IN BRIEF

➔ TECHNOLOGY

Cellulose synthase-like *CsIF* genes mediate the synthesis of cell wall (1,3;1,4)- β -D-glucans.

Burton, R. A. *et al. Science* **311**, 1940–1942 (2006)

The tough cell walls of many cereals consist largely of the polymer β -glucan, which is a bane to beer producers but contributes greatly to the soluble fibre content of these crops and is associated with many health benefits. This paper identifies the *CsIF* gene family as being responsible for the biosynthesis of β -glucan; a locus was identified as a major-effect QTL in barley, and then six genes were cloned from a syntenic region in the rice genome. The function of the genes was confirmed by the ability of three of these rice genes to produce β -glucan when expressed in *Arabidopsis thaliana*, which lacks the β -glucan polymer. This knowledge could be applied to improve the otherwise poor fibre content of wheat — either through traditional breeding or transgenic means — or to create improved material for biofuels.

➔ POPULATION GENETICS

The distribution of fitness effects of new deleterious amino acid mutations in humans.

Eyre-Walker, A. *et al. Genetics* 17 March 2006 (doi:10.1534/genetics.106.057570)

Describing the fitness effects of new mutations — the proportion of new mutations in our genomes that are deleterious, and to what degree — is central to many areas of biology, including understanding the genetic basis of disease and the maintenance of genetic variation. The authors have overcome the limitations of previous approaches to estimating fitness effects by analysing extensively sampled human SNP data alone. They show that the fitness effects of amino-acid changing mutations follows a gamma distribution. In addition, on average, a non-synonymous mutation reduces fitness by only ~4.3%. Any relaxation on selection that has occurred through improved medical care is therefore unlikely to cause a decline in genetic quality, although variants that underlie complex diseases might be harder to find than expected.

➔ RNA WORLD

A lentiviral RNAi library for human and mouse genes applied to an arrayed viral high-content screen.

Moffat, J. *et al. Cell* **124**, 1283–1298 (2006)

This paper describes a new resource for high-throughput RNAi screening in mammalian cell lines. The RNAi Consortium has produced and tested a lentiviral library of short hairpin RNAs (shRNAs) directed against 22,000 human and mouse genes, with an average coverage of 5 different shRNAs per gene. The lentiviral basis of the reagents allows delivery to non-dividing cells, including primary cell lines, which overcomes an important limitation of other delivery methods. The authors have also developed a protocol that allows a high-titre stock to be generated efficiently for each shRNA. The library is available from **Sigma-Aldrich** (<http://www.sigmaaldrich.com>) and **Open Biosystems** (<http://www.openbiosystems.com>), and details can be found at the **RNAi Consortium web site** (http://www.broad.mit.edu/genome_bio/trc).

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10.1038/nrg1860

URLs

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<http://www.sigmaaldrich.com>

Open Biosystems:
<http://www.openbiosystems.com>

RNAi Consortium

web site: http://www.broad.mit.edu/genome_bio/trc