

REGULATORY GENOMICS – DECODING DROSOPHILA REGULATORY SEQUENCES

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The precise regulation of gene expression is crucial for all animals. The regulatory information about when and where genes are to be expressed is located in defined genomic elements called enhancers that are able to activate gene expression in precise spatial and temporal patterns. We have developed a novel method (STARR-seq) to find such enhancers and measure their activity quantitatively across entire genomes. This allows us to trace enhancer activity across evolution and study its sequence basis.

Using STARR-seq, we screened the genomes of five closely related *Drosophila* species in *Drosophila melanogaster* S2 cells to trace cis-regulatory function across evolution in a constant trans-regulatory environment. STARR-seq reveals a surprising complexity of gene regulation with several independently functioning enhancers for single genes, including both developmental regulators (e.g. transcription factors) and broadly expressed genes.

Time: Friday, September 20th, 2013, 14:00 s.t. – 15.00

Location: Seminar room 44.22, 2nd floor, ZMB, Karl-Franzens University Graz,
Humboldtstrasse 48, 8010 Graz