



Sequencing Strepsiptera: NGS and museomics methods in a systematic study of the twisted-wing parasites

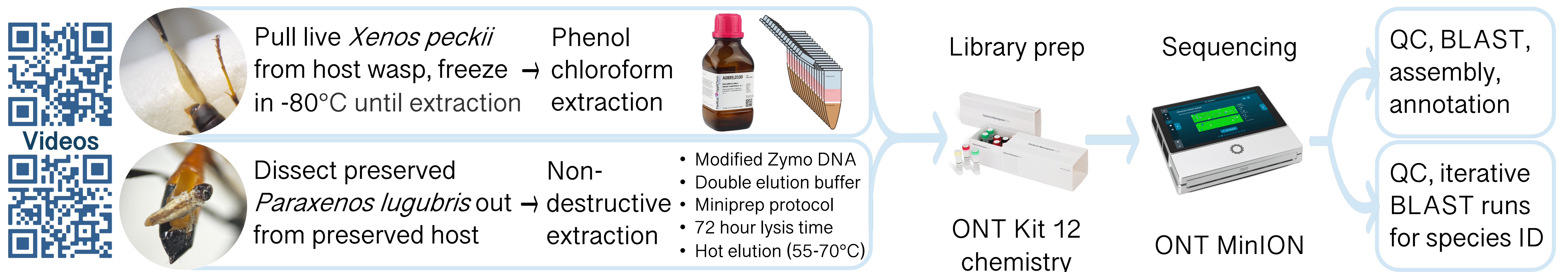
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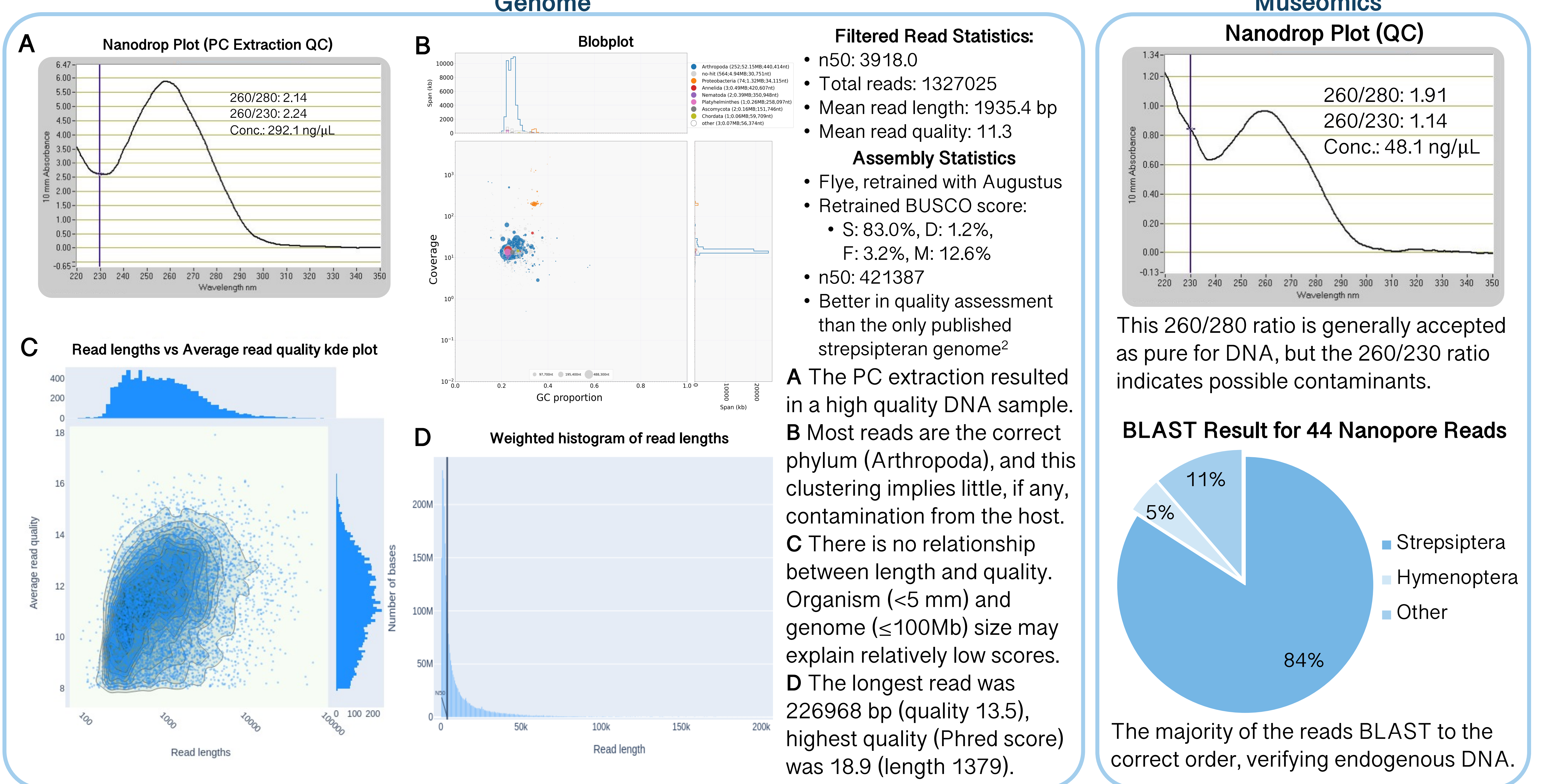
Introduction

- Strepsiptera, or the twisted-wing parasites, are a small and enigmatic order of Insecta that parasitize several other major insect groups.¹ Rarely collected afield, only one whole genome and one molecular phylogeny are currently published for the order.²
- “Museomics” refers to the study of genomics using museum specimens as molecular material.³ The advent of improved extraction protocols and next generation sequencing allow for the inclusion of decade-old preserved specimens in molecular phylogenies.
- We present our methods and quality assessments in using the Oxford Nanopore Technologies MinION to sequence two individuals: **1) the whole genome of a female *Xenos peckii* (Strepsiptera: Xenidae)** and **2) a test extraction of a female *Paraxenos lugubris* (Strepsiptera: Stylopidae) museum specimen, generated by our novel nondestructive DNA extraction protocol.**

Material & Methods



Results & Discussion



Conclusions & Future Directions

- Phenol chloroform extractions combined with nanopore sequencing can yield genome sequences for singular insect specimens < 5 mm in size.
- Nondestructive sampling methods on museum specimens can extract enough DNA for anchored hybrid enrichment (AHE) analyses.⁴

We will take more steps to polish this genome. It will eventually serve as a reference genome in the construction of our molecular phylogeny of Strepsiptera. All extant taxa sampled will be sourced from museums and extracted with our final nondestructive protocol. Currently, we are acquiring taxa, optimizing our protocol, and designing baits for the AHE analyses.

References

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