Journal of Cell Science

Consortia – the motion picture

These days cell scientists increasingly focus on the big picture. As former JCS Editor Gary Borisy put it, "cell biology has the real opportunity to burst the frames of cartoons [and] understand the emergent, self-organizing properties of interdependent systems" [Borisy, G. (2000). Beyond cell toons. *J. Cell Sci.* **113**, 749-750]. Genome sequencing, microarray analysis, live-cell imaging, high-throughput techniques for characterizing proteins: all of these encourage us to view cells and cellular processes at the system level – as networks. The study of networks – graph theory – is a science in itself, and great strides have been made in recent years. One of these has been the revelation that so-called 'scale-free' networks may describe phenomena as diverse as the Internet and cell signalling. In an article appearing on p. 4947 of this issue, Reka Albert introduces us to the basic features of scale-free networks and discusses how these can help cell biologists explore processes such as signal transduction, transcriptional regulation and metabolism. Establishing the biochemical hubs, modularity and motifs within these networks should allow us to make predictions of systems-level behaviour of cells and tissues, illustrating just how fruitful collaborations between biologists and mathematicians can be.

Interdisciplinary approaches are becoming increasingly common in all areas of cell biology. A good example is the Cell Migration Consortium (CMC), an NIH-funded initiative whose members are charting the network of interactions between signalling molecules, cytoskeletal components, adhesion receptors and the extracellular matrix that allow cells to move (see http://www.cellmigration.org). Spear-headed by another former Editor, Rick Horwitz, and Tom Parsons, the CMC involves investigators from over a dozen institutions, including cell biologists, mathematicians, biophysicists, chemists and computational scientists. Together they hope to define all the molecular players involved in migration and their locations, determine the structures of key migration complexes and develop new in vivo and in silico models of the process. In Cell Science at a Glance on p. 4917, Horwitz and colleagues sketch out an overview of cell migration, giving us a glimpse of the task the CMC has set itself. In an accompanying piece, they focus in on paxillin – a critical node in the migration network whose phosphorylation at multiple sites regulates its localization and adaptor activity. The CMC has used mass spectrometry to map all the phosphorylation sites in paxillin (see p. 4925). It has also tackled focal adhesion kinase (FAK; see p. 4931) and the integrin-binding protein talin (see p. 4921), and further phosphorylation maps of key migration molecules will appear in JCS over the coming months.

Other key nodes in the cell migration network are the Rho family GTPases Rho, Rac and Cdc42. These are critical cytoskeletal regulators controlled by guanine-nucleotide-exchange factors (RhoGEFs) that promote exchange of GDP for GTP. Recent work by several groups has identified an entirely new family of RhoGEFs – the CZH proteins. These contain a novel 'CZH2' GEF domain unrelated to the Dbl-homology (DH) domain present in previously identified RhoGEFs. On p. 4937, Nahum Meller and co-workers discuss the structure and evolution of CZH proteins and examine their roles in cell migration, as well as processes including phagocytosis, T-cell activation and neurite outgrowth. Spanning cell biology, apoptosis, immunology and neuroscience, this family alone illustrates the need for multidisciplinary approaches in the life sciences.

At JCS, we are enthusiastic about alliances of different scientists who come together to solve important and complex cell biological problems. We encourage such consortia to submit their work to the journal.

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