BIOSYNTHESIS

Sniffing out monoterpenes

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Roses have a distinctive fragrance that comprises hundreds of volatile compounds, including 2-phenylethanol, phenols and monoterpenes. The composition and abundance of these scent compound mixtures differ across rose hybrids, and breeding for features such as bloom longevity can diminish fragrance in the resulting varietals. Thus, tools for manipulating fragrant compound biosynthesis may be beneficial for the flower and fragrance industries. Magnard *et al.* now identify an unusual pathway used by roses to produce geraniol and other monoterpenes. Comparative amplification fragment length polymorphism–differential display and DNA microarray analysis revealed that a heavily scented rose cultivar (Papa Meilland, PM) expressed high levels of a gene with homology to the Nudix hydrolase family of pyrophosphatases relative to a lightly scented cultivar (Rouge Meilland, RM). The identified gene, which the authors termed *RhNUDX1*, encodes a cytosolic protein that is expressed predominantly in rose petals of PM (but not RM) during later stages of flowering. Further, RNAi knockdown experiments and quantitative trait locus (QTL) mapping revealed a functional linkage between *RhNUDX1* expression and geraniol production. RhNUDX1's biosynthetic role is shared by roses, as *RhNUDX1* expression correlates with monoterpene abundance in ten rose cultivars and, more generally, as heterologous expression of RhNUDX1 in tobacco plants resulted in the accumulation of geraniol and its glycosylated metabolites. Additional biochemical analysis revealed that geraniol production in roses is a two-step process: RhNUDX1 hydrolyzes geranyl diphosphate (GPP) to geranyl monophosphate, which is then converted to geraniol by a putative phosphatase in rose petals. These transformations were surprising given that GPP is the canonical substrate for terpene synthases that typically produce geraniol and other monoterpenes in plants. Though the biosynthetic source of GPP in roses remains unclear, the current RhNUDX1-dependent pathway defines an alternative mode of volatile monoterpene production in roses and offers promise for future engineering of more fragrant roses. *TLS*

PROTEOSTASIS

Death by cytoplasmic accumulation

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In addition to serving as energy factories for the cell, mitochondria control cell death through different pathways. Wang and Chen now identify a distinct mechanism of mitochondria-mediated cell death, which they call mitochondrial precursor overaccumulation stress (mPOS), that arises when proteins destined for mitochondrial import accumulate in the cytoplasm, overtaxing normal cytosolic protein homeostasis (proteostasis). To do this, they first screened for yeast multicopy suppressors capable of inhibiting cell death induced by $Aac2^{A128P}$, a misfolded ATP/ADP exchanger on the mitochondrial inner membrane not directly involved in protein import. The authors found 40 genes that could suppress $Aac2^{A128P}$-induced cell degeneration when overexpressed. Of these, 32 are already known to be involved in regulating proteostasis via such systems as mRNA silencing, translation and protein turnover. The identified antidegenerative suppressors are all localized to the cytoplasm and could enhance cell viability in mutants with diverse types of mitochondrial damage affecting the inner membrane integrity and functionality. These findings led the authors to suspect that mitochondrial damage not directly in the core protein import machineries is sufficient to reduce protein import and to induce the overaccumulation of mitochondrial precursor proteins in the cytosol followed by cell death. In addition, mPOS-induced cell death can be remediated by downregulating cytosolic protein production and other proteostatic processes. The authors could detect the accumulation of both mitochondrial and nonmitochondrial proteins in the cytoplasm of $AAC2^{A128P}$ cells using a proteomic approach. The accumulated nonmitochondrial proteins include Gis2—proposed to stimulate cap-independent translation—and Nog2—which inhibits nuclear export of the 60S ribosomal subunit. Although the precise mechanism remains unknown, Gis2 or Nog2 overaccumulation was shown to protect cells from mPOS-induced cell death. Overall, the study suggests a novel mechanism of mitochondria-induced cell death and identified a molecular network that protects cells from mPOS. *MB*

MICROBIOME

Adapting to mucus

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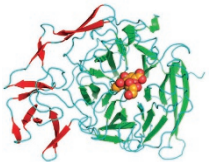

Disturbance of the normal gut microbiota can favor the growth of pathogenic species and has been linked to disease conditions such as inflammatory bowel disease (IBD). Within the gut, bacteria tend to populate the outer colonic mucus layer overlying the epithelium and their adherence and proliferation is influenced by carbohydrate modifications present on Mucins, the most abundant proteins in mucus. Mucin-associated glycan chains are often capped with terminal sialic acid moieties commonly used by pathogens to adhere to the mucosal surface. The expression of some forms of sialidase—enzymes capable of releasing terminal sialic acid caps on glycans—is known to promote bacterial survival in the mucosal environment. Taiford *et al.* report the discovery and characterization of an intramolecular *trans*-sialidase (IT-sialidase) called *NanH* in *Ruminococcus gnavus*, a commensal anaerobe commonly found in the human gastrointestinal tract that is also more prominent in individuals suffering from IBD. *NanH* had previously been identified as part of a *R. gnavus* gene cluster induced in the presence of mucins. Using recombinant *Rg*NanH, the authors showed that the enzyme specifically and efficiently processes α 2-3-linked sialic acids to release 2,7-anhydro-*N*-acetylneuraminic acid from glycan substrates, instead of free sialic acid, making it the first IT-sialidase of its class found within the human gut microbiota. The crystal structure of *Rg*NanH in apo and ligand-bound forms further revealed similarities to known IT-sialidases, in addition to providing details of NanH's specific catalytic mechanism. A prospective analysis of 124 metagenomes obtained from human stools also revealed a greater abundance of IT-sialidase encoding species in those with IBD as compared to healthy individuals. Bacterial IT-sialidases could thus be key to the adaptation of specific species to the sialylated-rich mucosal environment, and it will be interesting to study how they impact host-pathogen interactions and contribute to conditions associated with imbalances within the gut microbiome. *SL*

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