factors are regulated and how they pattern specific cell types in both wild-type and tpl-1 mutant embryos.

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Program/Abstract # 6
**Molecular dissection of germ cell development in the planarian *Schmidtea mediterranea***

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Freshwater planarians appear to utilize inductive signals to specify their germ cell lineage: germ cells are believed to form post-embryonically from the pluripotent somatic stem cells, known as neoblasts. Previously, we identified a planarian homolog of *nanos* (*Smed-nanos*) and demonstrated by RNA interference (RNAi) that this gene is required for the development, maintenance, and regeneration of planarian germ cells. We have performed microarray analyses to compare gene expression profiles between planarians with early germ cells and those without them. We identified ~300 genes that are significantly down-regulated in animals lacking early germ cells. This data set contains genes implicated in germ cell development in other organisms, conserved genes not yet reported to have germ cell-related functions, and novel genes. Analysis using putative domain functions (Clusters of Orthologous Groups) suggested diverse molecular functions, including cytoskeletal components, metabolism, RNA processing and modification, transcription, as well as signal transduction. Top hits have been validated by in situ hybridization. Functional analyses of these genes via RNA interference are being carried out. Thus far, we have identified several genes that, when knocked down by RNAi, cause various defects in germ cell development, including: impaired testes development; loss of spermatogonial stem cells; meiotic failure; and defects in sperm elongation. This work will contribute to our knowledge of conserved regulators of germ cell differentiation.

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Program/Abstract # 7
**Development rooted in interwoven networks**

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Specification and maintenance of cell identity are central processes of development. In an effort to understand the regulatory networks that control cell identity, we have profiled all cell types and developmental stages within a single organ, the *Arabidopsis* root. To acquire global expression profiles we developed technology (Clusters of Orthologous Groups) suggested diverse molecular functions, including cytoskeletal components, metabolism, RNA processing and modification, transcription, as well as signal transduction. Top hits have been validated by in situ hybridization. Functional analyses of these genes via RNA interference are being carried out. Thus far, we have identified several genes that, when knocked down by RNAi, cause various defects in germ cell development, including: impaired testes development; loss of spermatogonial stem cells; meiotic failure; and defects in sperm elongation. This work will contribute to our knowledge of conserved regulators of germ cell differentiation.

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Program/Abstract # 8
**Cdx2 and FGF cooperate to specify brachial and thoracic spinal identity of mouse embryonic stem cell–derived motor neurons**

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In the presence of retinoic acid and Sonic Hedgehog, embryonic stem (ES) cells differentiate to Hoxa5+ cervical spinal motor neurons (MNs) with high efficiency. However, the generation of Hoxc8+ brachial and thoracic MNs from ES cells is significantly less efficient. The goal of this study was to identify developmentally relevant extrinsic signals and intrinsic genetic programs that would facilitate high efficiency generation of caudal brachial and thoracic Hoxc8+ MNs from mouse ES cells. Newly born Hoxc8+ MNs expressed high levels of Cdx2 transcription factor whose expression peaks at the neural plate stage when cells are responsive to extrinsic rostrocaudal patterning signals. In addition, we found that Wnt is the principal signal inducing Cdx2 expression during MN differentiation. Using a newly generated ES cell line harboring a doxycycline inducible Cdx2 transgene, we observed that Cdx2 expression by itself was not sufficient to specify Hoxc8+ MNs. However, a brief induction of Cdx2 expression followed by the treatment of differentiating cells with FGF resulted in the high efficiency generation of Hoxc8+ MNs and the complete loss of Hoxa5 expression. We propose that Wnt directed Cdx2 expression followed by the activation of the FGF signaling cascade are prerequisites for efficient specification of Hoxc8+ brachial and thoracic spinal MNs from mouse ES cells.

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Program/Abstract # 9
**Vive la difference: The creation of sexual dimorphism in the soma and germline**

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The events that trigger sex determination in animals evolve rapidly, but we now know that the downstream events that translate this information into sexual dimorphism are more highly conserved. Recent work indicates that this conservation may extend between vertebrates and invertebrates, and flies and man. This is likely to be particularly true in gonad development, as the fundamental requirement for creating sperm and eggs is shared across animal species. One interesting aspect of gonad sexual dimorphism that we are currently investigating is the formation of the male vs. female germline stem cells and the niches for these stem cells created by the soma. In some species, such as humans, a germline stem cell population is only thought to exist in males but not females. In *Drosophila*, germline stem cells exist in both sexes, but there are clear differences in the development and regulation of these stem cell populations and their respective stem cell niches. How is the dramatic sexual dimorphism in germline stem cell development