IN BRIEF

TECHNOLOGY

Genome-wide detection of polymorphisms at nucleotide resolution with a single DNA microarray.

Gresham, D. *et al. Science* 9 March 2006 (doi:10.1126/science.1123726)

This paper describes a simple, inexpensive method for the genome-wide detection of intraspecific mutation and variation using a single microarray. The authors used a tiling array that provides roughly fivefold coverage of the *Saccharomyces cerevisiae* reference genome. Using known SNPs as a training set, they devised an algorithm that predicts the presence of single-nucleotide differences across the genome on hybridization to the array. In several scenarios, this approach provided sensitive, high-resolution detection of SNPs and also identified insertions and deletions, highlighting its potential for a range of applications.

NETWORK BIOLOGY

Genome-wide prediction of *C. elegans* genetic interactions.

Zhong, W. & Sternberg, P. W. *Science* **311**, 1481–1484 (2006)

Genetic interactions can be revealed by modifier screens but their success depends on easily scorable phenotypes and they are not feasible on a global scale in metazoans owing to their genome complexity. These authors used a computational approach to integrate interactome, gene-expression, phenotype and functional annotation data from baker's yeast, the fly and the worm. Pooling information from different species overcomes incompleteness of the data for any one organism. The result was a network of 18,183 functional genetic interactions in the worm, which is publicly available and serves as a cross-species genetic data search engine for genetic interactions.

LIFESPAN

Germ-cell loss extends *C. elegans* life span through regulation of DAF-16 by *kri-1* and lipophilic-hormone signalling.

Berman, J. R. & Kenyon, C. *Cell* **124**, 1055–1068 (2006)

SMK-1, an essential regulator of DAF-16-mediated longevity.

Wolff, S. *et al. Cell* **124**, 1039–1053 (2006)

These studies provide new insights into the specificity and integration of pathways that control lifespan. Berman and Kenyon showed that the *Caenorhabditis elegans* gene *smk-1* is essential for the control of longevity by the transcription factor DAF-16, which is the effector of the insulin signalling pathway. Furthermore, *smk-1* is needed specifically for DAF-16 to regulate stress responses that are involved in lifespan extension, but not for other physiological effects of the insulin signalling pathway. This indicates that lifespan regulation can be uncoupled from other potentially harmful functions of this pathway. As well as insulin signalling, reproductive status also affects longevity, and Wolff and colleagues showed how these two factors might be integrated. In a screen for new genes that are required for increased lifespan due to loss of germ cells, they identified *kri-1*, and showed that hormone signalling from the reproductive system to the intestine promotes DAF-16 function through the activity of this gene.