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PATHOGENOMICS Hybrid vs hybrid

Nature Genet. http://doi.org/bbxc (2016)

Triticale is an artificial hybrid cereal that combines wheat grain quality and yield with the robustness of rye. From its first commercial use half a century ago until 2001, triticale was resistant to powdery mildew, a devastating disease caused by the biotrophic fungus *Blumeria graminis*. Beat Keller at the University of Zürich, Switzerland, and colleagues now show that the pathogen has adapted to the hybrid cereal by undergoing hybridization itself.

The genomic sequences of different *B. graminis* strains indicate whether they infect wheat or rye. This also holds true for the newly emerging triticale-infecting isolates, which have large sequences from rye-infecting fungi merged into a mostly wheat-specific genomic background, a hallmark of hybridization followed by backcrossing. So, by combining their genomes, the pathogens have produced a hybrid strain with a host range expanded to include triticale. This event probably took place in Europe sometime after the development of triticale, and has occurred independently at least twice.

The molecular mechanism behind this host expansion is currently unknown, despite the authors checking the 'usual suspects' such as secreted effectors. Nevertheless, the discovery that pathogen evolution by hybridization closely mirrors host evolution, even in very short time frames, is of particular interest for agriculture, as it highlights the uncertain future of crop resistance to pathogens.

EPIDERMAL STRUCTURES Sculpting with RSL1 Curr. Biol. 26, 93-99 (2016)



Epidermal structures, such as unicellular rhizoids and multicellular propagules, played important functions in facilitating colonization of the land by plants. They promoted traits associated with land adaptation, such as nutrient acquisition, desiccation tolerance and reproduction. However, the genetic basis bolstering these epidermal structures remains largely unknown. Hélène Proust, of the University of Oxford, UK, and colleagues now find that the ROOTHAIR DEFECTIVE SIX-LIKE class 1(RSL1) transcription factors positively regulate the development of these epidermal structures.

Wild-type liverwort, *Marchantia polymorpha*, is abundant in epidermal structures, but two mutants showed no cells expanding out of the epidermis. The researchers identified an *MpRSL1* gene whose expression was disrupted in the mutants and whose overexpression restored

grassland ecology Nitrogen retention

New Phytol. http://doi.org/bbxf (2016)

Humans have approximately doubled the amount of biologically reactive nitrogen in the atmosphere over the past two centuries. Terrestrial plant communities can retain significant quantities of nitrogen, preventing its spread to the surrounding environment. Now, a series of glasshouse experiments suggests that the dominance, and not diversity, of plant traits determines the ability of grasslands to capture added nitrogen.

Franciska de Vries and Richard Bardgett of the University of Manchester, UK, examined the ability of 56 experimental grassland communities — comprised of various combinations of herbs and grasses, and differing in the diversity and dominance of various plant functional traits — to retain nitrogen. They fed the experimental plots with isotopically labelled nitrate and ammonium, and monitored uptake and retention over a 48-hour period. Nitrogen retention increased with root biomass, the abundance of herbs and the dominance of exploitative plant traits, namely a high specific leaf area and leaf nitrogen content, and a low leaf dry matter content. Whereas root biomass and herb abundance promoted plant nitrogen uptake, exploitative plant traits promoted soil microbial uptake.

Whether the nitrogen captured by exploitative plant communities is retained over longer periods of time will depend on its rate of remineralization. However, the researchers tentatively suggest that the ability of plants with exploitative growth strategies to capitalize on nitrogen additions in the short term may increase their abundance in the longer term. AA

research highlights

the epidermal structures. Five gain-offunction mutants with T-DNA inserted upstream of *MpRSL1* all developed ectopic rhizoids. Gene expression analysis confirmed that *MpRSL1* was specifically expressed in epidermal cells that developed into the epidermal structures.

The researchers showed that *RSL1* genes also controlled the development of rhizoids and axillary hairs in mosses. Moreover, transforming *MpRSL1* into the *Arabidopsis* mutant with defective *RSL1* function restored the root hairs, suggesting that the *RSL1* genes of *Arabidopsis* and liverwort are functionally conserved. It would seem that *RSL1* genes once regulated epidermal structures in the common ancestors of land plants, and retain that important function to this day. *JL*

GIBBERELLIN SIGNALLING Nectar control

Mol. Plant. http://doi.org/bbx4 (2015)

Flower and fruit development is one of the best-studied processes in plant biology. As well as petals, pollen, seeds and fruit, flowers also produce nectar, a sugary solution that attracts insects and other animals, either as pollinators or for defence. Auxin and jasmonic acid have both been implicated in the control of nectar production. Now, Lisa Wiesen at the University of Minnesota, USA, and colleagues have found a role for gibberellin (GA) in managing nectar flow.

A microarray investigation showed that GIBBERELLIN 2-OXIDASE6 (GA20x6), an enzyme that breaks down gibberellins and their immediate precursors, was overrepresented in nectar-producing nectaries. Furthermore, *Arabidopsis* mutants with non-functioning *ga20x6* genes produced significantly less nectar than wild-type plants, whereas an inhibitor of GA synthesis, paclobutrazol, restored their nectar production. Conversely, overexpressing *GA20x6* increased nectar volumes, and mutant plants with overactive GA synthesis produced less nectar than wild-type.

These experiments show that GA serves to suppress nectar accumulation or release but it is less clear how this is achieved. GA may reduce the starch reserves from which nectar sugars are synthesized, or possibly affect the transcription of genes directly involved in starch breakdown. However, the involvement of three of the major plant hormones in the production of nectar demonstrates the importance of precise control and release of this elixir. CS

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