

Stellingen

Behorende bij het proefschrift

‘Transcriptome profiling of infectious diseases and cancer in zebrafish’

1. Next generation sequencing methods allow the unbiased discovery of new infection-responsive gene products (chapters 2 and 3).
2. The complementary use of a microarray-based approach with tag-based (Tag-Seq) and full transcript (RNA-Seq) deep sequencing approaches presents the most complete characterization of innate immune transcriptome responses (chapter 3).
3. The identified overlap in infection- and cancer-related microRNAs as well as in their predicted target genes indicates common regulatory pathways in both processes that are still unexplored (chapter 4 and 5).
4. MicroRNA-146 mediates a feed back mechanism to properly control inflammatory responses and cancer-related processes (chapters 4 and 5).
5. Conservation at the level of microRNA expression between zebrafish and human liver tumors further supports the usefulness of zebrafish to study functions of microRNAs in the mechanisms of cancer (chapter 5).
6. Revealing the exact functions of microRNAs in gene regulation provides great potential for the therapy of pathological conditions such as cancer.
7. The emerging field of systems biology is highly dependent on advances in bioinformatics to integrate the wealth of information from seemingly disparate datasets.
8. Next generation sequencing is now transforming today's biology.
9. The post-genome challenge is to be able to interpret and use genomic data and to shift the focus from molecular characterisation to understanding of functional activity.

10. The European Framework Programmes for Research and Technological Development are beneficial to popularize zebrafish research in the Hungarian research community.
11. Feedback is the fundamental principle that underlies all self-regulating systems, not only machines but also the processes of life (Arnold Tustin, 1953).
12. Antisense is no nonsense.