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Shape, length and location of PAR polarity in asymmetric cell division

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Anterior-posterior (AP) polarity formation of cell membrane proteins plays a crucial role in determining cell asymmetry, which depends not only on the several genetic process but also biochemical and biophysical interactions. In *Caenorhabditis elegans*, a single fertilized egg cell (P0), its daughter cell (P1), and the germline precursors (P2 and P3 cells) form two exclusive domains of PAR proteins on the membrane along the anterior-posterior axis. Since a mother cell divides into two dissimilar daughter cells with different properties using this polarity, the shape and length scale of PAR domains are critical. Furthermore, the phenomenon of polarity reversal has been observed in which the axis of asymmetric cell division of the P2 and P3 cells is formed in an opposite manner to that of the P0 and P1 cells. The extracellular signal MES-1/SRC-1 has been shown to induce polarity reversal, but the detailed mechanism remains elusive. Here, I explore the mechanism of symmetry breaking and AP polarity formation using self-recruitment model of posterior proteins and show how the shape, length and location of PAR polarity can be form robustly. If time is allowed, I also introduce a multi-dimensional polarity model including cell's geometrical property and show how the cell geometry can give a critical effect on AP polarity.

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