1041292477
[Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

[Sequence 6 from Patent WO03087383](#)
 618543. 7 bp linear DNA
 Accession: AX930355.1 GI: 40312160
[Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

[METHOD OF TREATING AMINO ACID METABOLIC DISORDERS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS](#)
 618544. 7 bp linear DNA
 Accession: DD217800.1 GI: 88492517
[Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

[Sequence 6 from Patent EP1847614](#)
 618545. 7 bp linear DNA
 Accession: FB294362.1 GI: 161724094
[Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)



mes*	In-house
	413
	2,186
	3,715

ZIKA
 Human
 Coronaviru
 Hantavirus
 Lassa virus

SPECIFIC CASE

Samples: Human fecal samples (2 pairs mother-infant)

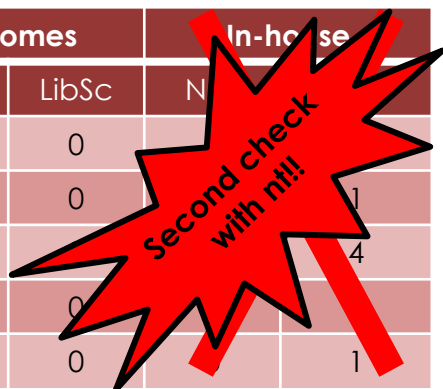
Library: LibScript (LibSc) vs. NEBNext (NEB)

Databases: RefGenomes vs. in-house

Family (RefGenomes)	D10_LibSc	D10_NEB
Ackermannviridae	46%	0%
Adenoviridae	35%	0%
Albetovirus	10%	95%
	D10-H_LibSc	D10-H_NEB
Parvoviridae	43%	0%
Poxviridae	11%	0%
	D40_LibSc	D40_NEB
Baculoviridae	1%	88%
Unclas. viruses	93%	0%
	D40-H_LibSc	D40-H_NEB
Astroviridae	29%	0%
Siphoviridae	23%	1%
Virgaviridae	36%	86%

No. positive samples

Virus	RefGenomes		In-house	
	NEB	LibSc	NEB	LibSc
West nile	0	0	0	0
Dengue	0	0	1	1
Zika	0	0	4	4
Bornavirus	0	0	0	0
Lassa virus	0	0	0	1



Enteric viruses (detected by RT-qPCR)

Virus	Sample (gc/L)	RefGenomes		In-house	
		NEB	LibSc	NEB	LibSc
NoV	D10 (2.02)	+	-	+	+
	D10-H (4.88)	-	-	-	+
HAstV	D40 (5.01)	-	+	-	+
	D40-H (6.26)	+	+	+	+
RV	D10 (3.39)	-	-	+	+
	D10-H (2.97)	-	-	+	-
	D40 (5.93)	-	-	-	-
	D40-H (3.55)	+	-	+	-

Conclusions

- **Human fecal virome are dependant of:**
 - **Pre-enrichment of the sample and library**
 - **Databases**
- **The detection of some viral groups is strongly influenced by the used databases**
- **Library sequencing kits can produce bias to DNA viruses.**

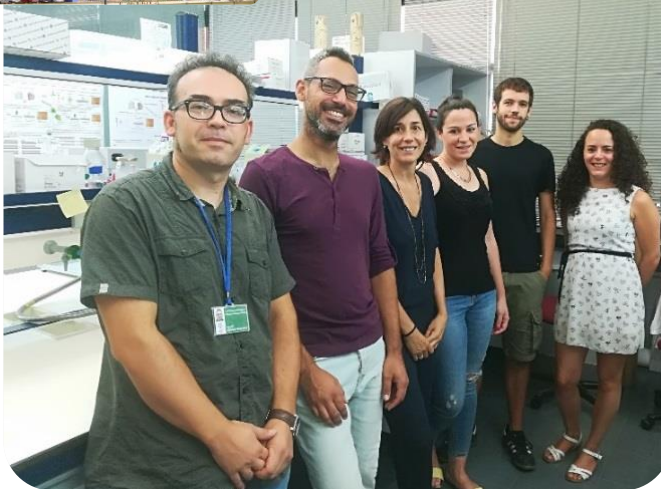




Travel grant

Thanks for your
attention!

:)



Food Viruses IATA

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*Members of



Fundings



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