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Linkage analysis in yeast

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In a paper published on March 28 in [Scienceexpress](#), Brem *et al.* describe how linkage analysis and gene expression profiling can be combined to dissect transcriptional regulatory networks in the budding yeast, *Saccharomyces cerevisiae* (DOI:10.1126/science.1069516). They crossed two yeast strains, a laboratory strain BY and a wild isolate RM from an Italian vineyard. Microarray analysis revealed 1528 genes expressed differentially between the two parent strains. They then used an [oligonucleotide array technique](#) to generate a genetic map with 3312 markers. The expression level of 570 genes showed linkage to at least one locus. Over 300 of these displayed parental differences in expression. Brem *et al.* suggest that regulatory patterns are complex and that many messages are affected by multiple loci (perhaps as many as five). They separated the results into those genes regulated by *cis*-acting modulators and sets of genes modulated by *trans*-acting loci. Thus, even single-celled organisms exhibit complex regulation of transcriptional variation that involves polygenic control.

References

1. *Scienceexpress*, [<http://www.scienceexpress.org>]
2. Direct allelic variation scanning of the yeast genome.