13. Ye, F., Breslow, D.K., Koslover, E.F., Spakowitz, A.J., Nelson, W.J., and Nachury, M.V. (2013). Single molecule imaging reveals a major role for diffusion in the exploration of ciliary space by signaling receptors. eLife *2*, e00654.
14. Pan, J., and Snell, W.J. (2005). *Chlamydomonas.* shortens its flagella by activating axonemal disassembly, stimulating IFT particle trafficking, and blocking anterograde cargo loading. Dev. Cell *9*, 431–438.
15. Engel, B.D., Ludington, W.B., and Marshall, W.F. (2009). Intraflagellar transport particle size scales inversely with flagellar length: revisiting the balance-point length control model. J. Cell Biol. *187*, 81–89.
16. Ludington, W.B., Wemmer, K.A., Lechtreck, K.F., Witman, G.B., and Marshall, W.F. (2013). Avalanche-like behavior in ciliary import. Proc. Natl. Acad. Sci. USA *110*, 3925–3930.
17. Tam, L.W., Ranum, P.T., and Lefebvre, P.A. (2013). CDKL5 regulates flagellar length and localizes to the base of the flagella in *Chlamydomonas*. Mol. Biol. Cell *24*, 588–600.
18. Hilton, L.K., Gunawardane, K., Kim, J.W., Schwarz, M.C., and Quarmby, L.M. (2013). The kinases LF4 and CNK2 control ciliary length by feedback regulation of assembly and disassembly rates. Curr. Biol. *23*, 2208–2214.
19. Berman, S.A., Wilson, N.F., Haas, N.A., and Lefebvre, P.A. (2003). A novel MAP kinase regulates flagellar length in *Chlamydomonas*. Curr. Biol. *13*, 1145–1149.
20. Cao, M., Meng, D., Wang, L., Bei, S., Snell, W.J., and Pan, J. (2013). Activation loop phosphorylation of a protein kinase is a molecular marker of organelle size that dynamically reports flagellar length. Proc. Natl. Acad. Sci. USA *110*, 12337–12342.

[1]MOE Key Laboratory of Protein Science, School of Life Sciences, Tsinghua University, Beijing 100084, China.
[2]Department of Cell Biology, University of Texas Southwestern Medical School, Dallas, TX 75390, USA.
*E-mail: William.Snell@UTSouthwestern.edu

http://dx.doi.org/10.1016/j.cub.2013.11.043

Insect Vision: Emergence of Pattern Recognition from Coarse Encoding

Neurogenetic tools of *Drosophila* research allow unique access to the neural circuitry underpinning visually guided behaviours. New research is highlighting how particular areas in the fly's central brain needed for pattern recognition provide a coarse visual encoding.

Antoine Wystrach*, Alex D.M. Dewar, and Paul Graham

Animals face complex visual worlds from which they must extract the right type of information to guide behaviour appropriately. How something as small as an insect brain can achieve this given the complexity of natural environments is a fascinating question. We know how insect visual systems extract motion information for flight control [1], polarisation information for course setting [2] or a moving-target for pursuit [3]. But little is known about the visual circuitry involved when insects discriminate patterns of a specific shape, such as flowers for foraging bees [4], panoramas for navigating ants [5] or artificial patterns for tethered *Drosophila* [6]. In a recent paper, Seelig and Jayaraman [7] have provided descriptions of the visual receptive fields of a population of neurons in a higher brain structure called the central complex, a region known to play a key role in sensory–motor integration in many insect species [2,6,8,9]. This is a significant breakthrough as it provides a description of an entire population of specific visual cells that appear to be involved in pattern recognition [10].

Seelig and Jayaraman [7] combined two-photon calcium imaging with the neurogenetic tools available to researchers working on the fruitfly *Drosophila melanogaster* to observe *in vivo* how populations of neurons in the fly's central brain respond to visual stimuli. They targeted the ring neurons R2 and R3/R4d; these receive input from glomeruli in the lateral triangle — presumably after pre-processing in the sensory areas — and project to the ellipsoid body of the central complex [11] (Figure 1A). By presenting black and white noise patterns to *Drosophila* and correlating the visual stimulus with cell responses, Seelig and Jayaraman [7] were able to determine the proprieties of the cell's

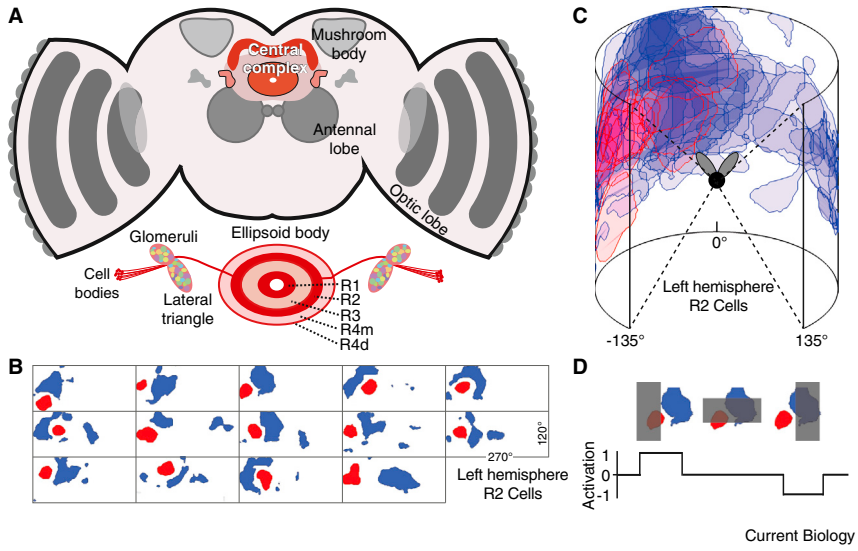

Figure 1. Ring neurons of *Drosophila melanogaster* central complex encode coarse visual information.

(A) Schematic of the fly's brain (top) and ellipsoid body of the central complex (bottom) (after [7]). The ring neurons receive input from the glomeruli of the lateral triangles and project to specific regions of the ellipsoid body. The different regions, and thus the different ring neurons play different roles in visuo-spatial behaviour. (B) Receptive fields of the 14 left hemisphere cells of R2 ring neurons that responded to visual stimuli, showing their excitatory (red) and inhibitory (blue) regions. The receptive field's shape and location on the visual field for each cell is stereotypic and coherent across flies [7]. Thus, those depicted here have been averaged across flies. (C) The same receptive fields as B overlaid on the fly's visual field. Note, the cells shown are all from the left brain. Each receptive field covers 90° or more of the fly's visual field. (D) Response of a R2 cell to vertical and horizontal bars. Since the inhibitory area is to the side of the excitatory one, the neuron responds maximally to vertically oriented bars.

receptive fields (Figure 1B). As the authors note, the receptive fields of *Drosophila* ring neurons share superficial properties with those of the so-called 'simple' cells of vertebrate primary visual cortex, such as the presence of distinct excitatory and inhibitory regions (Figure 1B). There are, however, fundamental differences in their distribution and organisation.

Vertebrate simple cells, as discovered by Hubel and Wiesel [12], have receptive fields made up of juxtaposed, elongated inhibitory and excitatory areas, so that they respond maximally to high contrast bars or edges of a particular orientation. These cells are regularly distributed across the entire visual field, and each region is served by many simple cells each responding maximally to different orientations. That way, visual scenes can be decomposed into high-frequency edge information enabling a detailed reconstruction of the visual world.

It is clear that the compound eyes of insects have a much lower resolution than the camera-like eyes of vertebrates. What is surprising is that the visual cells described by Seelig and Jayaraman [7] do not even approach the resolving power of *Drosophila* eyes (5°), but encode much coarser information. The receptive field of each ring neuron covers 90° of arc or more, which is around a third of the fly's visual field (Figure 1B,C). Moreover, there are only a few of these cells. Seelig and Jayaraman [7] found only fourteen R2 and seven R4d cells per hemisphere that were responsive to visual stimuli. With such a sparse and coarse encoding it is impossible to capture the details of a scene, so, unlike vertebrate simple cells, these cells may not have the role of reconstructing the visual world. Indeed, the analogue of simple cells may not be in the central complex, but rather earlier in the insect visual system [13–15]. So, we might ask, what kind of behaviours could be supported by the coarse information encoded by these ring neurons?

Flies, like many insects, exhibit spontaneous responses to particular visual patterns; for instance, *Drosophila* spontaneously orient towards vertical bars [16]. Similarly, Seelig and Jayaraman [7] observed that many of the ring neurons respond preferentially to vertically oriented bars (Figure 1D). At the level of a single cell, one can deduce what kind of stimulus would excite the cell by the shape of its receptive field (Figure 1D); however, understanding what information is encoded by a population of cells is a more complex problem. To this end, we simulated the visual input experienced by the group of R2 cells when a simulated fly inspects simple patterns (Figure 2). When the 'fly' scans the world, R2 cells as a group show a structured pattern of activation (Figure 2A). This suggests that the shape and location of these receptive fields are organised in a purposeful way. The activity of R2 neurons is greatest when the 'fly' is facing a narrow vertical bar, or the inner edges of a wide black stripe (Figure 2A), which, remarkably, corresponds to the spontaneous attractions observed in flies [17]. Given natural scenes, R2 cells would enable flies to orient towards trees in a field, or a leaf in a tree (Figure 2A).

Of course, a fly's behavioural repertoire is not limited to simple spontaneous responses; flies can also be conditioned to discriminate patterns. In a typical experimental paradigm, a fly is fixed by the head and thorax at the end of a wire and suspended within a drum showing two pairs of visual stimuli (Figure 2B). The torque exerted by the fly when trying to rotate is measured and the drum is then rotated in the opposite direction, so that the fly can control which pattern she is facing. In such a flight simulator, flies can be conditioned by an aversive stimulus to favour a particular pattern [18]. Successful learning indicates that flies are able to discriminate the patterns. Neurogenetic tools used in combination with such behavioural assays have shown that the R2/R4m neurons are required for the discrimination of at least four visual parameters: elevation, contour orientation, size and vertical compactness [10] (Figure 2C). Our simple simulation shows that the 'fly' would experience a difference in the group-level activation of R2 neurons when facing pairs of patterns varying along these dimensions (Figure 2C). The coarse encoding given by this small population of cells is likely insufficient to reconstruct the fine-details of these shapes (Figure 2B), yet enough information is retained to enable discrimination.

By describing the receptive field properties of ring neurons, Seelig and

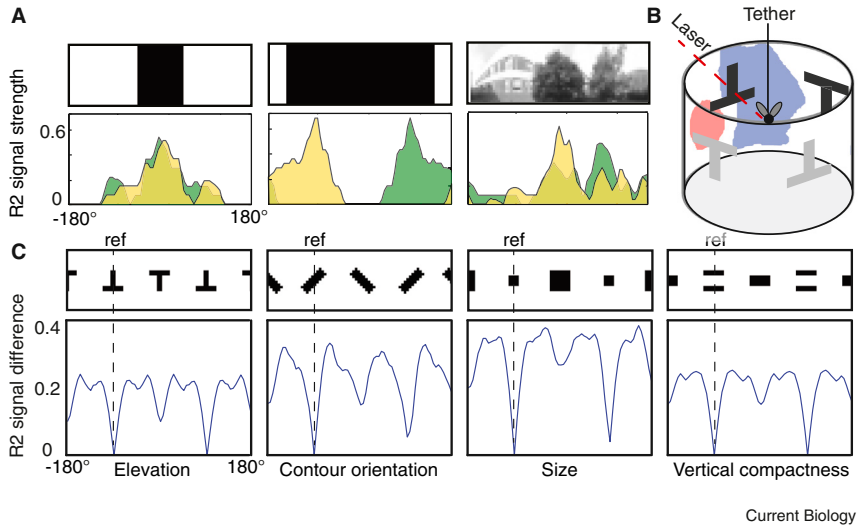

Figure 2. Group activity of R2 neurons relates to spontaneous and learnt behaviours.
(A) R2 neurons' collective activity as a function of the fly's orientation for the left (yellow) and right (green) hemispheres. For each orientation relative to the pattern, the proportion of R2 cells with current excitation greater than 1 S.D. from their average excitation is shown. R2 neurons respond maximally when the fly is facing a vertical bar or the inner edge of a larger black stripe. In natural scenes, R2 cells tend to respond preferentially when the fly is facing large high contrast objects. (B) Schematic of a fly simulator used to test whether flies can discriminate between pairs of patterns. The red (excitatory) and blue (inhibitory) areas indicate the scale of a typical R2 receptive field. (C) Absolute difference in group activity of the R2 cells for a simulated fly with varying orientation. The reference is the group activity when the fly faces the reference pattern ('ref').

Jayaraman [7] have begun a process of understanding how the complex visual information provided by the world is filtered to suit specific behavioural tasks. At first glance, it may be surprising how coarse the visual encoding is, far below the resolving power of *Drosophila* eyes. Nonetheless, this sparse encoding is sufficient to explain some spontaneous and learnt behaviour observed in flies. As often with insect studies [19], Seelig and Jayaraman's [7] discovery serves as a compelling example of how apparently complex problems can be solved with remarkably parsimonious solutions.

For a more complete understanding of sensorimotor behaviour in *Drosophila*, it will be interesting to see the receptive field proprieties of the other types of ring neuron, as we already know they are involved in different behavioural tasks [6]. Furthermore, the ring neurons of the ellipsoid body constitute only one step within much longer neural pathways [11]. For instance, neurons from the fan shaped body of the central complex seem to extract specific visual parameters from the patterns [20]. Finally, it is important to remember that the central complex is not only a visual area [6]. Indeed, only about half of the ring neurons targeted by Seelig and Jayaraman responded to visual stimuli [7]. Thus, we may be far from a complete understanding of the central complex, but we can be hopeful that co-ordinated behavioural, electrophysiological and genetic tools will together shed light on how a parsimonious nervous system can produce adaptive behaviour in a complex world.

References

1. Borst, A., Haag, J., and Reiff, D.F. (2010). Fly motion vision. Annu. Rev. Neurosci. *33*, 49–70.
2. Heinze, S., and Homberg, U. (2007). Maplike representation of celestial E-vector orientations in the brain of an insect. Science *315*, 995–997.
3. Nordström, K., and O'Carroll, D.C. (2006). Small object detection neurons in female hoverflies. Proc. R. Soc. Lond. B. *273*, 1211–1216.
4. Horridge, A. (2005). The spatial resolutions of the apposition compound eye and its neuro-sensory feature detectors: observation versus theory. J. Insect Physiol. *51*, 243–266.
5. Collett, M., Chittka, L., and Collett, T.S. (2013). Spatial memory in insect navigation. Curr. Biol. *23*, R789–R800.
6. Pfeiffer, K., and Homberg, U. (2014). Organization and functional roles of the central complex in the insect brain. Annu. Rev. Entomol. *59*, epub ahead of print.
7. Seelig, J.D., and Jayaraman, V. (2013). Feature detection and orientation tuning in the Drosophila central complex. Nature *503*, 262–266.
8. Bender, J.A., Pollack, A.J., and Ritzmann, R.E. (2010). Neural activity in the central complex of the insect brain is linked to locomotor changes. Curr. Biol. *20*, 921–926.
9. Ofstad, T.A., Zuker, C.S., and Reiser, M.B. (2011). Visual place learning in Drosophila melanogaster. Nature *474*, 204–207.
10. Pan, Y., Zhou, Y., Guo, C., Gong, H., Gong, Z., and Liu, L. (2009). Differential roles of the fan-shaped body and the ellipsoid body in Drosophila visual pattern memory. Learn. Mem. *16*, 289–295.
11. Young, J.M., and Armstrong, J.D. (2010). Structure of the adult central complex in Drosophila: Organization of distinct neuronal subsets. J. Comp. Neurol. *518*, 1500–1524.
12. Hubel, D.H., and Wiesel, T.N. (1959). Receptive fields of single neurones in the cat's striate cortex. J. Physiol. *148*, 574–591.
13. O'Carroll, D. (1993). Feature-detecting neurons in dragonflies. Nature *362*, 541–543.
14. Yang, E.C., and Maddess, T. (1997). Orientation-sensitive neurons in the brain of the honey bee (Apis mellifera). J. Insect Physiol. *43*, 329–336.
15. Spalthoff, C., Gerdes, R., and Kurtz, R. (2012). Neuronal representation of visual motion and orientation in the fly medulla. Front. Neural Circ. *6*, 72. http://dx.doi.org/10.3389/fncir.2012.00072.
16. Wehner, R. (1972). Spontaneous pattern preferences of Drosophila melanogaster to black areas in various parts of the visual field. J. Insect Physiol. *18*, 1531–1543.
17. Osorio, D., Srinivasan, M.V., and Pinter, R.B. (1990). What causes edge fixation in walking flies? J. Exp. Biol. *149*, 281–292.
18. Ernst, R., and Heisenberg, M. (1999). The memory template in Drosophila pattern vision at the flight simulator. Vis. Res. *39*, 3920–3933.
19. Wystrach, A., and Graham, P. (2012). What can we learn from studies of insect navigation? Anim. Behav. *84*, 13–20.
20. Liu, G., Seiler, H., Wen, A., Zars, T., Ito, K., Wolf, R., Heisenberg, M., and Liu, L. (2006). Distinct memory traces for two visual features in the Drosophila brain. Nature *439*, 551–556.

University of Sussex, School of Life Sciences, John Maynard Smith Building, Brighton, BN1 9QG, UK.
*E-mail: a.wystrach@sussex.ac.uk

http://dx.doi.org/10.1016/j.cub.2013.11.054

X-Inactivation: Xist RNA Uses Chromosome Contacts to Coat the X

The mechanisms by which Xist RNA associates with the X chromosome to mediate alterations in chromatin structure remain mysterious. Recent genome-wide Xist RNA distribution studies suggest that this long noncoding RNA uses 3-dimensional chromosome contacts to move to its sites of action.

Karen N. Leung[1,2] and Barbara Panning[1,*]

In organisms with XY sex chromosomes, chromatin modifications are directed to the X chromosomes (X) to equalize X-linked gene dosage between males and females. In flies and worms, the dosage compensation complexes are localized to the X by sequence specific binding to high affinity sites and subsequent spread to nearby lower affinity sites [1]. Despite over five decades of X chromosome inactivation (XCI) research, little is understood of the mechanisms controlling the localization of the mammalian dosage compensation machinery to the X. In XCI, a long noncoding RNA (lcnRNA), Xist RNA, recruits chromatin modifying complexes to the X. The *Xist* gene is encoded in the X-inactivation center (*Xic*), an X-linked *cis*-element that is essential for XCI. Xist RNA spreads from the *Xic* to coat the X and contributes to the initial establishment of silencing and subsequent maintenance of XCI [2]. In two recent studies, Engreitz *et al.* and Simon *et al.* used genome-wide approaches to map the DNA associated with Xist RNA to provide insight into how this lncRNA spreads [3,4].

Both groups utilized pools of antisense oligonucleotides complementary to the 17 kb Xist RNA to enrich for Xist RNA-associated genomic sequences in crosslinked cells. Comparison of Xist RNA distribution with data sets for genomic features provided clues about the mechanisms of Xist RNA localization and spread. During the maintenance stage of XCI the same pattern of Xist RNA distribution emerged in both studies. Xist RNA enrichment was observed across the entire X relative to autosomes. There was variability across the X, with gene-dense regions exhibiting the highest representation