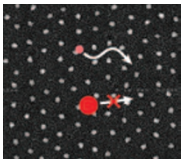
NANOTECHNOLOGY

## Receptors navigate an array

*Nano Lett.* doi:10.1021/nl404514e



JAY GROVES

The physical properties and spatial organization of membranes dictate their function. However, it has been difficult to visualize the spatial organization and to perform physical size measurements within membranes. To overcome these limitations, Caculitan *et al.* generated a supported membrane embedded with an array of regularly spaced gold nanodots between 40 nm and 180 nm apart. The nanodots create geometric constraints on the movement of proteins within the membrane where movement is blocked if protein clusters are too large to move between individual array nanoparticles. The authors looked at T-cell receptor (TCR) clusters to demonstrate the utility of the nanodot arrays for monitoring the spatial organization of protein clusters. The supported membrane was functionalized with peptide antigen-loaded major histocompatibility complex (pMHC) so that it could interact with TCR on living T cells. Monitoring TCR movement with a fluorescent antibody, the authors found that the 40-nm-spaced nanodot array impeded long-range TCR cluster transport, yet the signaling function was intact, whereas the 171-nm array allowed for unimpeded cluster movement. A panel of experiments where antigen density and nanodot array spacing were both varied revealed that the effective size of TCR clusters varied continuously with antigen density. Functional signaling clusters readily moved through 40-nm-spaced arrays at low antigen density, whereas at high antigen densities, TCR clusters had difficulty moving through 120-nm-spaced arrays. These findings highlight the ability of the supported membrane format to calibrate how TCR size varies with antigen density, which could not be easily determined by other methods. *MB*

NON-CODING RNA

## Lost on translation

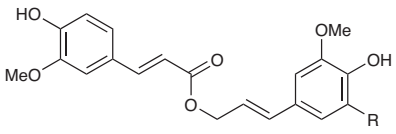
*Mol. Cell* **54**, 147–155 (2014)

In most eukaryotes, small noncoding RNAs (ncRNAs) are known to regulate gene expression at the translational level by pairing with ribosome-bound mRNAs. Yet because *Saccharomyces cerevisiae* lacks RNA interference pathways that are necessary to generate miRNAs, these regulatory pathways do not operate in yeast. A new study by Pircher *et al.* shows that yeast have an alternative mechanism for RNA-mediated translational control by identifying a small ncRNA that regulates ribosomal activity in response to stress. Building on their prior work that identified a class of small ribosome-associated ncRNAs in *S. cerevisiae*, the authors focused on an abundant 18-nucleotide ncRNA fragment of the *Trm10* transcript (Trm-ncRNA). *Trm10* knockout strains grow more slowly under hyperosmotic stress conditions, an effect that was independent of the Trm10-encoded methyltransferase protein but dependent on the presence of Trm-ncRNA. Genetic and polysome profiling experiments showed that Trm-ncRNA was stably expressed and associated with the 60S subunit of yeast ribosomes in cells. In response to hyperosmotic stress, Trm-ncRNA was redistributed to polysomes, where it blocked translation and decreased metabolic activity, permitting yeast to adapt to altered environmental conditions. Though it remains unknown how the 18-nucleotide fragment is generated from mRNA and where Trm-ncRNA acts on the ribosome, the study outlines a new mechanism for ncRNA regulation of translational activity by direct binding of the ribosome. *TLS*

CELL WALLS

## Designed for deconstruction

*Science* **344**, 90–93 (2014)




Conversations about biomass degradation often focus on oligosaccharides to be broken down or sugars that can be liberated during the process, but the plant cell wall also includes the complex aromatic polymer lignin, which complicates degradation. Previous work has shown that lignin biosynthetic pathways are promiscuous enough to incorporate alternative monomers, which can be used to create weak spots in the polymer matrix. Monolignol ferulate conjugates such as coniferyl ferulate are of particular interest as their structure will introduce labile ester bonds into the lignin backbone, and their insertion has been demonstrated *in vitro*. Wilkerson *et al.* now extend this strategy to intact plants. The authors first searched for an enzyme that could function orthogonally to the host plant, synthesizing the desired monomers instead of adding to existing monomer pools. Deep sequencing of the root tissue of a Chinese medicinal plant previously shown to contain coniferyl ferulate led to the discovery of a feruloyl coenzyme A monolignol transferase (FMT). Introduction of the encoding gene into a hybrid poplar using a xylem-specific promoter led to spatially and temporally controlled expression, with no obvious phenotypes in the growing plants. Chemical derivatization and characterization of the resulting lignin confirmed the incorporation (and thus production) of the monomers and yielded substantial improvements in digestibility using mild alkaline pretreatment. These results provide the first example of a mature plant designed to be degraded. *CG*

CHEMOTAXIS

## Small molecule GPS

*Proc. Natl. Acad. Sci. USA* **111**, 5896–5901 (2014)

The ability to manipulate the start and end point of a cell's migratory journey is an important tool for biological and therapeutic studies. However, co-opting the cell's chemotaxic machinery to promote directed movement remains difficult owing to the presence of signals in the cellular environment that can either misdirect or inhibit movement. As an alternative, Park *et al.* devised an approach using a modified G protein–coupled receptor (RASSL) that responds specifically to the biologically inert small molecule clozapine-*N*-oxide (CNO). Neutrophils transfected with the RASSL receptor exhibited cytoskeletal changes in response to CNO treatment and migrate toward a micropipette-generated gradient of CNO. The authors found that this system was applicable for a variety of cell types such as keratinocytes and endothelial cells, and neutrophils and T lymphocytes were shown to undergo trans-endothelial migration through a monolayer to reach the CNO signal. Finally, the RASSL system could be used *in vivo*, where intravenously administered RASSL-expressing T lymphocytes could localize to a microsphere releasing CNO. Overall, this RASSL-CNO system could be an interesting approach to direct cells to particular cellular destinations. *GM*

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