Marie Curie International Reintegration Grants (IRG) Call: FP7-PEOPLE-IRG-2008

"EVO-DEVOMICS" - DECODING DEVELOPMENTAL GENE REGULATORY PROGRAMS BY EVOLUTIONARY TRANSCRIPTOMICS

The goals of the proposed research were to: 1) to construct a molecular atlas for the developmental gene regulatory programs of seven nematode species and to test a model for developmental reprogramming, and 2) to directly test developmental reprogramming predictions in endoderm specification.

A description of the work performed since the beginning of the project,

1. An atlas for developmental gene regulatory programs across nematode embryology was constructed. Using this dataset, it was discovered that developmental milestones punctuate gene expression. The results were published in the journal Developmental Cell:
    a. http://www.cell.com/developmental-cell/abstract/S1534-5807(12)00142-6
    b. It was highlighted with a Preview article: http://www.cell.com/developmental-cell/abstract/S1534-5807(12)00198-0
2. A method for single cell RNA-Seq was developed which was both highly multiplexed and dependent upon linear amplification. This method was published in Cell Reports:
    a. http://www.cell.com/cell-reports/abstract/S2211-1247(12)00228-8
    b. It was highlighted in a recent review: http://www.nature.com/nrg/journal/v14/n9/full/nrg3542.html
3. We discovered a genomic bias for genotype-environment interactions in the C. elegans genome by examining gene expression of the C. elegans early embryo across five strains in five different conditions. We reported our findings in the journal Molecular Systems Biology.
    a. http://www.nature.com/msb/journal/v8/n1/full/msb201219.html
    b. We were also invited to submit a Review on these results in the journal Trends in Genetics: http://www.sciencedirect.com/science/article/pii/S0168952513000851

Expected final results and their potential impact. The final results have already been published and their impact already in sight. First, the atlas is being used by researchers of *C. elegans*. For every gene, users of the Wormbase site can see the gene expression profile from our atlas. For example, here is the profile for the gene tbx-43: http://www.wormbase.org/species/all/expr_pattern/Expr1012093#021--10. The Levin et al publication arising from this work (link above) has already cited 16 times since publication in 2012. A series of experiments have been planned following this work which has recently received funding from the ERC to the researcher (Itai Yanai). The CEL-Seq protocol developed as part of this project is a very successful method now used by many labs worldwide. Using this method, it is possible for any lab to examine individual cells at the whole transcriptomic level. Third, we discovered one important genomic biases for genotype-environment interactions. Though the work was done in the worm C. elegans, the insight derived there for the importance of trans effects is applicable to humans for detecting the advese effects of medicine. We are now collaborating with members of our medical school to follow up on this insight.