Next-generation DNA barcoding in the Auchenorrhyncha

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DNA barcoding, the sequencing of a standardized fragment of the mitochondrial COI gene (Hebert *et al.* 2003), is an important technique in modern systematics. Its application to Auchenorrhyncha has led to some important insights into species relationships (Hamilton 2014) and has great potential in allowing identification of females and nymphs when morphological characters are inadequate (Gopurenko *et al.* 2013). Recently developed techniques for sequencing the barcode region on next-generation sequencing (NGS) platforms, specifically the Illumina MiSeq, offer major technical improvements that will allow greater and more diverse applications of the technique (Shokralla *et al.* 2015, Meier *et al.* 2016).

The key difference between NGS and traditional Sanger sequencing lies in the ability of NGS to produce a discrete read from each individual molecule present in the sequencing library. Multiplexing using molecular indices thus allows thousands of individuals to be sequenced in a single run, for a major increase in throughput and significantly decreased cost. As well, the ability to obtain distinct barcodes from multiple taxa in a single sample opens up the possibility of ecological approaches to barcoding, such as simultaneous sequencing of auchenorrhynch hosts and their parasitoids. Multiplex amplification of nuclear genes alongside COI is also possible using NGS, allowing rapid and low-cost assembly of phylogenetic datasets.

I will present results from preliminary NGS barcode sequencing of a diversity of Auchenorrhyncha and their parasitoids. Technical and analytical challenges remaining, as well as future directions, will be discussed.

References

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