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Species boundaries of *Pardosa concinna* and *P. lapponica* (Araneae: Lycosidae) in the northern Nearctic: morphology and DNA barcodes

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Abstract

The Holarctic *Pardosa lapponica* (Thorell, 1872) and the Nearctic *P. concinna* (Thorell, 1877) are the only North American members of the *Pardosa lapponica* species-group. The morphological similarity between the two species raises the question of whether or not they should be treated as separate species. To examine the boundary between *P. lapponica* and *P. concinna*, morphological and genetic variation within and between the species was analysed. Copulatory organ characters of Nearctic specimens were analysed to determine if additional diagnostic characters exist, and the mtDNA COI region was sequenced to look for species-specific variation. Morphometric analysis of copulatory characters in females (e.g. length of median septum) and males (e.g. embolus length) of both species did not reveal diagnostic characters other than the terminal apophysis. No species-specific genetic patterns were found between the two species. The interspecific similarities in morphology and low genetic divergence between Nearctic specimens of *P. lapponica* and *P. concinna* contrasts with high genetic divergence between Palearctic and Nearctic specimens of *P. lapponica*. The results suggest a comprehensive taxonomic revision is necessary for the *P. lapponica* species-group.

Key words: morphometrics, COI, haplotype, spiders, arctic

Introduction

The genus *Pardosa* C.L. Koch, 1847 (Lycosidae) contains 46 species in North America, which have been arranged into 13 informal species-groups (Dondale & Redner 1990). Assignment to a species-group was based on morphological similarities in both noncopulatory and copulatory characters (Dondale & Redner 1990). Unfortunately, the morphological conservatism that allows species to be placed in these informal groups can also make identification difficult.

One such challenging group is the *Pardosa lapponica* species-group, which contains seven species (Zyuzin 1985). It is represented in North America by two species: the Holarctic *Pardosa lapponica* (Thorell, 1872), originally described from Lapland, and the Nearctic *P. concinna* (Thorell, 1877). *Pardosa concinna* was described by Thorell (1877) based on a single female specimen from Colorado, USA. Bishop (1949) described the first Nearctic female specimen of what is now recognised as *P. lapponica,* as *P. harperi* Bishop, 1949. Dondale and Redner (1986) synonymized *P. harperi* with *P. lapponica*.

Dondale and Redner (1986) treated *P. concinna* and *P. lapponica*, as separate species based on variation in the terminal apophysis of the male pedipalp. While the length of the median septum in females was suggestive of separate species, Dondale and Redner (1986) considered the terminal apophysis to be the only reliable diagnostic character. The terminal apophysis is often a key character for species delimitation in *Pardosa* (Zyuzin 1985), but variation may not be species-specific as once assumed.

Intraspecific variation in spider genitalia has not been well studied, owing to a long standing assumption of fast-paced genitalic coevolution (Huber 2004). Influenced by the lock-&-key hypothesis, many species were split based on any morphological variation observed in the genitalia as the variation was assumed to represent species boundaries. Variation within a single species, due to ontogenetic changes or phenotypic plasticity, was dismissed in the past (Huber 2004), and is only recently being recognised (Bennett 2006). This bias against intraspecific variation may have led to over-splitting of species.

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The removal of errors did not result in a barcode gap among all species, which means the divergence among sequences should not be the only statistic reported. In cases where no barcode gap exists, but separate species are suspected, fixed nucleotide substitutions have been used to show diagnostic differences between species (Hendrich *et al.* 2010). Interspecific variation between the Australian Dytiscidae (Coleoptera) species *Neobidessodes samkrisi* Hendrich and Balke, 2009 and *N. flavosignatus* (Zimmermann, 1922) was as low as 0.85% (Hendrich *et al.* 2010). Despite the low interspecific variation, there were five fixed nucleotide substitutions that Hendrich *et al.* (2010) used as diagnostic characters.

Examination of the barcodes of *Pardosa* species for fixed nucleotide differences agrees with the pattern found by Hendrich *et al.* (2010). Species-specific substitutions were present among morphologically distinct species that did not conform to the 2% barcode gap (Table 3). The Palearctic *P. lapponica* specimens were divergent from both the *P. concinna* and Nearctic *P. lapponica* specimens in both pairwise distance and fixed substitutions (Table 3). In contrast, neither a barcode gap nor fixed substitutions were observed between the Nearctic *P. lapponica* and *P. concinna* specimens.

The lack of divergence between the Nearctic specimens is evident in the close relationship among haplotypes from the two species, as well as the lack of species-specific clustering in the haplotype network that would be expected if the species were diversifying separately (Řezáč *et al.* 2008; Walker & Avise 1998). Shared haplotypes can be a sign of introgression between separate species, but the pattern of haplotype distribution does not support multiple species experiencing introgression. The shared haplotypes are found at multiple localities that are not in a suture zone between the ranges of the two species (Avise 2000) and are not in contrast with pronounced species-specific clustering (Lu *et al.* 2001).

The genetic divergence between Palearctic and Nearctic *P. lapponica* specimens, as well as the potential size difference and morphological variation in the median apophysis, suggests that *P. lapponica* may not, in fact, be a Holarctic species and that the synonymization of the Nearctic *P. harperi* (Bishop) with the Palearctic *P. lapponica* may not be justified. Considering the low morphological and genetic divergence between the Nearctic "*P. lapponica*" and *P. concinna* specimens, there may be justification for synonymizing *P. harperi* with *P. concinna* instead, although genetic study of specimens from the type locality of both species would be required. The *P. lapponica* species-group would benefit from taxonomic revision using morphological and molecular characters of all species. There may be undocumented morphological variations between the Palearctic and Nearctic "*P. lapponica*" specimens that would further support a species split. Examination of *P. concinna* specimens from the southern parts of its Nearctic range would determine whether these populations are conspecific with those in northern North America.

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