transcription is not yet known. To determine the role of Mediator in development, we analyzed the phenotypes caused by RNA interference. RNA interference assays showed that Med-6, Med-7, and Med-10 are required for the expression of developmentally regulated genes, but are dispensable for expression of ubiquitously expressed genes · tested in this study. Therefore, the gene-specific function of Mediator as an integrator of transcriptional regulatory signals is evolutionarily conserved and is essential for *C. elegans* development. We have characterized the biological functions of the *C. elegans* gene *med-6*, which is the homolog of the yeast mediator med-6. We first identified a genetic mutation in the *med-6* gene by comparing genetic and physical maps and determining the molecular lesion. Next, we demonstrated that *med-6* plays an important role in development by regulating the transcription of genes in several evolutionarily conserved signaling pathways. One pathway with which we found *med-6* to be associated is the Ras pathway, as is assayed in the hermaphrodite vulval development system. We also found that med-6 is involved in a transcription factor cascade and the Wnt pathway which work together to mediate male ray development. Thus, *med-6* mediates regulated transcription of genes in various metazoan developmental signaling pathways. Since Med-6 is universally conserved including in yeast, and the mediator-related proteins that function in vulval and male ray development are metazoan-specific, our results imply the role of *med-6* as a point of convergence where signals transmitted through metazoan-specific mediator-related proteins meet. In addition, RNAi experiments in *rde-1* background showed that maternal and zygotic *med-6* activities have distinct roles in development.

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Ethanol Sensitivity Genes in the Nematode *Caenorhabditis elegans*

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The mechanisms and sites of action of volatile anesthetics and ethanol are not fully understood. In the hope of understanding the mechanisms of ethanol, we first identified genes that control sensitivity to ethanol and anesthetics in the invertebrate system Caenorhabditis elegans. We identified 24 mutations that confer ethanol resistance either by EMS mutagenesis or transposon insertion mutagenesis. The genes are being cloned by positional cloning and analyses on the mutations are under way. In the next experiments, we used the cDNA microarray to identify genes that are either up-regulated or down-regulated by exposure of the animals to 7 % ethanol at various times. Several gene families including heat-shock protein family, glutamate receptor family, and gene families with unknown function, were up-regulated by ethanol after 6 hours. Also, there are gene families down-regulated. We are now examining these candidate ethanol-affected genes by northen analysis and in situ hybridization analysis. To establish an experimental system by which one can study Fetal Alcohol Syndrome using the nematode, we examined the effect of ethanol on embryogenesis. After incubating adult hermaphrodites in 7% EtOH for 12 hours, we observed egg-laying defects and abnormal embryogenesis. Based on this preliminary data, we will investigate and characterize the ethanol sensitivity genes involved in embryogenesis. In summary, we identified ethanol resistance genes by EMS or transposon mutagenesis; we identified genes whose transcription levels are altered by ethanol in the microarray analysis; and we established an experimental model system to study Fetal Alcohol Syndrome.