Poster Abstracts

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Genetical genomic approaches for understanding climatic adaptation in natural populations of Caenorhabditis elegans.

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Since Bergmann's observation in 1847 that mammals tend to grow bigger with increasing distance from the equator (Bergmann's rule) biologists have been fascinated by the geographical distribution of body size. It was discovered that not only mammals but also ectotherms, such as fish, bacteria, protists, invetrebrates and plants, grow larger in regions further away from zero latitude. This latitudinal size gradient correlates strongly with a thermal size gradient in which body size increases in colder environments. Although many explanations have been offered considering the underlying mechanism of Bergmann's rule, the molecular genetic control is unknown. A C. elegans strain (N2) from temperate regions (UK, min–max temperature 4–18°) complied with Bergmann's rule and grew bigger at lower temperatures, whereas a strain (CB4856) from tropical regions (Hawaii, min–max temperature 23–24°) did not. After crossing these strains and inbreeding for 20 generations we obtained a segregant population of SNP genotyped RILs. So far we have mapped several QTLs underlying body size changes at the respective temperatures of 12° and 24°. Presently we are exposing all RILs to the same temperatures, extracting RNA and hybridizing all RIL samples according to Fu and Jansen (in prep) using whole genome oligo arrays (obtained from GSC, Washinton University, St. Louis). The quality of the arrays is checked according to Prins et al. (in prep) and QTL analysis will be run on the expression profiles of the RILs. Using this genetical genomics approach we hope to unravel the linked genes which control Bergmann's rule in C. elegans.

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BABELOMICS: a suite of web–tools for functional annotation and analysis of groups of genes in high–throughput experiments

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We present Babelomics, a suite of web tools for functional analysis of groups of genes in high–throughput experiments, which includes the use of information on GO terms, interpro motifs, KEGG pathways, Swissprot keywords, analysis of predicted transcription factor binding sites, chromosomal positions and presence in tissues with determined histological characteristics, by means of five integrated modules: FatiGO, FatiWise, TransFAT, GenomeGO and TMT, respectively. Additionally, another module, FatiScan, provides a new procedure which integrates biological information in combination with experimental results in order to find groups of genes with modest but coordinate significant differential behaviour. FatiScan is highly sensitive and is able of finding significant asymmetries in the distribution of genes of common function across a list of ordered genes even in the case of these asymmetries were not extreme. The strong multiple–testing nature of the contrasts made by the tools is taken into account. All the tools are integrated in the gene expression analysis package GEPAS (http://www.gepas.org). Babelomics is the natural evolution of our tool FatiGO (http://www.fatigo.org, which analysed almost 22,000 experiments during the last year) to include more sources on information and new modes of using it. Babelomics can be find at: http://www.babelomics.org

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Genotyping Chip: A spotted array–based open mutation testing system

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The application of microarray technology for diagnostic mutation detection testing has the potential to change molecular genetics and personalized medicine. The simultaneous analysis of multiple mutations is expected to not only decrease the turn over time in the lab but also decrease the cost per genotype. Genotyping assays have been developed by several companies however they generally require that end users utilize the reagents, arrays and equipment from their company. Small specialized panels which focus on minority or ethnic groups are often not being developed due to their lack of profitability. This results in the need to use multiple platforms to perform several different tests. The aim of this study is to develop a spotted array–based mutation testing system which is compatible with most of the commercially available microarray scanners and reagents. The array