nature neuroscience

Looking back, looking ahead

This month is the first anniversary of *Nature Neuroscience*, leading us to reflect on what we have accomplished so far and where we hope to go next. From the beginning, our editorial view has been that neuroscience is fundamentally a single field. We believe that the common goal of understanding the brain should transcend the sometimes-baffling array of techniques, jargon and analytical approaches of its many practitioners. To reflect this view, we aim to publish papers that are not only influential within their own disciplines, but of broad interest to many neuroscientists. We also strive to maintain subject diversity by providing readers with examples of the best work from all areas of neuroscience. This month, for instance, the topics covered in our papers range from alternative splicing of calcium channels to the mechanism by which the human brain perceives second-order contours—such as picking out the zebras from the sea of stripes on our cover. Finally, we try to make our papers understandable to the widest possible range of neuroscientists. Are we succeeding? That is for our readers to judge, but we are encouraged that we consistently receive almost ten times as many papers as we can publish. We are grateful that so many authors have risked submitting their work to a new and unproven journal.

Looking beyond our own pages, the most important advance in neuroscience of the last year was arguably the completion of the genome sequence for the nematode *C. elegans*. We now have, for the first time, the complete instructions for building a simple nervous system[1]. The relevance of this information to more complex brains might be questioned, given the small size (302 neurons and about 5000 synapses) and stereotypical development of the *C. elegans* nervous system. Consider, however, the articles in this issue—with the exception of perhaps four that deal with higher brain functions, almost every one is about molecules or cellular events that have counterparts in worms. For example, we now know that the worm genome contains 5 calcium channels of the type discussed by Snutch and colleagues (page 407), about 50 potassium channels of the class identified by the Lazdunski group as targets for volatile anesthetics in mammals (page 422), 2 Slo potassium channels (page 416) and over 30 PDZ-domain proteins (page 447), as well as glutamate receptors (page 454) and transporters (page 427) and the major components of the exocytotic machinery (pages 434 and 440). In addition, migration of neuronal precursors (page 461) and olfactory coding (page 479) have both been dissected genetically in *C. elegans*.

To be sure, some important phenomena cannot easily be addressed in worms; for instance, they lack sodium spikes and have not demonstrated robust associative learning, and recording from their neurons is very difficult. Many of these gaps will soon be filled, however, by work on the fruitfly *Drosophila*, whose genome is likely to be fully sequenced by the end of 1999. In addition, the human genome sequence will soon become available, and its interpretation is likely to rely heavily on what has been learned from worms and flies. Perhaps the most important insight to emerge from large-scale sequencing has been the degree to which molecular mechanisms underlying cellular processes have been conserved, even among such distant phyla as nematodes, arthropods and chordates. Given that mammalian neurons are similar to those of invertebrates, it seems likely that many of the central problems of molecular and cellular neuroscience will be solved at least in part through the application of genetic methods in *C. elegans* and *Drosophila*.

What distinguishes the mammalian brain more than anything else is, of course, its size and connectivity, and to understand how the genome determines the structure and function of the brain, we must understand development. Although this is a major challenge, the hope is that much of the complexity of mammalian brain development will reduce to a limited number of core processes: for example, cell proliferation, migration and differentiation, axon targeting, selection of synaptic partners and formation and refinement of synaptic connections. If these processes can be understood in simple model systems, and if the underlying molecular mechanisms are conserved, then the prodigious complexity of the mammalian brain should be at least partly comprehensible as variations on a smaller number of themes. Much less is known about these processes than about (say) ion channels, but the initial findings are encouraging; for example, both the anterior–posterior and the dorsoventral patterning of the nervous system seem to show an impressive and previously unexpected degree of homology at the molecular level.

Thus, as *Nature Neuroscience* begins its second year, we intend to follow developmental neuroscience carefully, and in particular the interface between molecular genetics and development where much rapid progress is being made. As we learn more about the role of activity in brain development, it is becoming increasingly evident that there is no clear point at which development ends and mature function begins. Therefore it will become more and more critical for developmental biologists to talk to other neuroscientists and for all neuroscientists to be aware of the latest developments in molecular genetics. We hope to provide a forum for such conversation, and we welcome submissions in this area from researchers who are interested in communicating their findings to a broad audience.

1. Bargmann, C. I. Neurobiology of the *Caenorhabditis elegans* genome. *Science* **282**, 2028–2033 (1998).