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Hybrid Sequencing Approach for African Swine Fever Virus Whole Genome Assembly

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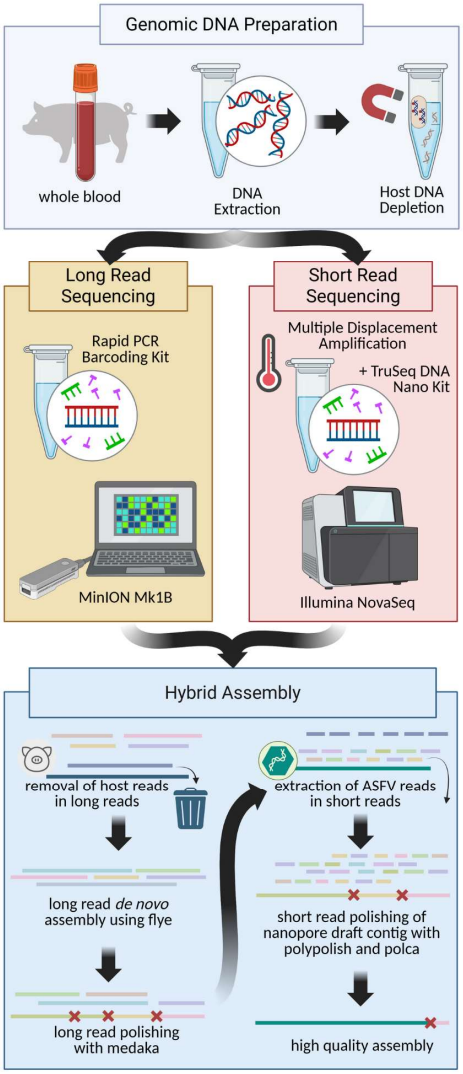
INTRODUCTION

African Swine Fever Virus (ASFV) is large dsDNA virus with a genome length of ~190 kbp. Its genome is characterized by homopolymer and repeat regions. Thus, it is challenging to elucidate the complete ASFV genome using only the widely used short read sequencing approach.

OBJECTIVE: To optimize a comprehensive workflow using long and short read sequencing approaches coupled with a hybrid assembly pipeline for the generation of high-quality genome sequences from ASFV-positive samples

METHODS



RESULTS AND DISCUSSION

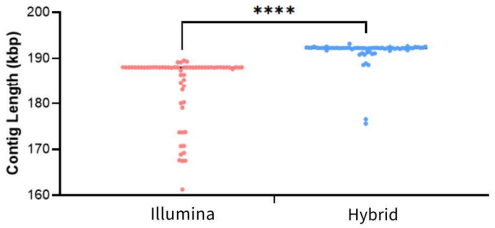


Figure 1. Sizes of the largest ASFV assembled contig per method. T-test showed that **hybrid** assemblies produced significantly **longer ASFV contigs** relative to Illumina-only assemblies. **** p<0.0001 (n=65 per group)

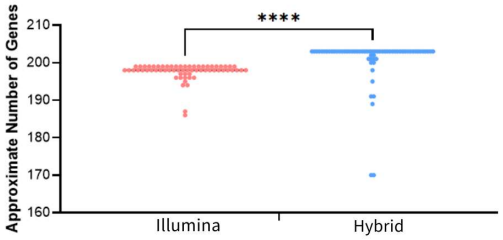


Figure 2. Approximate number of genes of the assembled contigs per method. Analysis showed significantly **higher gene count of hybrid assemblies** relative to Illumina-only assemblies. **** p<0.0001 (n=65 per group)

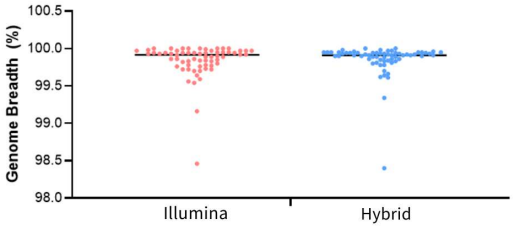


Figure 3. ASFV genome breadth with at least 10X depth of coverage between the two assembly approaches. Analysis showed that there is no significant difference in genome breadth between the two. But examination of the distribution showed increased IQR in hybrid . Half of Illumina-only assemblies fall within 99.78 to 99.95 range but **genome breadth IQR increased to 99.86 to 99.95 in hybrid assemblies**. Based on MIUViG standards, the generated draft assemblies cover at least 98% of the genome and are therefore high quality. (n=65 per group)

- Hybrid assembly approach combines the long read lengths of Nanopore approach and high accuracy of Illumina approach, producing more contiguous, more accurate, and more complete whole genome assemblies in comparison with Illumina-only assemblies.

CONCLUSION

High quality ASFV genomes were generated from 65 out of 72 samples using our sequencing approach and hybrid assembly pipeline. Our results demonstrate the scalability and suitability of the current protocol to assemble the large and complex ASFV genome, which has the potential to be adapted for routine viral genomic surveillance and characterization.

ACKNOWLEDGEMENTS

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REFERENCES