



Smooth as Silk: Transcriptomic Study of Silkworms Hints at the Genetic Basis of Silk Production

Silkworms are both a staple of the textile industry and symbols of longstanding historical, economic and cultural significance in China, where the mulberry silkworm *Bombyx mori* (*B. mori*) was domesticated nearly 5,000 years ago. Today, China remains the world's largest producer and exporter of *B. mori* cocoons and raw silk, which are primarily used in textile manufacturing. However, breakthroughs in genomics, manufacturing, and material sciences have suggested that silk holds some astounding intrinsic properties that may push it to the forefront of next-generation biomaterials used in regenerative medical treatments, advanced textiles, or bio-security. Unfortunately, the silk produced by *B. mori* typically exhibits poor color retention and lower tensile strength, precluding many of these exciting new applications.

Scientists have suggested that non-mulberry silkworms, especially of the *Saturniidae* family, may possess the ability to produce different silks, some that overcome the inherent deficiencies of *B. mori* silk. For example, these non-mulberry silks seem to hold onto color better, have a higher tensile strength, and are in general more robust than the silk coming from their domesticated counterpart. Unsurprisingly, silk from these worms already commands a hefty price because these silkworms have yet to be domesticated, and have a limited cultured population. However, functional genomics has provided several novel techniques for isolating and then utilizing valuable genetic traits present in non-domesticated variants of plants and animals — such as those exhibited by these wild silkworms — via gene mining, genetic manipulation or breeding efforts. With enough data, researchers might even be able to mine the genes that make *Saturniidae* silk distinctive and then modify the genetics of *B. Mori*.

The greatest hurdle in utilizing the genetic resources of other non-mulberry silk worms is a severe lack of genomic and genetic data on *Saturniidae* worms and their silk production which are necessary to make gene mining and genetic manipulation possible. In light of this problem, researchers from Dr. WANG Wen's group at the Kunming Institute of Zoology, Chinese Academy of Sciences led a joint-effort with researchers from the CAS Institution of Zoology, Kunming University of Science and Technology, Shenyang Agricultural University, Southwest University and the US-Based John's Hopkins University School of Medicine

to compare the transcriptomes of six different *Saturniidae* silk worms using next-generation sequencing technology.

Over the course of the investigation, WANG's team produced a substantial amount of transcriptomic and genomic data, with several key findings into the gene resources underlying the silk glands of several wild silkworm species. In particular, the number of genes specific to *Saturniidae* involved in development processes may help explain why their silk glands seem to develop differently and take different shape than those of *B. mori*. WANG's team also found evidence that the acidity of the silk producing environment may have a strong effect on the eventual strength of the silk fibers, suggesting that silk with greater tensile strength may need a more neutral production environment. Their results also identified a potential genetic basis of active catalytic progress associated with stable cocoon coloration.

In effect, the results of WANG's investigation suggest that the disparate features of silk — coloration, retention, strength — are likely not only due to silk proteins, but also to the environment of silk assembly, and more specifically, that stable silk coloration exhibited by some *Saturniidae* silkworms may be attributable to active catalytic progress in pigmentation. Moreover, these findings may prove useful in further comparative genomic explorations on the silk production, evolution of silk producers, and most especially further mining for genes involved in different aspects of silk-quality, providing potentially valuable gene resources of saturniid silkworms that may facilitate future genetic improvement and modification of mulberry silkworms. (By Andrew Willden from the Kunming Institute of Zoology)

