

## Example projects supported by the BAS Small Grants Scheme

### Leah Fitzpatrick – Expanding the arsenal: investigating Latrodectinae phylogeny and venom, with a focus on *Steatoda nobilis*.

Arguably the most popular species targetted by British newspapers is the Noble false widow spider (*Steatoda nobilis*), an imported species that has successfully thrived in the UK since the 1870s. One of the larger Theridiidae spiders (females can reach a body length of 13 mm), they are a synanthropic species that can look superficially similar to the notorious black widow (*Latrodectus*) spiders. Previous phylogenetic and venom transcriptomic work has suggested a close relationship between *Steatoda* and *Latrodectus* but a small sample size has limited a decisive conclusion, placing both genera (together with *Asagena* and *Crustulina*) in the subfamily Latrodectinae. It is not only the appearance of *S. nobilis* that has drawn much attention from the public; their venom has been noted to be potentially of medical significant\*, with recent documented cases of envenomation from the UK, Ireland and Chile. Symptoms are generally mild to moderate ranging from swelling around the entry wound to vomiting and abdominal cramps but on an island with few medically significant animals (let alone spiders), it can be difficult to explain the minimal risk these spiders represent to the public.

There are undeniable gaps in our knowledge of these two groups, with a need to provide more data and analysis to improve our understanding of the link between them. With this in mind, I approached BAS to seek a grant to help fund my MSc, which examined the relationship between *Steatoda* and *Latrodectus*, with a particular focus on *S. nobilis*. The Society graciously provided funding, which allowed me to:

1. Sequence three genes from 50 specimens representing over 20 species of Latrodectinae in order to build phylogenetic trees using both Bayesian and Maximum Likelihood methods.
2. Analyse the biogeography of this species, utilising the specimens collected for aim 1 above.
3. Bring 70 *S. nobilis* specimens to Galway to extract their venom for further analysis.
4. Investigate the position and placement of the venom system within selected Latrodectinae species, creating micro-computerized tomography (mCT) scanned 3D models to be used for public outreach as well as future research.

The final phylogenetic tree using both analytical methods included eight species represented by 22 specimens with a wide geographical distribution - it includes several species that not been used in previous phylogenies. The final trees offers a fascinating interpretation as a result of the placement of *Latrodectus* within *Steatoda*, raising questions about who is the real false widow. A 3D model of *Steatoda grossa* was produced, with the venom system highlighted within the scan, a first ever for Araneomorph spiders.

Unfortunately, while the venom from over 70 *S. nobilis* specimens was extracted in Galway, the results where unusable because of the quality of venom produced. In addition, many sequences had to be excluded from the final analysis due to either poor quality or contamination with fungus from the cuticle. However, the final results still produced a fascinating insight into the evolution of these animals and provided an interesting perspective on how *S. nobilis* has spread across Europe. With my supervisor, Dr. Michel Dugon, I am hoping to revisit this work post-COVID to help improve on these results.

A full account of this work will be published in the BAS Newsletter



A mCT scan of *Steatoda grossa*, with 3D venom canals and glands highlighted in purple

\*Medically significant is defined here as ‘requiring attention from a medical professional’. This does not imply that envenomation from *S.nobilis* is inherently life threatening nor that every bite will require medical attention but rather envenomation does have documented mild to moderate medical symptoms associated with it.

### **Geoff Oxford – Is *Eratigena atrica* (Agelenidae) one species or three?**

In 2013, it was suggested that the three ‘traditional’ species of large house spiders *Eratigena* (previously *Tegenaria*) *saeva*, *E. duellica* and *E. atrica* recognized in Britain were really one, albeit variable, species *E. atrica*. This was based on both molecular characterisation and morphological measurements made largely on continental European specimens where, it was claimed, distinctions could not be made. To investigate the possibility that the British populations differed from those on the continent, Angelo Bolzern and I examined the morphology of museum specimens from Britain, the continent and North America and sequenced mitochondrial DNA markers from a total of 50 newly collected British individuals of all three species. A BAS Small Grant in 2016/17 was invaluable in supporting the fieldwork involved in this study.

The results clearly showed that across the entire global ranges of the three species, morphological distinctions remained, demonstrating that there are indeed three species rather than one. The confusion over this matter arose because the original authors possibly did not appreciate fully the importance of viewing the sexual structures from a precise and

constant angle, and the fact that limited past and ongoing hybridisation between two of the species has confused the distributions of certain mitochondrial DNA markers. The latter point illustrates a growing realization that DNA 'barcoding' is sometimes not a substitute for traditional morphological examination in the determination of species.

For a full report of this project see:

Oxford, G. S. & Bolzern, A. 2018. Molecules vs. morphology – is *Eratigena atrica* (Araneae: Agelenidae) one species or three? *Arachnology* **17**: 337-357.

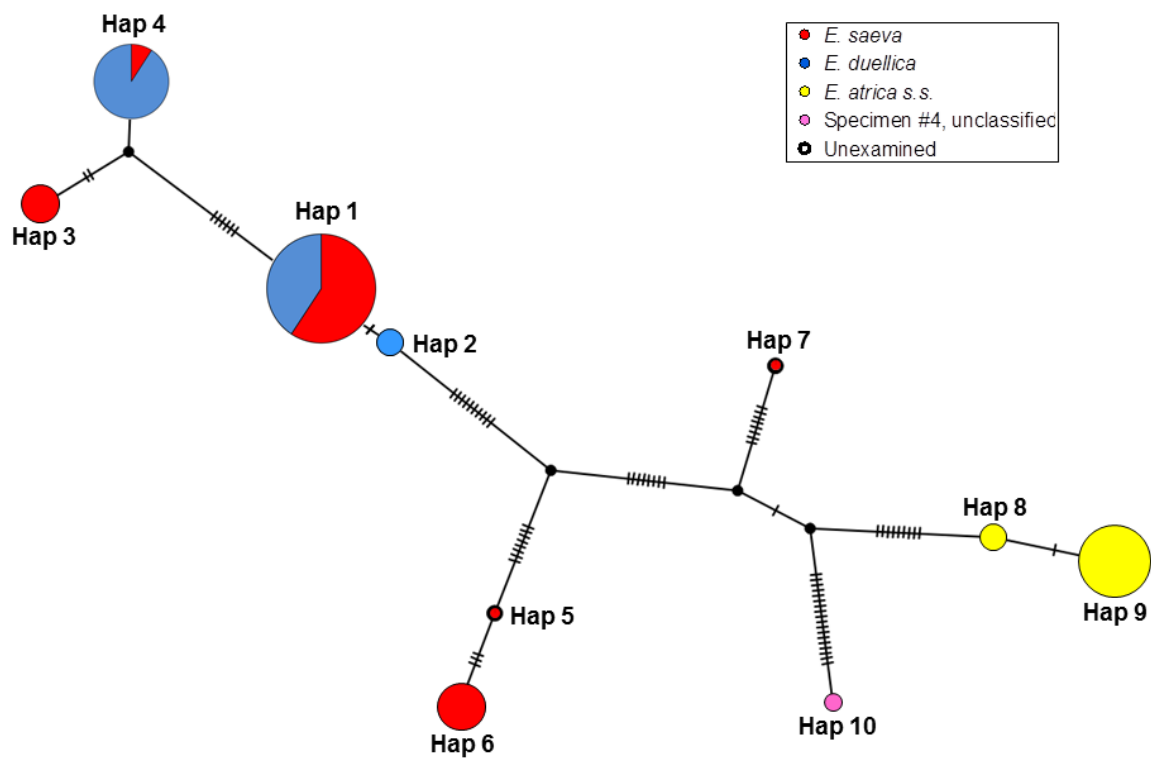


Diagram showing the sharing of mitochondrial DNA sequences Hap 1 and Hap 4 between *Eratigena saeva* (red) and *E. duellica* (blue) in British populations.