August 11

Nature

Structure and function of the global topsoil microbiome
Metagenomic, chemical and biomass analyses of topsoil samples from around the world reveal spatial and environmental trends in microbial community composition and genetic diversity.

Mitochondrial double-stranded RNA triggers antiviral signalling in humans
Mitochondrial double-stranded RNA can induce an interferon response if released into the cytoplasm, but self-recognition is prevented by SUV3 helicase and PNPase exoribonuclease. Somdutta Dhir, […] & Nicholas J. Proudfoot

Unique features of mammalian mitochondrial translation initiation revealed by cryo-EM
A cryo-electron microscopy structure of the mammalian mitochondrial translation initiation complex reveals unique features that are necessary to initiate mitochondrial translation and highlights a possible membrane-targeting peptide. Eva Kumme, , Marc Leibundgut, […] & Nenad Ban

Current Biology: Alert 31 July-07 August
Nutrient- and Dose-Dependent Microbiome-Mediated Protection against a Plant Pathogen
Pages 2487-2492.e3 Maureen Berg, Britt Koskella

Science
Developmental barcoding of whole mouse via homing CRISPR
George Church is at it again:
In vivo barcoding using nuclease-induced mutations is a powerful approach for recording biological information, including developmental lineages; however, its application in mammalian systems has been limited. We present in vivo barcoding in the mouse with multiple homing guide RNAs that each generate hundreds of mutant alleles and combine for an exponential diversity of barcodes. Activation upon conception and continued mutagenesis through gestation result in developmentally barcoded mice wherein information is recorded in lineage-specific mutations. We use these recordings for reliable post hoc reconstruction of the earliest lineages and investigating axis development in the brain. Our results provide an enabling and versatile platform for in vivo barcoding and lineage tracing in a mammalian model system.

Plant Cell
Disrupted Genome Methylation in Response to High Temperature Has Distinct Affects on Microspore Abortion and Anther Indehiscence
Yizan Ma, Ling Min, Maojun Wang, Chaozhi Wang, Yunlong Zhao, Yaoyao Li, Qidi Fang, Yuanlong Wu, Sai Xie, Yuanhao Ding, Xiaojun Su, Qin Hu, Qinghua Zhang, Xueyuan Li and Xianlong Zhang
Plant Cell 2018 30: 1387-1403. First Published on June 4, 2018; doi:10.1105/tpc.18.00074 **OPEN**
http://www.plantcell.org/content/30/7/1387.abstract
Integrated multi-omics data analysis reveals the role of genome methylation in male fertility, shedding light on the mechanism underlying male sterility in response to high temperature.
Van Treeck B, Parker R.
Emerging Roles for Intermolecular RNA-RNA Interactions in RNP Assemblies.
Cell. 2018 Aug 9;174(4):791-802.
PMID: 30096311 [PubMed - in process]

Ranaweera CB, Glaza P, Yang T, Zolkiewski M.
Interaction of substrate-mimicking peptides with the AAA+ ATPase ClpB from Escherichia coli.
Arch Biochem Biophys. 2018 Aug 6;. [Epub ahead of print]
PMID: 30092228 [PubMed - as supplied by publisher]

Ivanov P, Kedersha N, Anderson P.
Stress Granules and Processing Bodies in Translational Control.
Cold Spring Harb Perspect Biol. 2018 Aug 6;. [Epub ahead of print]
PMID: 30082464 [PubMed - as supplied by publisher]

Zlobin N, Evlakov K, Tikhonova O, Babakov A, Taranov V.
RNA melting and RNA chaperone activities of plant cold shock domain proteins are not correlated.
RNA Biol. 2018 Aug 6;. [Epub ahead of print]
PMID: 30081762 [PubMed - as supplied by publisher]

Liu Z, Wang C, Li Y, Zhao C, Li T, Li D, Zhang S, Liu C.
Mechanistic insights into the switch of Î±B-crystallin chaperone activity and self-multimerization.
J Biol Chem. 2018 Aug 3;. [Epub ahead of print]
PMID: 30076220 [PubMed - as supplied by publisher]

Kaya C, Akram NA, Ashraf M.
Influence of exogenously applied nitric oxide on strawberry (Fragaria Ã— ananassa) plants grown under iron deficiency and/or saline stress.
Physiol Plant. 2018 Aug 9;. [Epub ahead of print]
PMID: 30091474 [PubMed - as supplied by publisher]

Castillo MC, Coego A, Costa-Broseta Ã□, LeÃ³n J.
Nitric oxide responses in Arabidopsis hypocotyls are mediated by diverse phytohormone pathways.
J Exp Bot. 2018 Aug 2;. [Epub ahead of print]
PMID: 30085082 [PubMed - as supplied by publisher]

He SL, Hsieh HL, Jauh GY.
SMALL AUXIN UP RNA62/75 are required for the translation of transcripts essential for pollen tube growth.
Plant Physiol. 2018 Aug 9;. [Epub ahead of print]
PMID: 30093526 [PubMed - as supplied by publisher]

Kummer E, Leibundgut M, Rackham O, Lee RG, Boehringer D, Filipovska A, Ban N.
Unique features of mammalian mitochondrial translation initiation revealed by cryo-EM.
Nature. 2018 Aug;560(7717):263-267.
PMID: 30089917 [PubMed - in process]

Chotewutmontri P, Barkan A.
Multilevel effects of light on ribosome dynamics in chloroplasts program genome-wide and psbA-specific changes in translation.
PLoS Genet. 2018 Aug 6;14(8):e1007555. [Epub ahead of print]
PMID: 30080854 [PubMed - as supplied by publisher]

Employing Wheat's Bacterial Partners to Fight a Pathogen

Fusarium head blight is a devastating fungal disease affecting wheat and barley crops worldwide. According to the American Phytopathological Society, this disease has cost U.S. wheat and barley farmers more than $3 billion since 1990. USDA’s Agricultural Research Service scientists, together with land managers and other scientists at research universities, are taking a variety of approaches to solving this problem. These include breeding resistant cultivars, using massive disease-forecasting models and applying fungicides during critical junctures in crop growth to prevent fusarium head blight. Recently, many scientists have also become interested in the idea of employing microbial species that already live on and inside crop plants to do the dirty work of controlling disease epidemics. Read the full USDA blog.

USDA: Previously unknown rice blast resistance isolated

June 8, 2018 WASHINGTON, D.C., U.S. — A gene that gives rice resistance to a disease that has been costing about $66 billion a year in global damage has been isolated by a team of scientists led by U.S. Department of Agriculture’s (USDA) Agricultural Research Service (ARS) plant pathologist Yulin Jia.

Rice blast, caused by the fungus Magnaporthe oryzae, results in annual yield losses large enough to have fed 60 billion people each year, according to the team’s paper published in the journal *Nature Communications*.

In the U.S. mid-south rice-growing region, the cost of mitigating rice blast infection with fungicide applications can reach almost $20 per acre; plus, the fungus may still cause significant yield loss depending on the susceptibility of each rice variety and the degree of infection at the time of fungicide application, according to the USDA's Economic Research Service (ERS).

The disease resistance gene, Ptr, has a structure that has not been seen in plants before. It has been previously deployed unknowingly in blast-resistant rice cultivars because it has been tightly linked to another disease resistance gene, Pi-ta, which has a genetic structure that is well-described in scientific literature.

"Our research was able to separate the two genes and demonstrate that Ptr is independently responsible for its own broad-spectrum blast resistance without Pi-ta," Jia said. "This will provide a new strategy for developing blast-resistant rice cultivars."

The full genomic sequence of the Ptr gene was put into GenBank for use by public researchers worldwide.

Nat. Commun. 10.1038/s41467-018-04344-z, 10.1038/s41467-018-04721-8 (2018).

Decoding parasitic plant genomes

Parasitism has evolved multiple times in plants and resulted in some major agricultural pests, including relatives of the morning glory family called dodder or strangleweed. To examine the effects of parasitism on the genome, Vogel *et al.* and Sun *et al.* respectively sequenced the genomes of field dodder (*Cuscuta campestris*) and Australian dodder (*Cuscuta australis*). Both studies identified major gene losses, likely facilitating the transformation into leafless, rootless plants unable to photosynthesize. Vogel *et al.* documented more than 50 examples of gene transfer into field dodder from their hosts. Sun *et al.* examined transcriptomes of the haustoria, which are specialized organs that allow dodder to extract water and nutrients from host plants.

Cell: Alert 03 August-10 August

Krebs Cycle Reimagined: The Emerging Roles of Succinate and Itaconate as Signal Transducers Review article Pages 780-784 Michael P. Murphy, Luke A.J. O'Neill Download PDF

Krebs cycle intermediates traditionally link to oxidative phosphorylation whilst also making key cell components. It is now clear that some of these metabolites also act as signals. Succinate plays an important role in inflammatory, hypoxic, and metabolic signaling, while itaconate (from another Krebs cycle intermediate, *cis*-aconitate) has an anti-inflammatory role.

Emerging Roles for Intermolecular RNA-RNA Interactions in RNP Assemblies

Review article Pages 791-802 Briana Van Treeck, Roy Parker Download PDF

Eukaryotic cells contain large assemblies of RNA and protein, referred to as ribonucleoprotein (RNP) granules, which include cytoplasmic P-bodies, stress granules, and neuronal and germinal granules, as well as nuclear paraspeckles, Cajal bodies, and RNA foci formed from repeat expansion RNAs. Recent evidence argues that intermolecular RNA-RNA interactions play a role in forming and determining the composition of certain RNP granules. We hypothesize that intermolecular RNA-RNA interactions are favored in cells yet are limited by RNA-binding proteins, helicases, and ribosomes, thereby allowing normal RNA function. An over-abundance of intermolecular RNA-RNA interactions may be toxic since perturbations that increase RNA-RNA interactions such as long repeat expansion RNAs, arginine-containing dipeptide repeat polypeptides, and sequestration or loss of abundant RNA-binding proteins can contribute to degenerative diseases.

Challenges and Opportunities for Small-Molecule Fluorescent Probes in Redox Biology Applications

Xiqian Jiang, Lingfei Wang, Shaina L. Carroll, Jianwei Chen, Meng C. Wang, and Jin Wang

Antioxidants & Redox Signaling, Vol. 29, No. 6, August 2018: 518-540.
Abstract | Full Text | PDF (838 KB) | PDF Plus (783 KB)

Biological Production, Detection, and Fate of Hydrogen Peroxide

Christine C. Winterbourn

Antioxidants & Redox Signaling, Vol. 29, No. 6, August 2018: 541-551.
Abstract | Full Text | PDF (303 KB) | PDF Plus (355 KB)

Mechanisms and Applications of Redox-Sensitive Green Fluorescent Protein-Based Hydrogen Peroxide Probes

Leticia Prates Roma, Marcel Deponte, Jan Riemer, and Bruce Morgan

Antioxidants & Redox Signaling, Vol. 29, No. 6, August 2018: 552-568.

Abstract | Full Text | PDF (707 KB) | PDF Plus (543 KB)

***In Vivo* Imaging of Hydrogen Peroxide with HyPer Probes**

Dmitry S. Bilan and Vsevolod V. Belousov

Antioxidants & Redox Signaling, Vol. 29, No. 6, August 2018: 569-584.
Abstract | Full Text | PDF (1556 KB) | PDF Plus (760 KB)

Detection of Hydrogen Peroxide with Fluorescent Dyes

Flávia Rezende, Ralf P. Brandes, and Katrin Schröder

Antioxidants & Redox Signaling, Vol. 29, No. 6, August 2018: 585-602.
Abstract | Full Text | PDF (814 KB) | PDF Plus (641 KB)

Transgenic Organisms Meet Redox Bioimaging: One Step Closer to Physiology

Lija Swain, Maithily S. Nanadikar, Sergej Borowik, Anke Zieseniss, and Dörthe M. Katschinski

Antioxidants & Redox Signaling, Vol. 29, No. 6, August 2018: 603-612.
Abstract | Full Text | PDF (549 KB) | PDF Plus (368 KB)

Quantitative analysis of newly synthesized proteins
This protocol describes a proteomics approach for quantifying newly synthesized proteins (NSPs). NSPs are pulse-labeled with the methionine analog AHA or a heavy-isotope version of it, followed by AHA-peptide enrichment and LC-MS/MS analysis. Yuanhui Ma , Daniel B. McClatchy[…] & John R. Yates III

Combined expansion microscopy with structured illumination microscopy for analyzing protein complexes
This protocol describes how to combine expansion microscopy (ExM) with structured illumination microscopy (SIM). ExM–SIM is exemplified by super-resolution analysis of the synaptonemal complex (SC) and single-particle averaging of SC proteins. Yongfu Wang, Zulin Yu[…] & R. Scott Hawley

Molecular Cell
The Discovery of Ribosome Heterogeneity and Its Implications for Gene Regulation and Organismal Life Review Article *Pages 364-374* Naomi R. Genuth, Maria Barna

Quality Control of Orphaned Proteins
Review article Pages 443-457 Szymon Juszkiewicz, Ramanujan S. Hegde Download PDF
Integrated Functions of Membrane Property Sensors and a Hidden Side of the Unfolded Protein Response
Review article Pages 458-467 Roberto Covino, Gerhard Hummer, Robert Ernst Download PDF

Mettl1/Wdr4-Mediated m^{7}G tRNA Methylome Is Required for Normal mRNA Translation and Embryonic Stem Cell Self-Renewal and Differentiation
Original research article Pages 244-255.e5 Shuibin Lin, Qi Liu, Victor S. Lelyveld, Junho Choe, ... Richard I. Gregory
Download PDF

MitoCPR: Meticulous Monitoring of Mitochondrial Proteostasis
Pages 8-9 Radha Desai, Michelangelo Campanella Download PDF

Current Biology
Decoupling Yeast Cell Division and Stress Defense Implicates mRNA Repression in Translational Reallocation during Stress
In Press, Corrected Proof, Available online 2 August 2018
Yi-Hsuan Ho, Evgenia Shishkova, James Hose, Joshua J. Coon, Audrey P. Gasch
Download PDF