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EDITED AND REVIEWED BY  
Matjaz Kuntner,  
National Institute of Biology (NIB), Slovenia

\*CORRESPONDENCE  
Sean J. Blamires  
✉ sean.blamires@uts.edu.au

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# Grand challenges in arachnid genetics and biomaterials

Sean J. Blamires<sup>1,2,3\*</sup>

<sup>1</sup>School of Biological, Earth and Environmental Sciences, The University of New South Wales, Sydney, NSW, Australia, <sup>2</sup>Mark Wainwright Analytical Centre, University of New South Wales, Sydney, NSW, Australia, <sup>3</sup>School of Mechanical and Mechatronic Engineering, University of Technology, Sydney, NSW, Australia

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## 1 Introduction

Arachnids, particularly spiders, flourish in abundance within most ecosystems (Blamires et al., 2007; Oxbrough and Ziesche, 2013; Henneken et al., 2022; Agnarsson, 2023; Fonseca-Ferreira et al., 2023). Arachnids such as spiders, scorpions and mites create and/or secrete a range of biomaterials, including silks, glues, adhesives, nano-fibres, venoms and other toxins, and chitin associated molecules used to form sensory systems, armour, body colouration/luminescence, and locomotion (Kuntner, 2022). Studies focusing on the evolutionary and ecological aspects of these kinds of arachnid secretory products have established that extended phenotypic features enable arachnids their immense niche flexibility (Agnarsson et al., 2010; Blamires et al., 2012a; Blamires and Tso, 2013; Blamires et al., 2017a; Blamires et al., 2017b; Lacava et al., 2018; Viera et al., 2019; Henneken et al., 2022; Kuntner, 2022). Nonetheless, the genetic features and the expression patterns implicit in facilitating this flexibility remain largely unexplored.

Spiders readily build webs and/or produce silks in the laboratory, either by laying their threads onto a collecting platform or by force reeling using anaesthesia and a spooling mechanism (Blamires et al., 2012a; Blamires et al., 2012b; Blamires et al., 2015; Blamires et al., 2016a; Benamú et al., 2017; Blamires et al., 2018; Lacava et al., 2018; Blamires, 2022). Studies thus exploiting this have established a strong body of background knowledge about spider web and silk structural and functional variability across nano to macro scales (Vollrath and Porter, 2006a; Kluge et al., 2008; Porter and Vollrath, 2009; Blamires, 2010; Blamires et al., 2016b; Blamires, 2022; Blamires et al., 2022).

The genetic expression patterns for certain components of specific silks have now been sequenced for selected species of spiders (Babb et al., 2017; Garb et al., 2019; Kono et al., 2019), and a database of genetic and molecular structures and bulk fibre functions for the major ampullate (dragline) silks of over 1000+ spider species has been compiled (Araçawa et al., 2022). Nevertheless, such a strong body of knowledge does not exist for the other arachnid biomaterials (but see López-Cabrera et al., 2020; Lozano-Pérez et al., 2020, and Machalowski et al., 2020 for detailed reviews on cuticular structural materials, scorpion fluorescent molecules, and mite silks).

The accumulated work on spider silk means we now understand the genetic mechanisms by which environmental factors can affect differential protein (in spiders these are called spidroins, a portmanteau of spider fibroins) expression and biomaterial production, and the intricate complexity of these on phenotypic and extended phenotypic expressions. Recent advancements in genetic and other experimental (see Sane and McHenry, 2009; Craig et al., 2019; Craig et al., 2022; Blamires et al., 2023a) and computational (e.g. Blamires and Sellers, 2019; Craig et al., 2020; von Reumont et al.,

2022) tools mean that we can form solid testable hypotheses to explain the evolutionary trajectories of spiders and other arachnids, and how the expressed biomaterial products, including various types of silks, glues, venoms, cuticular molecules and pigments, influence those trajectories (Piorkowski and Blackledge, 2017; von Reumont et al., 2022); Joel et al., 2023).

Here I review three identified grand challenges (there are certainly more; see Kuntner, 2022; Agnarsson, 2023) in arachnid genetics and biomaterials relevant for this specialty section of *Frontiers in Arachnid Science*. They being: (1) Arachnid whole genome, transcriptome, and proteome sequencing and annotating, (2) Research on arachnid biomaterials as inspiration for new synthetic materials, and (3) the production and use of synthetic products inspired by arachnid biomaterials. My review focuses on work on spider silk. This is purely because it is the field where my own research has focused. Other arachnid biomaterials and applications of arachnid genetics are nonetheless of equal importance, and papers on these subjects will certainly be included in this specialty section of *Frontiers in Arachnid Science*.

## 2 Grand challenge 1. arachnid whole genome, transcriptome, proteome sequencing and annotating

Modern genomics methodologies have combined with advanced bioinformatics and allowed us to understand much about the diversity and evolutionary trajectories of complex organisms (McGuire et al., 2020). There are many areas where these technologies have the potential to exert an enormous scientific impact in arachnid research. These include: (i) managing and integrating large genomic, transcriptomic, and proteomic datasets, (ii) interpreting the functional significance of unique or specialized arachnid genes and proteins, and (iii) applying genomic, transcriptomic, and proteomic methodologies to the study of arachnid structural biomaterials.

### 2.1 Management and integration of large genomic, transcriptomic, and proteomic datasets

Managing and integrating vast amounts of genomic, transcriptomic, and proteomic data, including trait specific or whole genome or transcriptome data (e.g. Sanggaard et al., 2014; Babb et al., 2017; Garb et al., 2019; Kono et al., 2019; Correa-Garhwal et al., 2020) from different arachnid species poses substantial challenges (Garb et al., 2018; Agnarsson, 2023). The sheer diversity of extant arachnid species unfortunately introduces multiple complexities into any attempts to standardize and normalize genomic data derived from a variety of sources (Garb et al., 2018; Peng et al., 2020; Arakawa et al., 2022). Proteomics analyses present additional complexities when working with arachnids, depending on the proteomes in question (Ayoub et al., 2013; Haney et al., 2014; Peng et al., 2020; Arakawa et al., 2021). Silk

proteomes, for example, are extremely challenging to sequence and assemble due to the similarities of protein architectures across silk types and the extreme length and highly repetitive nature of most of the silk proteins (Ayoub et al., 2007; Liu and Zhang, 2011; Vasanthavada et al., 2012; Vienneau-Hathaway et al., 2017; Garb et al., 2018; Arakawa et al., 2021; Frandsen et al., 2023).

The distinctive genomic variations that different arachnid species exhibit make it difficult to establish a common analytical framework. Moreover, the scale of data generated when utilizing multiple -omics approaches necessitate the use of extremely sophisticated bioinformatics, advanced computational tools (including deep learning algorithms and AI) and vast storage infrastructures (Lischer and Excoffier, 2012; Sanggaard et al., 2014; dos Santos-Pinto et al., 2016; Arakawa et al., 2022; Stephan et al., 2022). The lack of any comprehensive genomic reference material for many arachnid species adds additional layers of difficulty for conducting meaningful comparative analyses (Garb et al., 2018; Zhu et al., 2023). As such, the underlying genetic structure and its subsequent expression patterns had been overtly simplified for arachnid biomaterials, such as silk and venom (Haney et al., 2014; Sanggaard et al., 2014; Malay et al., 2022; Frandsen et al., 2023; Zhu et al., 2023), which has hampered efforts aimed at mapping the evolutionary trajectories of silk development in spiders, and the creation of new silk or venom-like materials using recombinant and/or cloning technologies (Rising et al., 2005; Humenik et al., 2011; Heidebrecht et al., 2015; Malay et al., 2022; Zhu et al., 2023).

### 2.2 Interpreting the functional significance of unique arachnid genes and proteins

Of the available full-length spider genomes assembled, only one, that for velvet spider spiders (Sanggaard et al., 2014), was assembled using short-read sequences alone. The others have all relied upon long-read sequencing to some extent (Babb et al., 2017; Schwager et al., 2017; Garb et al., 2019; Kono et al., 2019; Adams et al., 2023; Wen et al., 2023). While long-read sequencing provide additional information that short reads do not, such as the details of nucleotide point mutations (Amarasinghe et al., 2020), there are many formidable challenges faced when applying long-read sequencing procedures to map whole genomes, particularly those associated with arachnid silk or venom proteins (Sánchez-Herrero et al., 2019; Amarasinghe et al., 2020; Fan et al., 2021; Sheffer et al., 2021; Zhou et al., 2021; Zhu et al., 2023). In arachnid silkomics or venomomics the challenges are exacerbated by the extensive variation present in motif length, repeating patterns, and allele orders, particularly among silk and venom genes (Arakawa et al., 2002; Clarke et al., 2014; Haney et al., 2014; Rao et al., 2022). For instance, spiders and mites exhibit a remarkable diversity in their silk producing genes (Arakawa et al., 2021; Arakawa et al., 2022; Zhu et al., 2023). The intricate motif size and composition variations are thought to directly contribute to their unique mechanical properties, yet few studies have directly assessed silk and/or venom genomic and transcriptomic variance side-by-side within

the same spiders (Blamires et al., 2018; Collin et al., 2018; Arakawa et al., 2022).

### 2.3 Applying genomic, transcriptomic, and proteomic methodologies to the study of arachnid structural biomaterials

The intricate interplay in place between the environment and genetic and epigenetic regulation adds an additional layer of complexity (Shendure and Ji, 2008), thus making it challenging to isolate and comprehend the specific functions of individual genes (Pigliucci, 2007). The highly specialized nature of some specific adaptations of arachnids might further complicate the task of identifying any genetic-environment (G x E) interactions, especially when it comes to applying genomic, transcriptomic, and proteomic information to understand the functional evolution of secreted biomaterials. Ecosystem engineering and niche construction mechanisms might, additionally, induce ecological feedback loops that could drive the evolution of extremely diverse features (Laland et al., 1999; Beckerman et al., 2016). Research that tackles integrating arachnid genomics, transcriptomics, and mechanistic analyses is thus needed to unravel the nuanced relationships between the environment, genetics, genetic expression, and various extended phenotypic traits.

### 3 Grand challenge 2. researching arachnid biomaterials as inspiration for new synthetics

Most synthetic plastic materials used by humans today build up in landfill and seep into the terrestrial and aquatic environment at alarming rates. These pollutants flow freely into the food chains of all ecosystems on Earth, including those utilized by humans. We accordingly may consider ourselves in a plastic pollution crisis (De Falco et al., 2018). Examining the functionality of natural materials appears to be the best way forward for designing new manufacturing innovations (Wolff et al., 2017a; Blamires et al., 2020; Stuart-Fox et al., 2023). Nevertheless, the question remains: where can we find examples of high performing natural materials to inspire the creation of these new functional biomaterials (Stuart-Fox et al., 2023)?

Spiders produce multiple types of silk, each of which are renowned for their unique and impressive mechanical and other properties. Spider silks thus represent a valuable source of inspiration for new low energy, high performance, biomaterials (Vollrath and Porter, 2009; Abdalla et al., 2017; Numata, 2021). A particular set of spider silk proteins, the major ampullate spidroins, or MaSps, has received a significant amount of attention from researchers (Vollrath and Porter, 2006b; Vollrath and Porter, 2009; Humenik et al., 2011; Blamires et al., 2017a; Numata, 2021; Li et al., 2022). This is because the major ampullate, or dragline, silk fibres they compose into show strength and toughness measurements comparable to those of the most extremely high performing

synthetic fibres, including Kevlar and aramid fibres (Blamires et al., 2020). The properties of major ampullate silk come about as a consequence of the silk proteins stacking into crystalline pleated  $\beta$ -sheets interspersed with 'amorphous' proteins forming into random and  $\beta$ -coils,  $\alpha$ -helices, and  $3_{10}$  helical structures (Tokareva et al., 2014; Blamires et al., 2017a; Liu and Zhang, 2011; Htut et al., 2021; Kono et al., 2021). The crystalline region bestows the silk its strength while the amorphous proteins give it extensibility. It is these unique secondary structure arrangements that give major ampullate its immense toughness (Htut et al., 2021; Blamires, 2022). This model is supported by findings that when spiders are placed on different diets, variations in crystalline and amorphous region structures correlate strongly with variations in bulk fibre properties (Craig et al., 2000; Tso et al., 2007; Blamires and Tso, 2013; Blamires et al., 2015; Blamires et al., 2017a; Blamires et al., 2018). Nevertheless, when scaled down to the atomistic level, no such correlations hold (Van Beek et al., 2002; Romer and Scheibel, 2008; Koebley et al., 2017; Blamires et al., 2022). We do not know why there is a disjunction between the nanoscale and bulk fibre properties (Blamires et al., 2022; Craig et al., 2022). More research is clearly needed to better understand how silk properties are induced across the different scales.

### 4 Grand challenge 3. production and use of arachnid inspired synthetic products

The plastic pollution crisis and other environmental sustainability issues have prompted researchers to seek inspiration from the natural world for the development of new materials for a diversity of useful properties (Lefèvre and Auger, 2016; Wolff et al., 2017a; Stuart-Fox et al., 2023). Spider silk, due to its impressive strength, toughness, and durability, and its synthesis from water and proteins, is one of the most popular natural materials being touted as an inspiration in the development of plastic replacements, and other environmentally friendly manufacturing applications (Blamires, 2022). There have recently been some significant advances in this field. For instance, a spider silk inspired polymeric amyloid fibre has been developed that exhibits strength and resilience on a par with that of spider silk (Li et al., 2021), thus presenting opportunities for developing new protective aerospace and military clothing, medical implants, environmental protection, and advanced electronics.

Supercontraction is a unique property of major ampullate silk, whereby the silk shrinks in length by up to 60% when wetted (Guinea et al., 2005; Blackledge et al., 2009; Blamires et al., 2012a; Madurga et al., 2016; Blamires et al., 2023b). This property is usually considered undesirable industrially and there is some expectation that advances in protein engineering will find a way to negate the property (Guinea et al., 2005; Meyer et al., 2014; Shi et al., 2014; Madurga et al., 2016). Nevertheless, harnessing it may be useful in some instances. For example, a spider silk inspired smart switch that can be incorporated into wearable products is being designed to utilize both supercontraction and the biocompatibility phenomena

of spider silk (Blamires et al., 2020; Flanagan et al., 2023). Finding more innovative ways to explore, minimize, or exploit the entire performance space occupied by spider silks accordingly represents a significant and industrially important grand challenge in arachnid biomaterials science (Agnarsson et al., 2009; Wolff et al., 2017a; Blamires et al., 2020; Blamires, 2022).

Other areas where arachnids are increasingly being seen as an inspiration in the development of novel materials includes examining spider leg movement patterns for inspiration in the development of moving robot parts (Landkammer et al., 2016), likewise the hair-like structures of spider and harvestmen feet are inspiring new adhesives for use in climbing robots, sensors, space exploration, and footwear (Wolff et al., 2014; Wolff et al., 2016; Wolff et al., 2017b; Borijindakul et al., 2021), and scorpion fluorescence molecules are inspiring the design and synthesis of molecular switches, chelates, and other therapeutic molecules (Samundeeswari et al., 2021).

## 4.1 Recombinant technologies and synthetic spider silk

The production of spider silk using recombinant technologies offers a sustainable alternative to traditional silk harvesting and addresses some ethical and environmental concerns associated with silk production (Karthik and Rathinamoorthy, 2017; Edlund et al., 2018). It has made some significant technological inroads of late, with full length MaSp2 proteins (other MaSp proteins are proving difficult for hosts to handle; Heidebrecht et al., 2015; Cao et al., 2017; Malay et al., 2022) being successfully expressed within a range of host organisms, including different bacteria, yeast, and tobacco plants (Ramezaniaghdam et al., 2022). This work shows that there is potential for the scalable and cost-effective production of synthetic spider silks in the very near future. Spinning the recombinant proteins into fibres that perform as well as spider silk fibres is nonetheless still proving to be significantly difficult. Some recent advances in microfluidic wet and dry spinning methodologies, such as computer-aided wet spinning, rotary microfluidic wet spinning, and channel-based wet spinning techniques, show excellent potential for creating bespoke fibrous materials from recombinant proteins (Lefèvre and Auger, 2016; Koeppel and Holland, 2017; Rohani Shirvan et al., 2022). With the continuing advancement of such technologies, it is highly likely that arachnids and their biomaterial products will inspire the production of a wide array of new functional materials (Koeppel and Holland, 2017).

## 5 Conclusion

I outlined herein three identified grand challenges in arachnid genetics and biomaterials: (1) Arachnid whole genome, transcriptome, and proteome sequencing and annotating, (2) research on arachnid biomaterials as inspiration for new synthetic

materials, and (3) the production and use of synthetic products inspired by arachnid biomaterials. A theme prevalent across each of these challenges is they involve managing and integrating large datasets, and interpreting the functional significance of unique arachnid genes and proteins, and their products. Solving issues around scaling up functionality when creating novel materials presents an ongoing challenge, as does exploring all the potential practical applications of arachnid biomaterial inspired synthetic materials. I touched on recent advances in arachnid genetics and experimental tools, as well as computational methodologies, emphasizing the exciting potential for developing solid, testable hypotheses to explain the evolutionary trajectories of spiders and other arachnids. I reviewed the abovementioned challenges through the lens of spider silk research, but this is not by any means the only research field in which these three challenges apply. Only with truly interdisciplinary research (e.g. biologists working intently with engineers and vice versa) will it be possible to adequately address these challenges and unlock the full potential of arachnid-inspired materials.

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SB: Conceptualization, Investigation, Project administration, Resources, Validation, Visualization, Writing – original draft, Writing – review & editing.

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