

## **Abstract:**

The genome of *Caenorhabditis elegans* encodes more than 280 nuclear hormone receptors (NHRs) in contrast to the 48 NHRs in humans and 18 NHRs in *Drosophila*. The majority of the *C. elegans* NHRs are categorized as supplementary nuclear receptors (supnrs) that evolved by successive duplications of a single ancestral gene. The evolutionary pressures that lead to the expansion of NHRs in nematodes, as well as the function of the majority of supnrs, are not known. Here, we have studied the expression of seven genes organized in a cluster on chromosome V: *nhr-206*, *nhr-208*, *nhr-207*, *nhr-209*, *nhr-154*, *nhr-153* and *nhr-136*.

Reverse transcription-quantitative PCR and analyses using transgenic lines carrying GFP fusion genes with their putative promoters revealed that all seven genes of this cluster are expressed and five have partially overlapping expression patterns including in the pharynx, intestine, certain neurons, the anal sphincter muscle, and male specific cells.

Four genes in this cluster are conserved between *C. elegans* and *C. briggsae* whereas three genes are present only in *C. elegans*, the apparent result of a relatively recent expansion. Interestingly, we find that a subset of the conserved and non-conserved genes in this cluster respond transcriptionally to fasting in tissue-specific patterns. Our results reveal the diversification of the temporal, spatial, and metabolic gene expression patterns coupled with evolutionary drift within supnr family members.