**Manuscript Title:** Ornamentation diversified faster than eco-morphology across Nearctic Dragonflies

**Year:** 2022

**File Name:** lib.spp.6sd.csv

**Description:** Species’ traits of Nearctic Libelluloidea dragonflies that were used in a supplemental analysis (see below) to compare the diversification of male wing melanization vs adult body length and relative wing size. Species in this analysis are those that are present in a pruned, maximum credibility phylogeny that was originally generated by Letsch et al. 2016 (Molecular Ecology). The pruned version of the phylogeny used in the analyses for these data has the file name ‘lib.na.phylo.tre’. The R scripts that use this dataset are named “main text annotated code.R”.

**Rows:** 72, excluding the header. Each row corresponds to a species present in the phylogeny lib.na.phylo.tre

**Columns:** 7. *log.size, log.size.se, log.rw, log.rw.se, log.color, log.col.se, binom*

*log.size*: ln-transformed adult body length. Taken as the mid-point of the total length (mm) listed in Paulson’s comprehensive field guides of North American odonates (2009, 2012)

*log.size.se*: standard error of the ln-transformed adult body length metric. Unlike in the analysis in the main text, this estimation assumed the phenotypic range listed in Paulson 2009, 2012 was 6 standard deviations across and was estimated using 15 individuals. See manuscript for more details

*log.rw*: ln-transformed relative wing size. Calculated by dividing the mid-point of the ln-transformed wing length (mm) by the ln-transformed total length (mm) listed in Paulson’s comprehensive field guides of North American odonates (2009, 2012)

*log.rw.se*: standard error of the ln-transformed relative wing size metric metric. Unlike in the analysis in the main text, this estimation assumed the phenotypic range listed in Paulson 2009, 2012 was 6 standard deviations across and was estimated using 15 individuals. See manuscript for more details

*log.color:* ln-transformed male wing melanization. See methods in main text for how this data was generated.

*log.col.se:* standard error of ln-transformed male wing melanization. Estimated directly from each species variability.

*binom:* Name of the dragonfly species