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THE AGE OF MUSEOMICS - HOW TO GET GENOMIC INFORMATION FROM MUSEUM SPECIMENS OF LEPIDOPTERA

par

Elsa Call

Thèse Univ. Lund, Suède

Billions of specimens can be found in natural history museum collections around the world, holding potential molecular secrets to be unveiled. The application of the latest Next-Generation sequencing (NGS) technologies to such specimens in called museomics. In this new age, these approaches open a window into the genetic past, and an exciting opportunity to expand our horizons. These methods provide the opportunity to study both extinct or difficult to collect taxa. Additionally, investigations into how factors, such as climate change, have shaped both the current and past diversity is possible. The aim of my thesis was to apply NGS techniques to museum specimens of Lepidoptera, to better investigate the types of data generated and their uses.

Firstly, we demonstrate the use of a targeted enrichment (TE) approach to sequence hundreds of nuclear loci from dry pinned specimens. Secondly, we used the data generated from the targeted enrichment to investigate the phylogenetic relationships of three Geometroidea moth families. Thirdly, we compare the recovery rate of a targeted enrichment approach vs whole-genome sequencing (WGS) for Geometroidea museum specimens. Finally, we investigated the usefulness of WGS for population genomics approaches based on specimens of a variety of ages using Pieris napi as an example.

Beyond the technology itself, museomics also open the door for answering plenty of interesting scientific questions. The potential for such approaches can have a considerable impact on phylogenomics and population genetic studies, as we saw here, but on more ecological perspectives as well, particularly by accessing data from an era before climate changes. The limits are our imagination of thinking of the biological question we want to investigate, and our creativity to develop methods that will help us answer these questions. The age of museomics is upon us.

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