

Reductionism and context simplification in Developmental Biology

Some considerations from a study case

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In the so called “post-genome era”, after the complete sequencing of the genome of several animals and plants, we are left with the challenge of dividing the complete DNA sequence into functional units and understanding their roles during the lifespan of living organisms. Developmental genetics study the expression patterns and functions of genes during the embryonic development using several vertebrate and invertebrate models. The big difficulty of such an analysis is to understand complicated and interconnected regulatory patterns that take place during the most intense and crucial moment of an organism’s life, its development.

Big advances in genetic engineering and bioinformatics led to an exponential increase of our knowledge in the last years. Nevertheless, decoding transcriptional regulation (identification and characterization of targets of transcription factors in non-coding DNA) and post-transcriptional control remains a challenge, and some questions remain to date difficult to answer with the available approaches. Here, I analyze some contributions and some limitations of the reductionist approach, which is at the basic of the functional genome analysis based on experimental biology.

As an example I report briefly some results of a project aimed to identify the function of a novel transcription factor (*Tshz1*) in the development of a cell population in the mouse olfactory bulb (the complete work is published in the form of dissertation and available at the link http://www.diss.fu-berlin.de/diss/receive/FUDISS_thesis_000000003544).

The reduction of complexity and the simplification of context led to some success in the functional analysis, although the identification of a causal and regulatory network underlying the analyzed phenotype was so far not possible. I suggest that, although it is hard to imagine how a holistic approach would lead to success with the tools available to date, reductionism might be a hindering factor when approaching a system whose variables are not only big in number, but also mostly unknown. In particular, reduction of genetic diversity, simplification of multiple causal pathways, formulation of the questions, fragmentation of the brain anatomy and of the genome in putative functional units, and attempt of a clear separation of causes and effects are considered specifically in the example reported, and their contribution to the final result is discussed.