spt/ntl double mutants lack all trunk and tail mesoderm, including tissues that form in either single mutant. Thus ntl and spt are required for formation of all posterior mesoderm. To identify T-box downstream targets for functional analysis, the lab performed a microarray screen, generating an extensive list of potential Ntl and Spt targets, including t-box gene 6 (tbx6) and mesogenin (msgn1). Knockdown strategies demonstrate that tbx6, a T-box transcription factor, is required for non-axial trunk and tail mesoderm formation. In contrast, characterization of a mutant null for msgn1, a bHLH transcription factor, reveals that msgn1 plays a relatively small role in zebrafish mesoderm formation. This is surprising since studies of msgn1 in other vertebrates reveal significant roles in posterior mesoderm development. Currently, we are investigating the roles of tbx6 and msgn1 by characterizing their genetic interactions with ntl, spt, and other T-box targets.

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Program/Abstract # 155
	tbx24 is required for proper dermomyotome formation in the posterior trunk of zebrafish
Nathan C. Birda, Frank Stellabotteb, Stephen H. Devotoa
aDept. of Biol., Wesleyan Univ., Middletown, CT, USA
bHouse Ear Institute, Los Angeles, CA, USA

Several genes are differentially required for segmentation at various axial levels. We found only one, fused somites (tbx24), which is also required for dermomyotome development and patterning. We quantified the defect in fss mutants by counting the number of dermomyotome cells in a standard somite. In fss, Pax7+ dermomyotome cells are absent in the central third of the somite lateral surface, but are present in the dorsal and ventral thirds of the somite. Total Pax7 cell number is half that of heterozygous siblings. The defect is only found posterior to about S9. The presence of normal anterior trunk dermomyotome indicates that the defect is not solely due to missing segment boundaries. The dermomyotome defect is detectable at the earliest stages of somite morphogenesis, suggesting tbx24 may be necessary for initial dermomyotome specification. To test dermomyotome behavior in fss, we perturbed Hh and BMP signaling using cyclopamine or heat shock-driven shh and bmp2b. Both BMP2b overexpression and cyclopamine added at tailbud stage similarly increase the total number of Pax7+ dermomyotome cells at all axial levels. The gap in the central dermomyotome is not significantly affected by loss of Hh or gain of BMP2b signaling. Shh overexpression abolishes nearly all Pax7+ cells in both het and fss siblings. Our results indicate tbx24 is required for dermomyotome formation, particularly within the central region of the somite lateral surface, but not for myogenic differentiation of the dermomyotome. We are now examining the nature of the tbx24 requirement for the central region of posterior trunk dermomyotome.

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Program/Abstract # 156
The p38-MAP Interacting Protein (p38IP) regulates somite and vertebral development
Sunita Warriera, Irene E. Zohna,b
aCenter for Neuroscience, Children’s Research Institute, Children’s National Medical Center, Washington DC USA
bSupported by grants from the March of Dimes Foundation and the Spina Bifida Association.

The droopy eye (drey) mouse line harbors a hypomorphic mutation in p38-MAP Interacting Protein (p38IP), displaying an array of incompletely penetrant phenotypes such as gastrulation and neural tube defects including exencephaly and spina bifida. A null genetrap allele (p38IPpRK) exhibits fully penetrant gastrulation and other defects in mesoderm development. In addition, p38IPpRK/RRK mutants show fusion and loss of posterior somites. In this study, we explore defects in somite development in hypomorphic p38IPpRK/RRK mutants. Skeletal staining of p38IPpRK/RRK hypomorphs at E15.5–17.5 reveals fusions of the ribs and vertebrae. To determine if rib and vertebrae fusions originate from defects in somitogenesis, expression of somite markers was examined in E9.5–10.5 p38IPpRK/RRK hypomorphs. Mutant embryos exhibit reduced and disorganized expression of markers for the posterior somite compartment (Unca4.1) and the sclerotome (Pax5). Furthermore, these embryos show reduction in the expression of Notch ligands Dll1 and Dll3 in the presomatic mesoderm. Formation of the regular metameric pattern of somites is controlled by the somite clock, which is regulated by Notch along with Wnt and Fgf pathways. Future experiments aim to determine if p38IP impinges on these pathways to gain a better understanding of how mutation of p38IP results in disruption of somite formation.

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Program/Abstract # 157
The regulation of somite epithelialization by paraxis
Megan Rowtona, Pilar Ramose,b, Douglas Andersona, Heather Cunliffeb, Alan Rawlsa
aSchool of Life Sciences, Arizona State University, Tempe AZ, USA
bTGen, Phoenix AZ, USA

generates an extensive list of potential Ntl and Spt targets, including tbx24, which is required for proper dermomyotome formation in the posterior trunk of zebrafish. We are now examining the nature of the tbx24 requirement for the central region of posterior trunk dermomyotome. The expression array of psm and somitic tissue from E9.5 paraxis−/− embryos has revealed a role for the gene during early events in somitogenesis, including mesenchymal-to-epithelial transition (MET), maintenance of anterior/posterior polarity, and cell proliferation. MET is associated with an increase in adherens junctions and desmosomes along the apical junctions and focal adhesion along the basal surface. Studies performed in chick embryos predict that paraxis and Mesp2 coordinate the differential activation of the rho family members, Rac1 and Cdc42 in the acquisition of epithelial morphology. Further, interactions between EphA4 receptor and its ligand, ephrinB2 serve as the catalyst for MET at the segmental boundary. The gene targets of paraxis and how this promotes and maintains MET in the newly formed somite remain poorly understood. Here we present a differential gene expression array of psm and somitic tissue from E9.5 paraxis−/− and paraxis+/+ embryos. The role of paraxis in regulating the transcription of genes linked to cell adhesion and MET will be presented.

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Program/Abstract # 158
Structure and function of AGAMOUS in a basal eudicot
Theadora R. Tolkin, Kacie McCarty, Kelsey Galimba, Veronica Di Stilio
Dept. of Bio., U of Washington, Seattle, WA, USA

A major feature of angiosperm evolution is the trend from indeterminate floral patternning in basal lineages to tightly determinate growth resulting in 4 four well-defined whorls of organs along the floral axis in core eudicots. Modification of this floral plan during evolutionary time may have required changes in the regulation of genes affecting floral meristem determinacy and organ identity. In Arabidopsis, a core Eudicot, the C-class gene in the ABC model of flower development, AGAMOUS (AG), has been shown to play a role in stamen and carpel identity as well as floral determinacy, with function being determined by
timing and location of gene expression. Here, we analyze the genomic sequence of ThAG-1, including its regulatory region, in two related species for which natural mutants, in the form of horticultural varieties, are also available, *T. thalictroides* and *T. delavayi*. Among several horticultural mutant varieties, we identified four with a phenotype resembling an AG loss of function. In these mutants, we characterized ThAG-1 structure and function using genomic sequencing and RT-PCR as compared to wild-type. Using Viral Induced Gene Silencing (VIGS), we were able to phenocopy many characteristics of our mutants in wild-type plants. About 10% of silenced plants also exhibited a complete re-initiation of the floral meristem, which we did not find in any *Thalictrum* mutants but which has been described in *Arabidopsis* AG loss of function mutants. We will discuss how these complementary approaches help elucidate interesting aspects of the conservation and divergence of C class gene function and regulation in early eudicots.

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Program/Abstract # 159
Temporal regulation of development by the MED12–MED13 module of Arabidopsis mediator
Stewart Gillmorah, Matthew Willmanna, Scott Poethiga
aDepartment of Biology, University of Pennsylvania, Philadelphia, PA USA
bNational Laboratory for Biodiversity Genomics (LANGEBIO), CINVESTAV-IPN, Irapuato, Guanajuato, Mexico

Multicellular development involves precise temporal coordination of sequential developmental programs. The life cycle of flowering plants such as *Arabidopsis thaliana* can be divided into early seed development (embryo pattern formation), late seed development (accumulation of seed storage proteins and desiccation tolerance), germination, vegetative development (leaf production), and reproductive development (flowering). We have recently described a role for the transcriptional regulators *MED12/CCT* and *MED13/GCT* in temporal regulation of pattern formation in early embryogenesis (Gillmor et al., Development 137:113). Further morphological and molecular characterization of *cct* and *gct* mutants demonstrates that these genes play a global role in regulating the transitions between different phases of the Arabidopsis life cycle. Microarray analysis demonstrated that *cct* and *gct* mutants continue to express seed specific transcripts after germination. During vegetative development, *cct* and *gct* mutants delay the onset of adult leaf traits such as an elongated shape, a complex vascular system, and the appearance of ventral leaf hairs. *cct* and *gct* also affect the transition to reproductive development, delaying flowering by several weeks. The morphological and molecular phenotypes of *cct* and *gct* mutants suggest that a primary function of the *MED12* and *MED13* genes is to sharpen the temporal boundaries of phase-specific transcriptional programs during the Arabidopsis life cycle.

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