REFERENCES

Aida, M., Beis, D., Heidstra, R., Willemsen, V., Blilou, I., Galinha, C., Nussaume, L., Noh, Y.S., Amasino, R., and Scheres, B. (2004). Cell *119*, 109–120.

Di Laurenzio, L., Wysocka-Diller, J., Malamy, J.E., Pysh, L., Helariutta, Y., Freshour, G., Hahn, M.G., Feldmann, K.A., and Benfey, P.N. (1996). Cell *86*, 423–433.

Ebel, C., Mariconti, L., and Gruissem, W. (2004). Nature *429*, 776–780.

Helariutta, Y., Fukaki, H., Wysocka-Diller, J., Nakajima, K., Jung, J., Sena, G., Hauser, M.T., and Benfey, P.N. (2000). Cell *101*, 555–567.

Inze, D. (2005). EMBO J. *24*, 657–662.

Sabatini, S., Heidstra, R., Wildwater, M., and Scheres, B. (2003). Genes Dev. *17*, 354–358.

van den Berg, C., Willemsen, V., Hendriks, G., Weisbeek, P., and Scheres, B. (1997). Nature *390*, 287–289.

Weigel, D., and Jürgens, G. (2002). Nature *415*, 751–754.

Weinberg, R.A. (1995). Cell *81*, 323–330.

Wildwater, M., Campilho, A., Perez-Perez, J.M., Heidstra, R., Blilou, I., Korthout, H., Chatterjee, J., Mariconti, L., Gruissem, W., and Scheres, B. (2005). Cell, this issue.

Pushing Back the Expansion of Introns in Animal Genomes

Sudhir Kumar[1,*] and S. Blair Hedges[2]

[1]Center for Evolutionary Functional Genomics, Biodesign Institute, and School of Life Sciences, Arizona State University, Tempe, AZ 85287, USA

[2]Department of Biology and NASA Astrobiology Institute, Pennsylvania State University, University Park, PA 16802, USA

*Contact: s.kumar@asu.edu

DOI 10.1016/j.cell.2005.12.007

In a recent paper in *Science*, Raible et al. (2005) surveyed the position of introns in 30 genes of a marine annelid and showed that over 60% of the introns occupy positions identical to those in human homologs. In contrast, both human and marine annelid genes share only 30% of their introns with other invertebrates. These observations suggest that the common ancestor of most animal phyla had intron-rich genes and reinforce the notion that introns proliferated early in the evolutionary history of eukaryotes.

Introns were discovered in eukaryotic genes in 1977 (Sambrook 1977; Gilbert 1978) and are now known to be important for generating diversity in RNA and proteins in animal cells. Analyses of the completely sequenced genomes of vertebrates (such as humans, mice, and fish) and invertebrates (such as the fruit fly and nematode) have shown that the former contain a larger number of introns per gene (5.2–7.9) than the latter (3.1–5.5) (Lynch 2005). Using completely sequenced animal genomes along with those of plants and fungi, researchers have attempted to discern which of the following two hypotheses is true. The first is the gain-of-introns hypothesis, which states that the genome of the last common ancestor of arthropods (for example, insects) and deuterostomes (for example, vertebrates) was intron poor and then gained introns during the evolution of its vertebrate descendants (Rogozin et al., 2003). The second is the loss-of-introns hypothesis, which states that the genome was intron-rich and then lost introns in the evolutionary lineage leading to arthropods (Roy and Gilbert 2005).

To decide which hypothesis is correct would require obtaining many partial or complete genome sequences, especially from invertebrates. However, until recently, the invertebrate genomes used in the computational analyses were primarily from only two phyla—arthropods and nematodes—both of which are intron poor. Moreover, these lineages represent only a fraction of all animal phyla (see Figure 1A). In a recent paper in *Science*, Raible et al. (2005) provide a glimpse into the intron composition of the phylum Annelida by sequencing a total of 2.3 megabases of the genome of the segmented worm *Platynereis dumerilii* and by predicting 30 gene transcripts. These transcripts contain an average of 7.8 introns, very similar to the number seen for homologous genes in humans (8.4 introns per gene), and the highest yet found in any invertebrate (assuming that the remainder of the annelid genome yields a similar number).

Given that both of the two debated hypotheses of animal phylogeny (see Figures 1B and 1C) place annelid worms closer to arthropods than to deuterostomes, there are only two ways that the annelid could have an

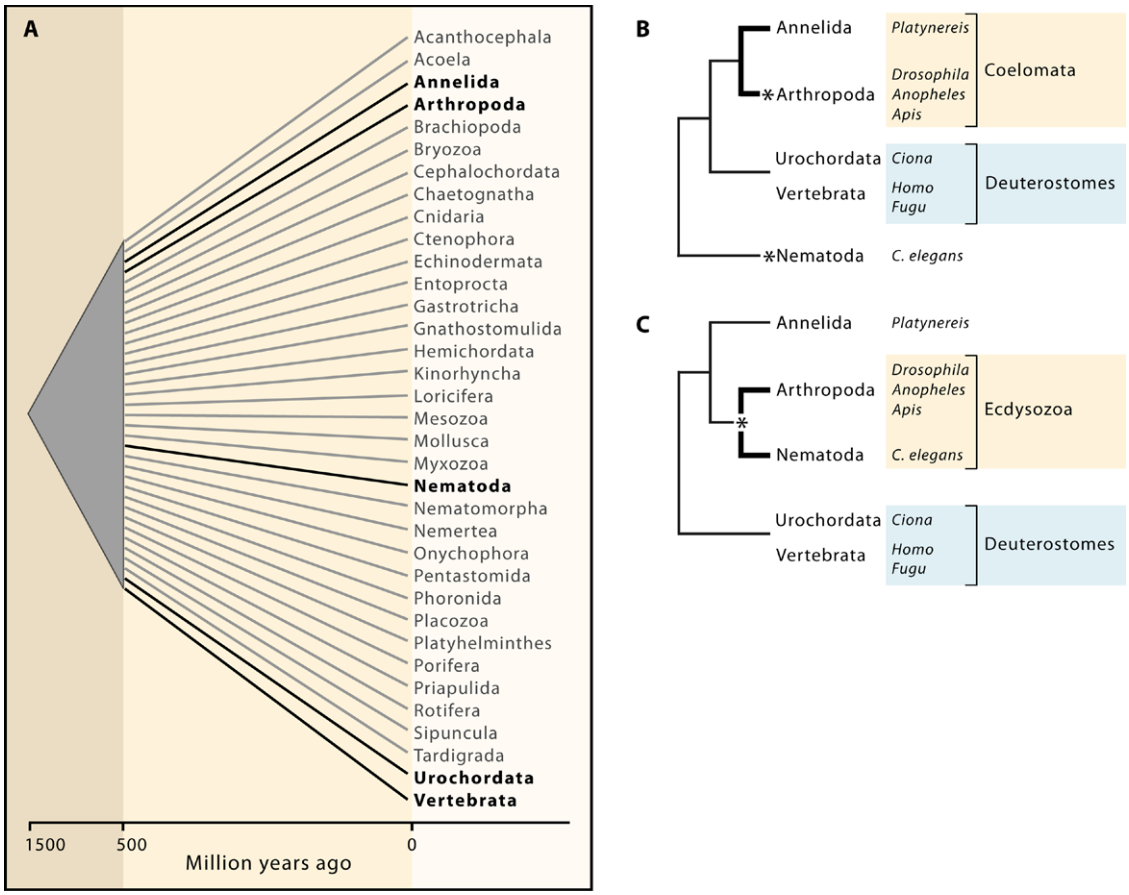

Figure 1. Diversity of Animal Groups and Their Evolutionary Relationships

(A) Names of major groups containing all living animals, along with the range of divergence times derived from molecular data (Blair et al., 2005). Raible et al. (2005) analyzed member species from the five highlighted groups to infer intron richness in the common ancestor of arthropods and nematodes, which represents a deep divergence among animals.

(B and C) Two contrasting phylogenies relating the five groups. The Coelomata hypothesis places annelids as the closest relatives of arthropods (B). In contrast, the Ecdysozoa hypothesis proposes that nematodes and arthropods are most closely related (C). The black asterisks indicate potential points when introns may have been lost.

intron-rich genome: (1) It was retained from the last common ancestor of arthropods and deuterostomes, or (2) it acquired the higher number of introns secondarily. To determine which explanation is more likely, the authors scored the number of shared introns between the genes of the marine annelid and other animals. An intron was considered to be shared if it was found in the same amino acid position and the same codon position (the same intron phase). Interestingly, annelid genes shared more than 60% of introns with the human genome but fewer than 30% with the other invertebrate genomes examined (those of the honey bee, fruit fly, and nematode). This observation supports the idea that intron richness is an ancient trait that has been preserved in the marine annelid genome. It also provides experimental support for the recent conclusion that a large number of introns in living animals are quite old (Roy and Gilbert 2005). The reason why this marine annelid retained introns when some other invertebrates lost most of them remains a mystery. Raible et al. (2005) also found that *Platynereis* shows a slow rate of protein sequence evolution, but, at present, it is unclear whether the high intron retention is causally related to a lower rate of protein evolution.

The phylogenetic scenario assumed by Raible et al. (2005) is the Ecdysozoa hypothesis, which postulates that nematodes and arthropods are close relatives (see Figure 1C). This hypothesis proposes that introns were lost in the Ecdysozoan common ancestor. The competing Coelomata hypothesis instead assumes that nematodes branched from the animal tree before the split of arthropods and deuterostomes (see Figure 1B). Under this scenario, introns were lost independently in the lineage leading to nematodes and the lineage leading to arthropods. On the other hand, if the last common ancestor of arthropods and deuterostomes was intron poor (e.g., Rogozin et al., 2003), a different scenario of intron gain and loss would need to be postulated.

However, current inferences about the evolution of introns are at best tentative because virtually no information exists about intron content for a vast majority of animal phyla and major clades. The sampling of species from each group is meager, and our ability to reliably map the intron gain and loss on ancestral evolutionary lineages is highly limited. A case in point is the observation that the tunicate *Ciona*, a deuterostome, contains far fewer introns per gene than its closest relatives (fish and human). If its genome were the only one available for deuterostomes, we would have erroneously inferred that deuterostomes lost introns early in their evolutionary history.

Finally, the observation of intron loss in several independent lineages of animals may be an indication that the increased number of alternatively spliced gene products in the cell, afforded by an increased intron content, was not the prelude to a higher phenotypic complexity of animals. Perhaps, as suggested by Lynch and Conery (2003), the evolution of introns is attributable to smaller population sizes of bigger (more complex) organisms. This allows introns to escape natural selection and to become fixed in the genome without initially having an adaptive role. In this case, the complexity and diversity of advanced animal body plans arose independently of the intronic enrichment of their genomes.

REFERENCES

Blair, J.E., Shah, P., and Hedges, S.B. (2005). Evolutionary sequence analysis of complete eukaryote genomes. BMC Bioinformatics *6*, 53.

Gilbert, W. (1978). Nature *271*, 501.

Lynch, M. (2005). Mol. Biol. Evol. Published online November 9, 2005. 10.1093/molbev/msj050.

Lynch, M., and Conery, J.S. (2003). Science *302*, 1401–1404.

Raible, F., Tessmar-Raible, K., Osoegawa, K., Wincker, P., Jubin, C., Balavoine, G., Ferrier, D., Benes, V., de Jong, P., Weissenbach, J., et al. (2005). Science *310*, 1325–1326.

Rogozin, I.B., Wolf, Y.I., Sorokin, A.V., Mirkin, B.G., and Koonin, E.V. (2003). Curr. Biol. *13*, 1512–1517.

Roy, S.W., and Gilbert, W. (2005). Proc. Natl. Acad. Sci. USA *102*, 1986–1991.

Sambrook, J. (1977). Nature *268*, 101–104.

Playing Ping Pong with Pins: Cortical and Microtubule-Induced Polarity

Julie Ahringer[1,*]

[1]The Gurdon Institute and Department of Genetics, University of Cambridge, Tennis Court Road, Cambridge CB2 1QN, United Kingdom

*Contact: jaa@mole.bio.cam.ac.uk

DOI 10.1016/j.cell.2005.12.011

Cortical cell polarity controls mitotic spindle orientation in many cell types. In this issue of *Cell*, Siegrist and Doe (2005) turn this around and show that the transfer of polarity information between the cortex and the spindle is not just one way. In *Drosophila* neuroblasts, the spindle also has polarizing activity on the cortex.

Many animal cells have polarized functions. They can separate inside from outside, undergo directed migration, grow in a defined direction, or divide to give daughters of different fates. So it is important to understand how cells become polarized and how this polarity is communicated and coordinated with cellular functions.

A popular model system for addressing these questions is the study of neuroblasts in the fruit fly *Drosophila* (reviewed in Betschinger and Knoblich, 2005)In *Drosophila* embryos, neuroblasts delaminate basally from a polarized epithelium, the neuroectoderm (Figure 1). These neuroblasts become polarized along their apical/basal axes and undergo asymmetric cell divisions to generate two daughter cells of different sizes and fates, a larger apical neuroblast and a smaller basal ganglion mother cell. Before division, the spindle rotates to orient along the apical/basal polarity axis. Understanding how cortical polarity information controls the orientation of the mitotic spindle is a major focus of research. Siegrist and Doe (2005), in this issue of *Cell*, show that information does not just flow from the cortex to the inside of the cell but that the spindle also communicates to the cortex to ensure the robust coordination of spindle orientation with cortical polarity.

The cortical polarity of neuroblasts is controlled by a set of apically localized proteins: the conserved Par complex (consisting of Bazooka, Par-6, and atypical protein kinase C) and the Inscuteable protein (reviewed in Betschinger and Knoblich [2004]). Disruption of the Par/Insc pathway leads to defects in spindle orientation and mislocalization of basal proteins