

Processes such as breathing, locomotion, and ingestion require a well-connected network of cells that are in turn regulated by a network of genes. The nematode *C. elegans* allows us to integrate the study of the gene and cellular networks associated with locomotion. The cellular network that we are investigating involves a cross-inhibitory network composed of the DD and VD motor neurons (collectively termed the D motor neurons (mns)) and the muscles they innervate. The D mns contribute to the animal's sinuous pattern of locomotion by causing muscle relaxation. The gene network includes two transcription factors UNC-30 and ALR-1 and a large number of genes involved in the anatomical and physiological characteristics of the D mns. We have used two approaches to analyze the relationships between the gene and cellular networks: bioinformatics and genetics. In the bioinformatics approach, potential transcription factor binding sites in the upstream regulatory region of a neuropeptide gene in the D mns, *flp-11*, were analyzed using software, such as MUSSA and TESS. The two candidates that emerged were then analyzed using a genetic approach. We reasoned that if these two transcription factors regulated *flp-11*, then the pattern of a *pflp-11::gfp* reporter would be altered in a mutant background. *pflp-11::gfp* was crossed in an *alr-1* and an *unc-30* mutant backgrounds. The normal *pflp-11::gfp* pattern expression was observed in an *unc-30* mutant background, but not in an *alr-1* mutant background. In future studies, we will continue to bind these two approaches to study the relationship between gene and cellular networks.