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Making sense of antisense

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The yeast *Candida albicans* is the major pathogen causing human fungal infections. *C. albicans* is not amenable to functional genomic strategies used for other micro-organisms, because of mating difficulties, its diploid nature and the lack of random insertional mutagenesis methods.

In the March Nature Biotechnology, Marianne De Backer and colleagues describe an approach to overcoming these limitations, in order to perform a genome-wide screen for gene function (*Nature Biotechnology* 2001, **19:**235-241). The technique combines antisense RNA and promoter interference technology and involves the development of an integrative vector to drive transcription of antisense RNA in an inducible manner.

De Backer *et al* created a library of clonedC. albicansDNA fragments, introduced these into *C. albicans* and screened for the effects of gene suppression on yeast growth. About 10% of transformants showed a growth phenotype and it was possible to identify 86 different genes, of which 38% have no homologues in other organisms.

They also showed that these crippled strains could be used effectively in high-throughput screening assays to identify possible antifungal drugs. This is because reduced expression of a gene renders the yeast more sensitive to drugs that act on its protein product or associated molecules in the same pathway.

References

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2. *Nature Biotechnology*, [http://www.nature.com/nbt/]

3. *Candida albicans* sequence at Stanford University, [http://www-sequence.stanford.edu/group/candida/index.html]