

HYBRID VIGOUR

Infertility rescue

Sci. Rep. **5**, 11274 (2015)

Heterosis, or 'hybrid vigour', causes cross-bred offspring to have growth or other characteristics that are more advantageous than either of their purebred parents. Though helpful in agriculture, the heterotic advantage is rarely passed beyond the first generation. Now, Singh *et al.* have developed a genetic system to ensure consistent production of hybrid seed.

A number of approaches exist to suppress self-fertilization and ensure hybrid seed production, including the laborious removal of anthers from 'female' parents, chemical poisoning of the pollen, and biotechnological systems involving ribonuclease and ribonuclease inhibitor expression.

This new approach relies on sabotaging pollen production in the female parent. The maternal line is transfected with an expression cassette containing the gene for BECLIN1 an autophagy related protein from *Arabidopsis*. BECLIN1 is under the control of a promoter specific for the tapetum — a layer of cells which supports the developing male gametophyte. This promoter is mutated so that it requires a variant form of transcription factor (TBPm3) not present in the normal plant but co-supplied in the expression cassette. BECLIN1 interferes with programmed cell death in the tapetum; an essential part of its function. The male sterility thus induced is rescued in hybrids because TBPm3 is tagged with an additional protein fragment used by the ubiquitin ligase, COP1, to target proteins for degradation. The intended 'male' parent has a second expression cassette containing COP1 also

under the control of a tapetum-specific promoter. In hybrid plants (which contain both cassettes), COP1 drives degradation of TBPm3, preventing BECLIN1 synthesis, thus restoring tapetal cell death and male fertility.

This system is less labour intensive than mechanical or chemical approaches and should circumvent some of the biosafety concerns that accompany existing biotechnological approaches. Singh *et al.* demonstrated the functioning of their system in *Nicotiana tabacum* but its elegant simplicity should ensure its utility in commercial cereal and pulse breeding. CS

THERMOTOLERANCE

Waste management

Nature Genet. **47**, 827–833 (2015)

Breeding heat-tolerant crops is exceptionally important in the context of global warming. However, our understanding of the genetic basis of plant thermotolerance remains limited. By studying the African rice (*Oryza glaberrima*) adapted to tropical environments, Xin-Min Li, of the Shanghai Institutes for Biological Sciences, and colleagues uncovered a gene contributing to crop thermotolerance.

Utilizing a segregating population derived from a heat-tolerant African rice accession and a heat-sensitive Asian variety, the researchers narrowed down a major thermotolerant quantitative trait locus, *TT1*, to a gene encoding a 20S proteasome $\alpha 2$ subunit. Overexpressing *TT1* in Asian rice enhances thermotolerance, while silencing this gene causes heat sensitivity. Compared with the Asian allele, the African allele contains several nucleotide substitutions, including an arginine-to-histidine mutation.

Ubiquitylome analyses showed lower accumulation of ubiquitinated proteins in the African genotype during heat stress. Such higher proteasome activity suggests a higher protection against heat stress by eliminating cytotoxic denatured proteins.

Natural variations occurred on both coding and regulatory sequences of the *TT1* gene. The African specific haplotype, containing the arginine-to-histidine substitution, shows long-term heat tolerance, Asian varieties exhibit differential *TT1* expression, highly correlated with short-term heat tolerance and geographical distribution, suggesting the modulation of *TT1* for local adaptation at both protein and mRNA levels.

Introgression of the African *TT1* allele into the Asian variety increased yield under heat stress. Transforming this allele in *Arabidopsis* and tall fescue also enhanced their thermotolerance, showing its potential for breeding heat-tolerant varieties of a wide range of crops. JL

GENOME EVOLUTION

From big to immense

New Phytol. <http://doi.org/5ms> (2015)

The diversity in plant nuclear genome sizes spans three orders of magnitude. Recently, extremely compact genomes (60–80 Mb) have been sequenced, probably close to the theoretical limit to code all the genes needed for an average plant to function. Laura Kelly and colleagues sought the other extreme, and partially sequenced the 45-Gb genome of two diploid species of the lily relative *Fritillaria*, in order to understand what drives the expansion in these genomic giants.

The genomes of both species have expanded tremendously since they diverged. The majority of this expansion comes from a heterogeneous mix of low-abundance sequences, and not from a few highly repetitive elements, like in barley or cotton. The mechanism behind this appears to be the amplification of diverse repeats combined with a slower rate of deletion, resulting in the accumulation of ancient, highly diverged decayed DNA, originally derived from repetitive sequences.

This mechanism of DNA accumulation may be shared by other large-genome organisms, such as salamanders and lungfish. In the future it will be interesting to understand the evolutionary costs and benefits of maintaining such large and complex genomes, and whether they are on a trajectory towards extinction. GT

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ECOLOGY

Sourcing water in a savannah

Ecology **96**, 1466–1472 (2015)

Climate-driven shifts in rainfall regimes could alter the vertical distribution of water in soils, with potential consequences for the balance of deep- and shallow-rooted species. However, the extent to which trees and grasses compete for the same water source has remained unclear, particularly in tropical and subtropical savannahs.

Ricardo Holdo, of the University of Missouri, and Jesse Nippert examined the sensitivity of tree and grass transpiration to depth-specific variations in soil water content in a lowland savannah ecosystem in South Africa over the course of a growing season. Tree transpiration was inferred from measurements of sap flow, and grass transpiration from measurements of canopy temperature. The stable isotope signature of soil and xylem water was used to determine the source of the soil water. Tree transpiration proved to be positively correlated with soil water content at 40-cm depth, but largely insensitive to variations in soil moisture at shallower depths. In contrast, grass transpiration increased with soil water content at 5-cm depth, but was unaffected by variations at greater depths.

The differential sensitivity of trees and grasses to different sources of soil water adds to the evidence for depth-dependent niche partitioning among trees and grasses in savannah systems. AA