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Divergent evolution of arrested development in the dauer stage of *Caenorhabditis elegans* and the infective stage of *Heterodera glycines*.

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BACKGROUND: The soybean cyst nematode *Heterodera glycines* is the most important parasite in soybean production worldwide. A comprehensive analysis of large-scale gene expression changes throughout the development of plant-parasitic nematodes has been lacking to date. **RESULTS:** We report an extensive genomic analysis of *H. glycines*, beginning with the generation of 20,100 expressed sequence tags (ESTs). In-depth analysis of these ESTs plus approximately 1,900 previously published sequences predicted 6,860 unique *H. glycines* genes and allowed a classification by function using InterProScan. Expression profiling of all 6,860 genes throughout the *H. glycines* life cycle was undertaken using the Affymetrix Soybean Genome Array GeneChip. Our data sets and results represent a comprehensive resource for molecular studies of *H. glycines*. Demonstrating the power of this resource, we were able to address whether arrested development in the *Caenorhabditis elegans* dauer larva and the *H. glycines* infective second-stage juvenile (J2) exhibits shared gene expression profiles. We determined that the gene expression profiles associated with the *C. elegans* dauer pathway are not uniformly conserved in *H. glycines* and that the expression profiles of genes for metabolic enzymes of *C. elegans* dauer larvae and *H. glycines* infective J2 are dissimilar. **CONCLUSION:** Our results indicate that hallmark gene expression patterns and metabolism features are not shared in the developmentally arrested life stages of *C. elegans* and *H. glycines*, suggesting that developmental arrest in these two nematode species has undergone more divergent evolution than previously thought and pointing to the need for detailed genomic analyses of individual parasite species.

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