Nature Reviews Genetics | AOP, published online 13 May 2008; doi:10.1038/nrg2387

IN BRIEF

YEAST GENETICS

The chemical genomic portrait of yeast: uncovering a phenotype for all genes.

Hillenmeyer, M. E. *et al. Science* **320**, 362–365 (2008)

In *Saccharomyces cerevisiae*, only ~20% of genes are essential under optimal growth conditions. To test the general validity of this number, the authors carried out a chemical genetics experiment in which >1,000 heterozygous and homozygous deletion strains were subjected to a range of 400 chemicals and various environmental stresses. Almost all (97%) strains showed a measurable growth phenotype, suggesting that most genes are essential in at least one condition.

QUANTITATIVE GENETICS

Gene-centric genomewide association study via entropy.

Cui, Y. *et al. Genetics* 1 May 2008 (doi:10.1534/genetics.107.082370)

Current designs for genome-wide association studies largely rely on linkage between a SNP or haplotype and the causal disease variant, which makes many results difficult to replicate owing to variations in linkage disequilibrium patterns. This paper describes a new design in which all variants within one gene are treated as a single unit. The power of this gene-centric approach is illustrated by comparing the false positive rate of such a method with a single-SNP design under various parameters, and using real and simulated data.

SYNTHETIC BIOLOGY

A synthetic *Escherichia coli* predator–prey ecosystem.

Balagaddé, F. K. *et al. Mol. Syst. Biol.* **4**, 187 (2008)

The authors have generated one of the most complicated and best resolved of synthetic circuits — one that reproduces interactions between predators and prey. The two populations, derived from a single population of *Escherichia coli*, influence each other's abundance through interconnected quorum-sensing modules. The strength of this synthetic ecosystem lies in being able to relate population dynamic behaviours to variations in the parameters of the circuit. Similar design principles can be used to examine the interplay of environment, gene regulation and population dynamics.

GENE REGULATION

Identification of active transcriptional regulatory modules by the functional assay of DNA from nucleosome-free regions.

Yaragatti, M. *et al. Genome Res.* 25 Apr 2008 (doi:10.1101/gr.073460.107)

Most approaches for identifying *cis*-regulatory modules do not explore the functional activity of the candidate sequences. This paper describes an approach that addresses this issue by isolating and assaying DNA fragments specifically from nucleosome-free regions (NFRs) — the regions of the genome that contain regulatory elements. The method uses the enzymatic accessibility of NFRs to isolate them from other genomic DNA, followed by cloning the resulting fragments into reporter plasmids to assay their regulatory activity. The authors identified more than 100 new regulatory modules using this approach.