

# Recent progress and prospects for advancing arachnid genomics

Jessica E Garb<sup>1</sup>, Prashant P Sharma<sup>2</sup> and Nadia A Ayoub<sup>3</sup>

Arachnids exhibit tremendous species richness and adaptations of biomedical, industrial, and agricultural importance. Yet genomic resources for arachnids are limited, with the first few spider and scorpion genomes becoming accessible in the last four years. We review key insights from these genome projects, and recommend additional genomes for sequencing, emphasizing taxa of greatest value to the scientific community. We suggest greater sampling of spiders whose genomes are understudied but hold important protein recipes for silk and venom production. We further recommend arachnid genomes to address significant evolutionary topics, including the phenotypic impact of genome duplications. A barrier to high-quality arachnid genomes are assemblies based solely on short-read data, which may be overcome by long-range sequencing and other emerging methods.

## Addresses

<sup>1</sup> Department of Biological Sciences, 198 Riverside Street, Olsen Hall 414, University of Massachusetts Lowell, Lowell, MA 01854, USA

<sup>2</sup> Department of Integrative Biology, 352 Birge Hall, 430 Lincoln Drive, University of Wisconsin-Madison, WI 53706, USA

<sup>3</sup> Department of Biology, 204 West Washington Street, Howe Hall, Washington and Lee University, Lexington, VA 24450, USA

Corresponding author: Garb, Jessica E ([Jessica\\_Garb@uml.edu](mailto:Jessica_Garb@uml.edu))

Current Opinion in Insect Science 2018, 25:51–57

This review comes from a themed issue on **Insect genomics**

Edited by **Christopher Childers, Anna Childers and Stephen Richards**

For a complete overview see the [Issue](#) and the [Editorial](#)

Available online 21st November 2017

<https://doi.org/10.1016/j.cois.2017.11.005>

2214-5745/© 2017 Published by Elsevier Inc.

## Introduction

Arachnids are an arthropod class containing over 130 000 described species in 12 extant orders including Araneae (spiders), Scorpiones (scorpions), Acariformes (mites), Parasitiformes (ticks), Opiliones (harvestmen) and Thelyphonida (vinegaroons) (Figure 1a; [1,2]). Despite their diversity and key phylogenetic position, the first arachnid genome became available as recently as 2008 and genomes have only become accessible for non-acarine (mite and tick) arachnids in the last four years [3–5,6<sup>••</sup>,7<sup>••</sup>,8].

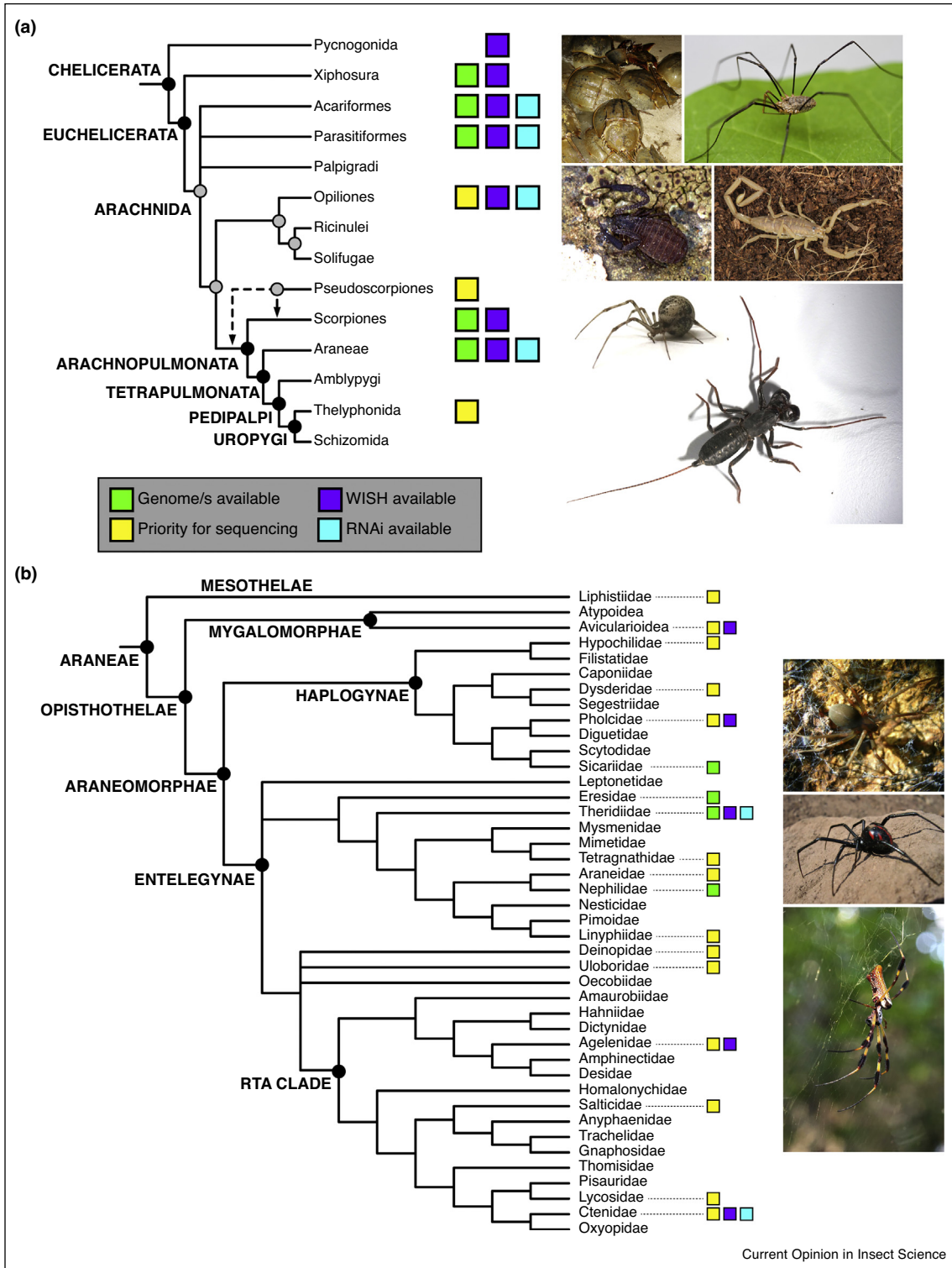
The earliest arachnid genome sequencing focused on members of the Acari that are important plant and animal pests, such as *Ixodes scapularis* (black legged tick, transmitter of Lyme disease), *Varroa destructor* (honeybee mite), *Tetranychus urticae* (red spider mite), *Rhipicephalus microplus* (southern cattle tick), and *Galendromus occidentalis* (western predatory mite) [9–11]. More recently, two scorpion and five spider genomes were deposited in NCBI (Table 1; [3–5,6<sup>••</sup>,7<sup>••</sup>]), several of which were produced as part of the i5k, an initiative to sequence 5000 medically and agriculturally important arthropods [4]. In this review we focus on significant findings uncovered by new spider and scorpion genomes and make recommendations for additional genomes urgently needed to address research questions of broadest scientific interest.

## Spider silk biology

A spider-specific trait of particular economic interest is silk production due to the impressive mechanical properties and biomimetic potential of these fibers. Although silk production has evolved multiple times in arthropods, it has reached greatest sophistication in spiders, which can make up to seven distinct types of silk fibers and glues [12]. These include dragline silks with toughness that exceeds Kevlar, prey capture threads that can reversibly extend 300% [12], and environmentally responsive silk glues [13]. Spider silk fibers are primarily composed of different members of a spider-specific family of structural proteins (spidroins) that dictate their divergent material properties. Genomes, in concert with transcriptomic and proteomic data, are an important resource to comprehensively characterize spidroins as well as other proteins composing silks. High quality sequences are required to produce silk-like synthetic fibers using genetic engineering [14,15].

A particular challenge to assembling spidroin gene sequences is that they encode long, highly repetitive proteins. Of the five available spider genomes, only one (the social velvet spider) successfully assembled multiple full-length spidroins using short-read sequences alone [5]. This was attributed to the low heterozygosity of this highly inbred species. A promising solution for assembling full-length silk genes from an outbred species was to use genomic information from spidroin gene fragments for long-distance PCR of full-length genes [6<sup>••</sup>]. These PCR products were subsequently sequenced completely with Pacific Biosciences (SMRT) methods [6<sup>••</sup>]. This approach remarkably recovered 20 full-length

Figure 1



Established and targeted genomic resources across arachnids. Colored icons indicate availability of genomes (green), whole mount in situ hybridization techniques for RNA expression assays (purple), and functional tools (blue). High-value targets for genomic sequencing are indicated with yellow icons. **(a)** Simplified phylogeny of Chelicerata from Sharma *et al.* [2] showing well resolved nodes (black circles) and nodes recovered only by slowly evolving genes (gray circles). Photographs clockwise from top left: the horseshoe crab *Limulus polyphemus* (photo: P. Funch); the harvestman *Phalangium opilio* (photo: arthropod i5k wiki); the scorpion *Centruroides sculpturatus* (photo: G. Giribet); the vinegaroon *Mastigoproctus giganteus* (photo: G. Giribet); the cobweb spider *Parasteatoda tepidariorum* (photo: E.V.W. Setton); and the pseudoscorpion

Download English Version:

<https://daneshyari.com/en/article/8878536>

Download Persian Version:

<https://daneshyari.com/article/8878536>

[Daneshyari.com](https://daneshyari.com)