Genetic relations within and among Dolomedes aquatic spiders Marija Vugdelić

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Abstract

The fen raft spider *Dolomedes plantarius* (Clerk) is a species with a Palaearctic distribution, which has nevertheless experienced population declines across its range. Consequently, it has been Red listed in many countries, and has been a subject of an ongoing conservation programme in the UK.

In the research described in this thesis, molecular markers were used to investigate several aspects of *D. plantarius* ecology and evolution. Mitochondrial gene sequences and nuclear microsatellites were used to assess the genetic status of several *D. plantarius* populations from across Europe, and to infer the extent to which diversity has been affected by recent population dynamics and more ancient, historical processes. Analysis of mitochondrial genes revealed the maintenance of ancestral haplotypes, a degree of population divergence, but a weak spatial structure in haplotype distribution, which was only significant at a broad geographic scale. Nuclear microsatellites have similarly revealed allele sharing amongst populations and a degree of population divergence, although a lack of straightforward geographic affiliation of particular alleles. It is argued that these spatial patterns of genetic diversity have been created by the recent population dynamics, although these may be partly obscured by processes that took place during historic range expansions and contractions associated with glaciations.

Paternity analysis of a limited sample of *D. plantarius* progeny by means of microsatellite genotyping, has found evidence of multiple mating by females, and suggests a possible cryptic female choice.

A congeneric species with a similar distribution, *D. fimbriatus*, has also been subject to genetic analysis using mitochondrial markers. The analyses revealed that this species shows different population genetic patterns to that of *D. plantarius*. This is attributed primarily to the ecological differences between the two species. However, it is also suggested that the difference could be due to the selective sweep driven by infection with maternally inherited bacterial endosymbiont *Wolbachia*, whose presence has been detected in *D. fimbriatus* by the means of PCR assays.

Finally, a molecular phylogenetic analysis of eleven *Dolomedes* species, including two European and nine East Asian species is constructed for the first time, and it strongly suggests an Asian origin of European *Dolomedes*.

It is anticipated that inferences regarding *D. plantarius* biology obtained through this research can be used to inform the ongoing conservation programme of this species. In addition, it is believed that this research contributes to the understanding of the colonisation of Europe by semi-aquatic species, and extends the knowledge of molecular ecology and evolution of the genus *Dolomedes* and spiders in general.