

Identification of all gene functions within reach

A new approach enables stem cell researcher Jürgen Knoblich to investigate the function of genes across an organism's whole genotype simultaneously. In future this will make it possible to tackle the identification of the causes of illnesses even more systematically.

Our genes determine how we look, but also what illnesses we suffer from. Since the beginning of this century, all human genes have been identified. But what function does each gene have in the organism? For humans this question will remain unanswered for some time to come, but for a model organism like the fruit fly an answer is already possible. In the next edition of the renowned professional journal *Nature*, IMBA stem cell researcher Jürgen Knoblich and his post-doctoral researcher Jennifer Mummery-Widmer describe the functions of no less than 2,600 of approximately 13,000 known genes in the fruit fly genome together with the networks linking them.

Simultaneous analysis of all genes possible for the first time

This quantum leap is the result of a new procedure with which makes it possible to analyse complex biological processes in all the genes of the fruit fly simultaneously. This unusually extensive gene analysis was only made possible by using the IMP-IMBA fly library, which was compiled by neurobiologist Barry Dickson. The database contains 20,000 strains of flies and in each of these exactly one gene is deactivated.

More systematic development of therapies

This amounts to a paradigm shift as far as medical progress is concerned. When faced with a clinical picture, the old approach was to search for the responsible gene, the proverbial needle in a haystack. In principle, all genes are now known, and the question is a much more systematic one: what exactly do the genes related to the illness control in the body? Which biochemical pathways and signal chains are being interrupted, and what approach can be used to get them going again? Jürgen Knoblich is convinced: "This is exactly how medication has to act in order to fight an illness. We want to find out which of these gene networks is responsible for the growth of tumours and controlling stem cells in humans," is how Jürgen Koblich explains the next steps.

Publication:

Mummery-Widmer, J.L., Yamazaki, M., Stoeger, T., Novatchkova, M., Bhalerao, S., Chen, D., Dietzl, G., Dickson, B.J. and Knoblich, J.A. (2009). Genome-wide analysis of Notch signalling in *Drosophila* by transgenic RNAi. *Nature*.