EXPLORING THE GENOMIC BASIS OF AN UNDERWATER TAPE: THE EVOLUTION OF SILK BIOSYNTHESIS AND ASSOCIATED BEHAVIOUR IN CADDISFLY LARVAE

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Motivation and Results

Properties of caddisfly silk (polymerization in aquatic environments, high tensile strength/extensibility, sticks under water) make this material an interesting target for inter-disciplinary and industrial research.

• We identified termini of the heavy (h-) and assembled the genomic region that encodes for light (l)-fibroin, proteins that form the basis of caddisfly silk1
• Genome size varies 12.6-fold, from 170MB in net-spinning to 2130MB in case-building species (Fig. 2)
• Genome size variation may be linked to the functional diversification of silk characteristics and use in caddisflies

1 Caddisfly larval silk is used to construct a variety of underwater architectures
2 Genome size evolution in Trichoptera.3 Genome sizes are given on the y-axis in Mbp. Illustrations from Thomas et al. 2020*
3 Examples for repeat abundance in two caddisfly suborders.2 Illustrations from Thomas et al. 2020*

Contribution to SGN Program Portfolio

• From ideas to application: Collaborative projects with bio-technologists will gauge the potential of caddisfly silk as technical material
• Infrastructure: Our data is part of a newly established taxonomically broad genome collection: Senckenberg Biodiversity Genome Collection
• Documenting and analyzing biodiversity in an Earth system context

Outlook

• We are beginning to disentangle strands of silk to predict the underlying metabolism and mediation of silk characteristics
• We are applying new sequencing technologies to solve the problem of assembling the highly repetitive h-fibroin
• We will characterize the pattern of genome size evolution in a phylogenetic context

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References