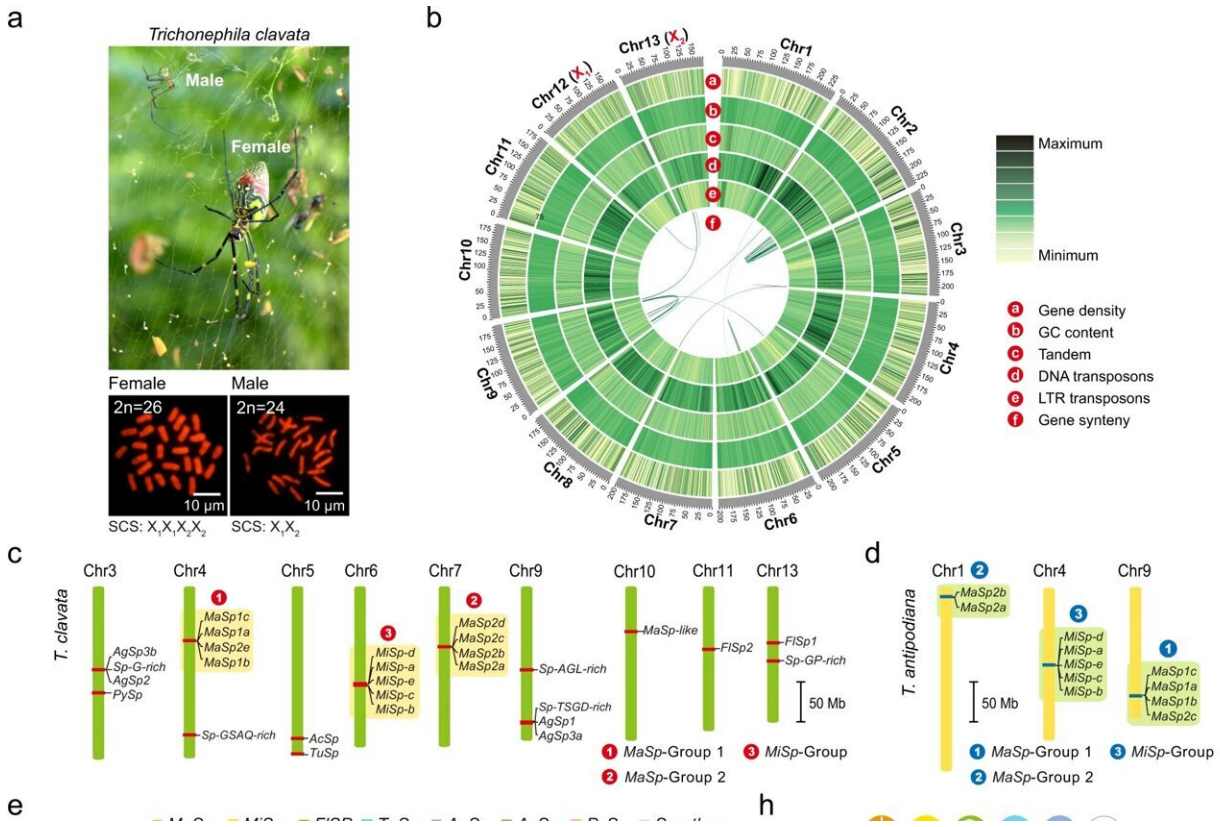
Molecular atlas of spider silk production could help bring unparalleled material to market

March 3 2023, by Justin Jackson



Chromosomal-scale genome assembly and full spidroin gene set of T. clavata. **a** Photograph of *T. clavata* showing an adult female and an adult male on the golden orb-web (above) and the female and male karyotypes (below). SCS, sex chromosome system. **b** Circular diagram depicting the genomic landscape of the 13 pseudochromosomes (Chr1–13 on an Mb scale). **c** Twenty-eight *T. clavata* spidroin genes anchored on chromosomes. **d** Spidroin gene groups of another orb-

web spider, *T. antipodiana*. The published genomic data of *T. antipodiana* was analyzed to identify the location information of spidroin genes. **e** Spidroin gene catalog of six orb-web spider species. **f** Expression clustering of silk glands (major and minor ampullate (Ma and Mi), flagelliform- (Fl), tubuliform- (Tu), aggregate- (Ag), and aciniform & pyriform (Ac & Py) glands) and venom glands. The pink line shows the closest relationship between the Ma and Mi glands. **g** Morphology of *T. clavata* silk glands. Similar results were obtained in three independent experiments and summarized in Source data. **h** Expression patterns of 28 spidroin genes in different types of silk glands. Source data are provided as a Source Data file. Credit: *Nature Communications* (2023). DOI: 10.1038/s41467-023-36545-6

Researchers from Southwest University in China have constructed the entire chromosomal-scale genome assembly and complete spidroin gene set of the golden orb-weaving spider, Trichonephila clavata, known for its especially strong, golden-colored webs.

They attest that their work "Provides multidimensional data that significantly expand the knowledge of spider dragline silk generation…" and the researchers plan on using this new "molecular atlas" to better understand how spiders manufacture their silk.

Published in the journal *Nature Communications*, the paper details the steps the researchers took, from wild spider capture to multiomic analysis, in revealing the interplay of genes within the spider's major ampullate gland, the gland responsible for producing dragline silk.

Spider dragline silk is a true material marvel with many potential medical and industrial applications. It is lighter and stronger than steel while maintaining an elastic stretching ability that rivals rubber. Unlike many synthetic materials, spider silk is non-toxic, biodegradable, and biocompatible, making it an ideal material for surgical implants,

biosensors, and tissue reconstruction.

The only limitation to adopting spider silk as a replacement for a long list of materials we currently use is how difficult it is to manufacture. There was an effort in the past to produce the proteins in goat milk by a company called Nexia, and it worked, but not at a scale required for mass production.

And despite the obvious benefits of spider silk, no one has stepped up to start spider farming on the scale required. Researchers expect that by better understanding silk production at a molecular level in spiders, they will gain practical insights to help bring this unparalleled material to market.

Making a molecular atlas with multiomics

To obtain the genome, the research team used the Oxford Nanopore platform, which can produce the most extended contiguous reads of any gene sequencer, as well as Illumina sequencing machines for more accurate yet shorter read capture lengths and Hi-C for chromosome mapping. By combining these three different sets of genomic data, the researchers were able to bioinformatically reconstruct a detailed model of the spider's chromosomal-scale genome assembly and complete spidroin gene set.

Having this genomic data allows connections to be made between gene expression and, ultimately, the proteins found in spider silk, which is exactly what the researchers did next. The team performed transcriptome (messenger RNA), protein, and metabolite (signaling molecule) analysis of the three segments of the major ampullate gland; the tail, sac, and duct.

Liquid chromatography-mass spectrometry analysis identified 28

proteins: 10 were spidroins, the proteins that make up spider silk, 15 were spider silk-constituting elements, and one was related to venom. With the core components identified, the researchers could rank them in order of intensity-based absolute quantification.

Further analysis allowed them to characterize the specific biological functions of the Tail, Sac, and Duct related to silk production based on the function of genes and gene products. The Tail omics mostly revolved around the synthesis of organic acids, those in the Sac primarily focused on lipid production, and the Duct omics were related to ion exchange and chitin synthesis.

Previous research has found some elements discovered in the current study, but none have put the whole picture together in such a complete and comprehensive way.

More information: Wenbo Hu et al, A molecular atlas reveals the tri-sectional spinning mechanism of spider dragline silk, *Nature Communications* (2023). DOI: 10.1038/s41467-023-36545-6