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The evolutionary expansion of nematode-specific glycine-rich secreted peptides

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We analyzed the glycine-rich secreted peptides (GRSPs) of 10 species genomes: *Homo sapiens*, *Dani rerio*, *Drosophila melanogaster*, *Caenorhabditis elegans*, *Caenorhabditis briggsae*, *Arabidopsis thaliana*, *Monosiga brevicollis*, *Saccharomyces cerevisiae*, *Dictyostelium discoideum*, and *Guillardia theta*. The number of Grsps in each genome was 4, 6, 53, 93, 78, 52, 0, 0, 5 and 0, respectively. Interestingly, there were fewer Grsps in human genome than in *D. discoideum* genome, despite the greater complexity of humans. The two nematode species *C. elegans* and *C. briggsae* possessed the highest abundance of Grsps, of which 98.7% were orthologous. Mapping these Grsps strengthened clustering and illustrated the clear co-linearity between the chromosomes of the two nematodes. In particular, most of Grsps were found on chromosome V: 44 of 93 *C. elegans* and 41 of 78 *C. briggsae*. A comparative analysis of orthologous Grsps from other species resulted in the successful annotation of 17 *C. elegans* Grsps with DAVID and 21 *C. elegans* and 3 *C. briggsae* Grsps with Blast2Go. This observation highlighted the nematode-specific expansion of Grsps originating from tandem duplications during ecological adaptation of the two nematodes. The phenomenon goes against the general rule that gene families also experience evolutionary expansion in abundance in increasingly complex species.

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