CDB SEMINAR

Silke Rinkwitz

Brain and Mind Institute

Sydney Medical School, University of Sydney

Wednesday, October 14, 2009

16:00~16:45 A7F Seminar Room

Genome architecture and new strategies to analyze gene regulation and activity

Summary

We performed an enhancer detection screen in the zebrafish, which gave rise to 1200 zebrafish lines that express YFP in the developing embryo. About 330 of these lines were deemed interesting and the insertions mapped to the genome. Identification of the corresponding genes was based on GO terms and on expression pattern of genes across the chromosomal insertion site. Among the genes identified are transcriptional regulators, growth factors, pathway modulators, genes involved in neuronal patterning, path finding as well as micro RNAs. We frequently find that the target gene with the same expression pattern as the reporter gene can be at a genomic distance of 100-200 kb. Insertions close to Hox genes revealed the expression patterns of the genes in early as well as late developmental stages with the cytoplasmic YFP distributing uniformely within the cell and axonal projections of neurons. With focus on the Hox4 genes neuronal subtypes that express the genes could be elucidated. Often, the non-coding sequences surrounding the targeted genes have strong conservation indicating a putative regulatory role for the gene they surround. We show, with Hox4 genes as example, how this information can be used to dissect the cis-regulatory landscape of the genes. The study further reveals that enhancers that regulate Hox genes can act outside the clusters as regular enhancers. The results will be discussed.

Host:

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