Fish Oil Turns the Tide on Insulin Resistance

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Inflammation mediated by macrophages promotes insulin resistance in obesity. Oh et al. now identify the G protein-coupled receptor 120 (GPR120) on macrophages and fat cells as a receptor for omega-3 fatty acids (ω-3 FAs). The authors show that GPR120 activation by ω-3 FAs inhibits inflammation pathways in macrophages and can reverse insulin resistance in mice. These results provide a molecular basis for the anti-inflammatory effects of ω-3 FAs and suggest that anti-inflammatory treatments may ameliorate insulin resistance in obesity.

West Nile Virus Stopped at Its Source

PAGE 714

West Nile virus, a potentially deadly virus in humans, propagates in mosquitoes. Cheng et al. now find that infection of West Nile virus triggers mosquito cells to produce the lectin protein mosGCTL-1. This C-type lectin enhances entry of the virus into additional mosquito cells through its interaction with a protein tyrosine phosphatase receptor, which is homologous to human CD45. Blocking mosGCTL-1 with an antibody disrupts the infective cycle of West Nile virus in mosquitoes, suggesting a new strategy for controlling viral dissemination.

Antibodies Are Double-Trouble for Cancer

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Monoclonal antibodies are standard therapeutics for several cancers, including the anti-CD20 antibody rituximab for B cell non-Hodgkin lymphoma (NHL). However, antibodies are not curative and must be combined with cytotoxic chemotherapy for clinical benefits. Now, Chao et al. identify CD47 as an antibody target in NHL and demonstrate that combining anti-CD47 antibody with the rituximab antibody eradicates human NHL in mice. The synergistic mechanism used by these two antibodies may be applicable to combined antibody treatments for many types of cancers.

ATAC Wears Two HATs in MAPK Signaling

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Extracellular cues often trigger MAP kinase (MAPK) signaling pathways, which then activate downstream transcription factors like c-Jun. Here, Suganuma et al. demonstrate that the ATAC histone acetyltransferase (HAT) governs the response to MAPK signaling by serving as both a coactivator of transcription and a suppressor of upstream signaling in the MAPK pathway. The authors show that ATAC acetylates histone H4 at JNK target genes, which then serves as a positive cofactor for basal transcription. In addition, ATAC directs upstream MAPKs to the site of c-Jun binding and restricts the levels of JNK activation.

A Multitasking Leader mRNA

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Bacterial mRNAs often contain leader sequences that regulate transcription of the adjacent coding region by binding metabolites and ions. For example, the leader of the mRNA for the Salmonella Mg²⁺ transporter gene mgtA responds to Mg²⁺. Now, Park et al. demonstrate that this leader also contains a short open reading frame with many proline codons, translation of which places mgtA expression under the control of cytoplasmic proline concentrations as well as Mg²⁺. Thus, leader mRNAs can use distinct mechanisms to sense multiple intracellular signals.

Vivid Memories of Days Gone By

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Light responses and photoadaptation in the fungus Neurospora depend on the circadian transcription factor White Collar Complex (WCC) and its negative regulator Vivid (VVD). Mazhan et al. now demonstrate how WCC and VVD cooperate to discriminate light intensities over more than five orders of magnitude during the day. At night, previously synthesized VVD serves as a molecular memory of the sun’s brightness during the preceding day and suppresses responses to light cues of lower intensity, such as moonlight.
Cell Polarity Goes with the Flow

Planar polarization of epithelial cells allows the uniform alignment of hairs, cilia, and other cellular structures with tissue shape. Now, Aigouy et al. combine experimental and theoretical approaches to show that polarity patterns in the *Drosophila* wing arise during growth. Specifically, cell polarity is reoriented from a radial to a proximal-distal axis when mechanical stresses during growth cause the cells to rotate or “flow” with respect to each other. Linking planar polarity to morphogenesis provides a simple mechanism for coordinating the global polarity pattern with tissue shape.

Com-plexin’ with Semaphorins

Semaphorins and their receptors, Plexins, are widely expressed protein families that mediate repulsive signaling during cell guidance. Here, Liu et al. present two X-ray crystal structures of PlexinC1, one in complex with the Semaphorin Sema7A and another in complex with the Semaphorin mimic A39R from the smallpox virus. In both structures, the Semaphorin interacts with a PlexinC1 dimer in a novel edge-on, orthogonal geometry. These findings suggest that Plexins are activated by ligand-induced dimerization during cell guidance.

Interspecies Organogenesis

A goal of regenerative medicine is to derive organs from a patient’s pluripotent stem cells (PSCs), but in vitro organogenesis is complex. Here, Kobayashi et al. generate a functioning rat pancreas in mice without a pancreas by injecting rat PSCs into mouse blastocysts. These interspecific chimeras provide proof of principle for in vivo generation of organs derived from donor PSCs and for interspecific blastocyst complementation.

A Wormhole to the Origin of the Cortex

The cerebral cortex or pallium controls the highest-order processing in mammals, but its evolution remains enigmatic. Now, Tomer et al. develop an expression profiling technique to generate a gene expression map for the developing brain of the segmented worm *Platynereis dumerilii*. Comparison of this map with that observed for the developing cerebral cortex suggests a common evolutionary origin for the mammalian cortex and the worm’s mushroom body, a brain region in invertebrates that processes sensory input.

Will the Real Chromosomal Proteins Please Stand Up

Proteomic analysis of large cellular structures is frequently hindered by the presence of contaminants. In their analysis of mitotic chromosomes, Ohta et al. overcome this problem by integrating proteomics with additional quantitative and bioinformatic data—effectively adding a final purification step in silico. This approach successfully pinpoints hitchhikers from amongst the ~4,000 identified proteins and provides insight into the functional relationships among the genuine constituents, including evidence that many more kinetochore-associated proteins exist than recognized previously.