palate, the penetrance of which is increased to 100% in the presence of a single Snai1-null allele. This phenotype is due to a failure of the elevated palate shelves to fuse, caused by a lack of apoptosis and the persistence of periderm cells at the medial epithelial edge (MEE). Moreover, deletion of the remaining Snai1 allele using the neural crest-specific Wnt1-Cre results in multiple craniofacial defects, including a distinct cleft palate phenotype. Unlike Snai1+/−;Snai2−/− embryos, clefting in these embryos results from a failure of the Meckel's cartilage to extend the mandible and thereby allow the vertical palate shelves to elevate, a defect similar to that seen in the Pierre–Robin sequence in humans. This work demonstrates that Snail family members play multiple, critical roles in craniofacial development in mice.

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Program/Abstract # 49
Cell-autonomous accumulation of the *Drosophila* HIF-α homologue Sima in tracheal cells contributes to tracheal extra-sprouting in hypoxia
Pablo Wappner, Andres Dekanty, Lazaro Centanin
Instituto Leloir, Buenos Aires, Argentina

The *Drosophila* tracheal system is a network of ramified tubes that deliver oxygen to every tissue in the organism. Tracheal development relies mostly on guided cell migration in which the FGF homologue, Branchless (Bnl), is expressed outside the tracheae and attracts the extension of tracheal branches by binding to the FGF receptor homologue, Breathless (Btl), that is expressed in tracheal cells. By the end of embryogenesis, this genetically specified phase of tracheal development has been completed and later, in larval stages, terminal tracheal branches are plastic and have the capacity to sprout-out projections towards oxygen-starved areas in target tissues, very much like angiogenesis in mammals. This oxygen-dependent effect has been also reported to depend on the upregulation of Bnl in target tissues. Here we report that in hypoxic *Drosophila* larvae, the HIF-α homologue, Sima, accumulates mainly in tracheal cells, provoking transcriptional upregulation of Btl. Loss-of-function mutants for the HIF prolyl hydroxylase gene, *fatiga*, a well-known negative regulator of Sima, exhibit extra-tracheal branches but this effect is reduced by lowering *btl* dose. Specific over-expression of Sima or Btl in tracheal cells induce an increase in the number of terminal branches, suggesting that upregulation of the receptor is sufficient for tracheal extra-sprouting. We propose that upregulation of Btl in response to cell-autonomous accumulation of Sima in tracheal cells is a cardinal event in hypoxia-dependent tracheal terminal branching.

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Program/Abstract # 50
Regulation of growth by the Fat tumor suppressor pathway
Ken Irvine, Eunjoo Cho, Yongqiang Feng, Hiroyuki Ishikawa, Binnaz Kucuk, Yaopan Mao, Oh, Cordelia Rauskolb
Howard Hughes Medical Institute, Waksman Institute and Department of Molecular Biology and Biochemistry, Rutgers The State University of New Jersey, Piscataway, NJ 08854, USA

It has long been appreciated that organ growth is influenced by organ patterning, but the molecular mechanisms that link them have remained unclear. We have begun investigating a new intercellular signaling pathway, the Fat pathway, that links patterning to growth. *fat* encodes a large protocadherin, mutation of which influences both tissue polarity and growth in the imaginal discs of *Drosophila*. Characterization of the functional relationships among *Drosophila* tumor suppressors led us to identify the kinases Discs overgrown and Warts as components of a Fat signaling pathway. *fat*, *discs overgrown* and *warts* regulate a common set of downstream genes in multiple tissues, including *wingless*, *Serrate*, *four-jointed*, *Diap1*, *cyclin E* and *expanded*. Fat signaling also interconnects with Hippo signaling at multiple levels, but both genetic and molecular experiments suggest that they act largely in parallel to regulate disc growth, with Hippo signaling regulating Warts phosphorylation, and Fat signaling regulating Warts stability. We will present our current understanding of the molecular basis for signal transduction downstream of Fat, and of the regulation of Fat by the graded expression of its ligand, Dachsous and the Golgi protein Four-jointed.

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Program/Abstract # 51
Fgf8 is essential for development of the male reproductive tract
Yutaka Ueda [1], M. Lewandoski [2], S. Plisov [1], C. Wilson [2], N. Sharma [1], C. Elder [2], Perantoni
[1] *Laboratory of Comparative Carcinogenesis, NCI, Frederick, MD, USA*
[2] *Cancer and Developmental Biology Laboratory, NCI, Frederick, MD, USA*

Fgf8 plays a major role in the development of several tissues, including the midbrain–hindbrain region, branchial arches, limb bud and metanephros. An examination of mutants with pan-mesodermal inactivation of *Fgf8* due to tissue-specific recombination, using the primitive streak-specific TCre transgene, revealed a novel *Fgf8*-dependent phenotype in the male reproductive tract. Whole-mount immunohistochemistry and in situ hybridization using riboprobes for *Fgf8*, *Pax2*, *Lim1* and *Shh* demonstrated that TCre; *Fgf8* embryos lack the cranial aspect of the mesonephros, including the mesonephric tubules at E11.5. This results in the loss of the efferent ductules, the head and body of the epididymis and most of the vas deferens in