Exploring Viral Metagenomics in ASFV-Positive Samples from the Philippines Reveals Co-Infection With Other Swine Pathogens

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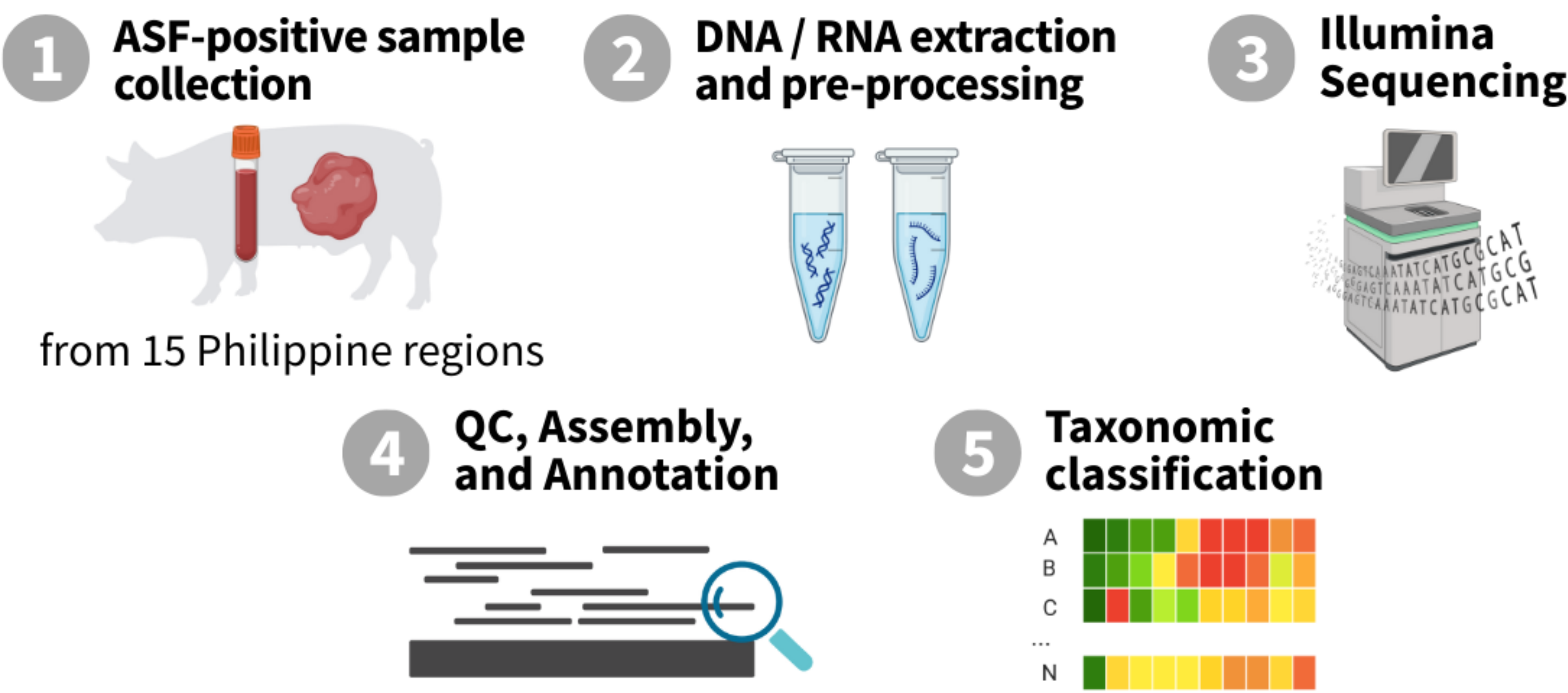
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INTRODUCTION

Co-infections are common in swine and can influence disease outcomes. While co-infections of various swine pathogens are increasingly recognized, the presence of other DNA or RNA viruses in ASF-infected swine remains largely uncharacterized.

OBJECTIVE: To identify co-infecting swine viruses in ASF-positive samples using a metagenomic sequencing approach

METHODS

1. **ASF-positive sample collection**
from 15 Philippine regions

2. **DNA / RNA extraction and pre-processing**

3. **Illumina Sequencing**

4. **QC, Assembly, and Annotation**

5. **Taxonomic classification**

RESULTS AND DISCUSSION

(a)

(b)

Figure 1. Heatmaps displaying the relative abundance of the top 10 vertebrate-associated viral families (y-axis) identified through k-mer-based taxonomic classification using Kraken2 on **(a)** DNA sequencing and **(b)** RNA sequencing data, presented on a $\log_{10}$ reads per million (RPM) scale across samples. The color intensity corresponds to the $\log_{10}$(RPM) values, as shown in the legend. The x-axis refers to sample IDs representing samples collected from individual pigs from different regions of the Philippines.
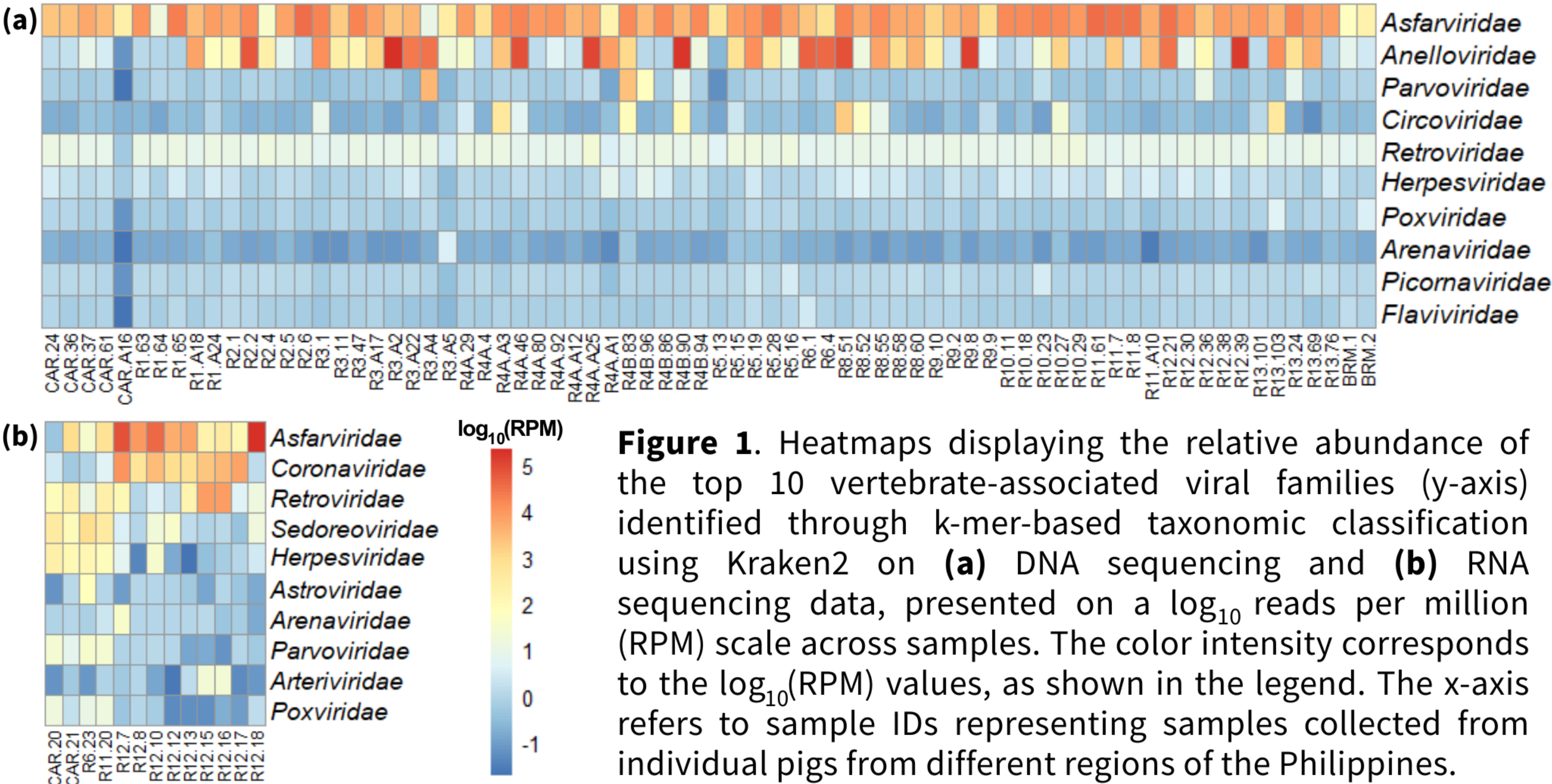
Table 1. List of viruses with near to complete-length genome assemblies from DNA and RNA sequencing.

Method	Family	Genus	Species	Contigs	Length (kb)	Prevalence	Seen with ASFV before?
DNA-seq	*Anelloviridae*	*Iotatorquevirus*	Iotatorquevirus suida1a	159	1.5 - 5.8	58.67%	Yes[1]
		Kappatorquevirus	Kappatorquevirus suidak2a	29	1.5 - 2.8	20%	No
			Kappatorquevirus suidak2b	16	1.5 - 3.0	21.33%	No
	Circoviridae	*Circovirus*	Circovirus porcine2	17	1.7	21.33%	Yes[2,3]
	Parvoviridae	*Tetraparvovirus*	Tetraparvovirus ungulate2	1	5.2	1.33%	Yes[4]
		Copiparvovirus	Copiparvovirus ungulate2	1	5.6	1.33%	No
			Copiparvovirus ungulate4	3	3.4 - 5.7	4%	No
RNA-seq	*Sedoreoviridae*	*Rotavirus*	Rotavirus alphagastroenteritidis	6*	0.5 - 2.3	14.29%	No

*Near to complete-length sequences of this virus' coding regions were assembled

In summary, **63 out of 75 (84%) DNA samples** and **2 out of 14 (14.29%) RNA samples** showed the presence of at least one viral species other than ASFV.

CONCLUSION

To our knowledge, this is the first report to explore co-infection in ASFV-infected swine using an unbiased sequencing approach.
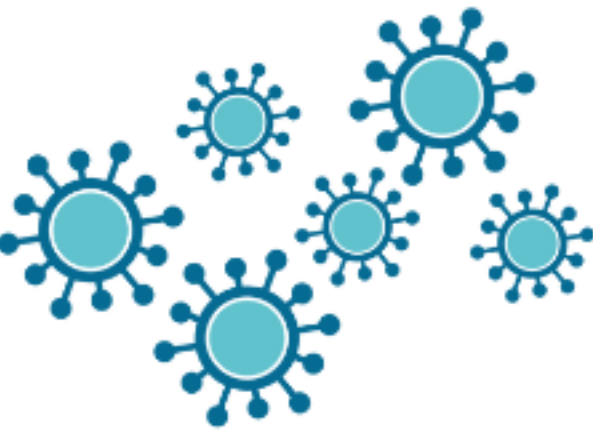
These findings provide baseline data on swine viral diversity to aid in further investigations of viral co-infections in correlation with clinical signs.

ACKNOWLEDGEMENTS

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