

## **Genomic evolution of underwater silk in caddisflies (Insecta: Trichoptera) and other freshwater arthropods**

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Aquatic insects have been neglected in genomic studies. However, they exhibit a suite of ecologically relevant key innovations and adaptive traits, the evolution and genetic background of which remain poorly understood. This project is designed to fill this gap by generating and analyzing genomic data to study the evolution of adhesive underwater silk in Trichoptera (caddisflies) and other (semi-) aquatic arthropods. Caddisflies exhibit the greatest diversity of underwater silk uses. This exciting key innovation has potentially facilitated their radiation across a multitude of different aquatic environments. Further, the unique properties of under water silk (polymerization in aquatic environment, enormous tensile strength, elasticity) makes this system interesting for applied sciences. Using a comparative genomics framework and targeting mechanisms such as gene family expansion, selection, presence/absence of genes and variation in gene sequences (e.g. repeat motifs in important silk gene clusters), the project aims to uncover the genomic basis of the evolution of genes and gene families encoding for silk phenotypes in Trichoptera and other freshwater arthropods. Further, by looking at different developmental stages, genetic modulation and regulation of the different properties of silk will be investigated, i.e., the role of gene expression and post-transcriptional modifications (e.g., alternative splicing) and potential methylation patterns in silk genes will be examined. Understanding the genomic evolution and molecular mechanisms of silk production will not only address questions regarding molecular adaptations responsible for the diversification in aquatic environments but also lay the foundation to gauge the potential of underwater silk for biomedical and biotechnological applications.

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