Supplementary Tables

Supplementary Table S1. Statistics for the spider species used in this study.

Supplementary Table S2. Significantly enriched KEGG pathways and GO biological processes for 20 positively selected genes ($q < 0.05$) in group-living spiders. Categories associated with nutrient metabolism are in orange, and categories associated with autophagy are in blue.

Supplementary Table S3. Significantly enriched KEGG pathways and GO biological processes for 54 convergent genes ($q < 0.05$) in group-living spiders. Categories associated with nutrient metabolism are in orange, and categories associated with autophagy are in blue.

Supplementary Table S4. Classification of autophagy, nutrition, nerve, and immunity modules of "group-lving dataset"

Supplementary Table S5. Significantly enriched KEGG pathways and GO biological processes for 73 accelerated genes in group-living spiders. Categories associated with nutrient metabolism are in orange.

Supplementary Table S6. Fisher's Exact Test of accelerated/decelerated terms and four modules.

Supplementary Table S7. Significantly enriched KEGG pathways and GO biological processes for 86 decelerated genes in group-living spiders. Categories associated with autophagy are in blue.

Supplementary Table S8. Fisher's Exact Test of accelerated/decelerated genes and four modules.

Supplementary Table S9. Classification of autophagy, nutrition, nerve, and immunity modules of "route dataset"

Supplementary Table S10. Result of relative evolutionary rates analysis in "route dataset". Categories associated with nutrient metabolism are in orange, and categories associated with autophagy are in blue.

Supplementary Tables S1-S10 are listed as a separate file due to their large size.