Although rice might look different from tomato and *Arabidopsis*, there are similarities in the way that they grow. The main stem produces leaves with associated axillary meristems, and the meristems that are closest to the base can develop into tillers — grain-bearing branches. Li *et al.* found a spontaneous mutation that causes a loss of vegetative axillary meristems and, therefore, tillers, as well as a reduction in plant height and reproductive branching. The mutated gene — *MONOCULM1* (*MOC1*) — is homologous to *LS*. So, it seems that *LS* gene function is widely conserved.

RNA *in situ* hybridization analysis showed that *LAS* is expressed in the cells from which axillary meristems develop, whereas *MOC1* is transcribed in axillary meristems from the earliest stages of development. Mutant analysis indicated that, in leaf axils, *MOC1* is genetically upstream of the known rice meristem regulators *OSH1* and *OsTB1*. Similarly, *LAS* is needed in *Arabidopsis* for the correct expression of *SHOOTMERISTEMLESS* (*STM*) and *REVOLUTA* (*REV*) — important genes that are required for meristem function. *LAS* and *MOC1* might activate transcription directly as they are members of the plant-specific GRAS family, which are believed to be transcription factors. Consistent with this, Li *et al.* show that a MOC1–GFP fusion protein is localized in the nucleus.

The high level of conservation of *LAS* and *MOC1*, together with their upstream positions in known genetic hierarchies, indicates that they might be master regulators of axillary meristem formation. Therefore, these genes are likely to be a hot area for future research. Not only will this work contribute to our understanding of plant development, but it might also have an important agronomic impact because tiller production in cereals is a key determinant of grain yield and the level of tomato branching can affect fruit size.

Catherine Baxter

References and links

ORIGINAL RESEARCH PAPERS Li, X. *et al.* Control of tillering in rice. *Nature* **422**, 618–621 (2003) | Greb, T. *et al.* Molecular analysis of the *LATERAL SUPRESSOR* gene in *Arabidopsis* reveals a conserved control mechanism for axillary meristem formation. *Genes Dev.* **17**, 1175–1187 (2003)

WEB SITES

Jiayang Li's laboratory: http://www.genetics.ac.cn/xywwz/Faculty/jyli.htm

Klaus Theres' laboratory: http://www.mpiz-koeln.mpg.de/~theres

These results are stunning, as a standard assumption has been that Y chromosomes drift faster than mtDNA because males are more promiscuous and vary more in their reproductive success than do females. If the results are replicated in other populations the implications could be important — more realistic estimates of the rates of genetic drift might completely change our interpretation of human mtDNA and Y-chromosome data.

One thing is for sure: in Iceland, at least, it seems that girls do grow up faster than boys!

Nick Campbell

References and links

ORIGINAL RESEARCH PAPER

Helgason, A. *et al.* A population wide coalescent analysis of Icelandic matrilineal and patrilineal genealogies: evidence for a faster evolutionary rate of mtDNA lineages than Y chromosomes. *Am. J. Hum. Genet.* **72**, 29 April 2003

WEB SITE

deCODE Genetics: http://www.decode.com

IN BRIEF

FUNCTIONAL GENOMICS

Genomic gene clustering analysis of pathways in eukaryotes.

Lee, M. J. & Sonnhammer, E. L. L. *Genome Res.* **13**, 875–882 (2003)

Although operons are rare in eukaryotes, genes that act in the same pathways might still be clustered. The authors looked for clustering in five eukaryotic genomes for genes that have been assigned to the same pathway in the KEGG database. Although genes associated with 30–98% of pathways cluster to some extent, surprisingly, there is little conservation between genomes as to which genes are clustered, perhaps reflecting lineage-specific evolutionary-events.

FUNCTIONAL GENOMICS

Discovering novel *cis*-regulatory motifs using functional networks.

Etteiller, L. M. *et al. Genome Res*. **13**, 883–895 (2003)

Data from DNA-binding experiments, microarrays and genome comparisons have been used to facilitate regulatory-motif discovery. These authors use protein–protein interactions and metabolic networks in combination with *Saccharomyces cerevisiae* genome data to predict upstream regulatory motifs. They describe 42 potential sites, some of which are new and are associated with genes that are probably co-regulated. Their results show that interacting proteins are often transcriptionally coordinated, even if there is no evidence for their co-regulation in gene-expression data sets.

MOUSE MODELS

Mutations in dynein link motor neuron degeneration to defects in retrograde transport.

Hafezparast, M. *et al. Science* **300**, 808–812 (2003)

The genetic basis of most motor neuron diseases (MND) is unknown. But a promising breakthrough has been made from the study of two mouse mutants — *Legs at odd angles* and *Cramping 1*. These mice have progressive neurodegenerative disorders and share a similar pathology to human MND. Both mutants carry a missense point mutation in the cytoplasmic dynein heavy chain, which is needed for microtubule-mediated retrograde transport in axons.

CLONING

Molecular correlates of primate nuclear transfer failures.

Simerly, C. *et al. Science* **300**, 225–227 (2003)

So far, no one has successfully cloned a primate, let alone a human, by nuclear transfer. Cloned rhesus monkey embryos fail to develop beyond early stages because many of the cells are aneuploid as a result of aberrant mitotic-spindle formation. Two proteins, NuMA and HSET, are needed for correct spindle organization, but in primates — unlike other mammals — these proteins are exclusively associated with the chromosomes in unfertilized egg cells. As these chromosomes are removed during nuclear transfer, spindle organization is disorganized in primates and chromosome segregation fails.