

# Study provides new data about the laws governing embryo development in organisms

July 11 2007

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Research aimed at understanding the mechanisms underlying embryo development has taken a step forward thanks to collaborative work between biologists specialized in the study of the fruit fly (*Drosophila melanogaster*) and scientists specialized in the design of mathematical models that simulate the functioning of biological systems.

Specifically, a study of wing formation in *Drosophila*, led by the researchers Marco Milán, from the Institute for Research in Biomedicine (IRB Barcelona), and Javier Buceta, from the Centre for Research in Theoretical Chemistry (CeRQT), both located within the Barcelona Science Park (PCB), has led to the discovery of a new genetic function involved in this process, and furthers our understanding of the internal laws which regulate it. The article will be published on 11 July in the journal PLoS One.

The development of a living being is based on general laws written into the genetic code of each cell and which enable them to develop a specialist function, modifying the way they divide, their form and their behaviour. These changes are coordinated through a series of instructions that must be correctly interpreted within the cell, and this means that the information must pass along a pathway of signalling molecules. These pathways have been conserved across evolution, and therefore studies using models such as the fruit fly provide information about these same processes in humans and other animals.

The Developmental Biology of *Drosophila* Group from the IRB

Barcelona, led by Marco Milán, studies the signals that guide wing development in *Drosophila*. The wings are generated from a set of cells grouped into different segments or compartments that never mix with one another, and which enable the symmetrical construction of the dorsal and ventral parts starting from a given limit or border. This process of subdivision into compartments also takes place during the formation of the vertebrate central nervous system, and the genes and signalling pathways involved are conserved in both *Drosophila* and vertebrate species.

Although biologists already had an intuitive idea of how the limit or border between these compartments was generated, there had been no systematic study taking into account all the relevant elements. Therefore, and with the backing of a group from the CeQRT of the PCB, led by Javier Buceta, they decided to turn to mathematical modelling as a way of understanding better the internal mechanisms which regulated this process. In this way they identified certain interactions in the signalling pathways that brought to light a number of contradictions and showed that a key step was missing in their model. As Milán explains: “Thanks to this computer simulation we have found a new genetic function that ensures the stability of the system and has enabled us to test its robustness. This study shows that modelling is a highly useful tool for describing *in silico* new properties of a biological system and being able to corroborate them subsequently *in vivo*”.

In this regard, Buceta, who leads a group dedicated to modelling biological processes (the SiMBioSys) in the CeRQT, explains that “the advantage of these modelling techniques is that they can simulate genetic and cell interactions as a set of mathematical equations and, therefore, to determine the feasibility of a biological mechanism”. In order to study the stability of the system they conducted around 45,000 different *in silico* experiments, introducing variations in twenty parameters. The results have enabled them to identify the most important system

parameters and showed that the biological mechanism maintained its functionality in 91% of the cases analyzed. According to Milán and Buceta “this study confirms the hypothesis that if this gene network has been maintained across evolution in both vertebrates and insects, it is precisely because it is highly stable and robust”.

Source: Institute for Research in Biomedicine

Citation: Study provides new data about the laws governing embryo development in organisms (2007, July 11) retrieved 25 April 2024 from <https://phys.org/news/2007-07-laws-embryo.html>

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