



Comparative Analysis of Whole Genome Sequencing and Target Capture of Ultra Conserved Elements for Phylogenetic Studies in Hymenoptera.

Juanita Rodriguez (CSIRO, Australian National Insect Collection); Olivia Evangelista (CSIRO, Australian National Insect Collection); Alicia Grealy (CSIRO, National Collections and Marine Infrastructure).

In this study, we present a comparative analysis of Whole Genome Sequencing (WGS) and Target Capture of Ultra Conserved Elements (UCE), within the context of phylogenetic research. We utilized a set of aculeate Hymenoptera (Pompilidae, Mutillidae, Colletidae, and Apidae) as our study subjects. We extracted DNA from 205 fresh and museum specimens and prepared libraries in miniaturized reactions with an initial quantity of 5 ng of DNA. The libraries underwent two processing methods: 1) target capture in pools of 16 using the UCE Hymenoptera 2.5Kv2A bait set, followed by sequencing, and 2) whole genome sequencing at a target 10x coverage, assuming genome sizes of 300Mb-600Mb depending on the taxon. UCE loci, were extracted with Phyluce from assemblies derived from both approaches. Our findings indicate that whole-genome sequencing surpasses target capture when applied to fresh specimens, in terms of ultra-conserved elements (UCEs) recovered and contig length at coverage levels exceeding 10x. However, under conditions of DNA degradation, target capture can potentially outperform whole-genome sequencing. This study not only elucidates the relative advantages and limitations of these methodologies but also underscores their adaptability to specific taxonomic groups.

Juanita Rodriguez: juanita.rodriguez@csiro.au