Identifying genetic factors that contribute to trait variation among species is difficult. Weiss *et al.* developed a method for unbiased genome-scale mapping of trait differences and used it to work out how a range of yeast species evolved. When crossed, these yeast species produce sterile offspring, preventing the use of traditional genetic-mapping techniques. However, by reciprocal hemizygosity analysis via sequencing (RH-seq), alleles that contributed to differences in thermotolerance were spotted that diverged between two species. Surprisingly, these turned out to map to essential housekeeping genes. Thus, without taking a candidate locus approach, RH-seq allowed identification of genes responsible for traits that differ between species.
Nat. Genet. **50**, 1501 (2018).

https://www.sciencemag.org/news/2018/11/researchers-launch-plan-sequence-66000-species-united-kingdom-s-just-start?utm_campaign=news_weekly_2018-11-02&et_rid=328058488&et_cid=2465523
The Earth BioGenome Project aims to sequence the genome of every complex organism on Earth — that's 1.5 million species — and will probably cost $US4.7 billion. The project brings together more than a dozen existing ventures that focus on various slices of life, such as specific types of animal or the creatures of a particular country. Among the largest commitments to the effort so far is a plan by the the Wellcome Sanger Institute to decode the genomes of all the eukaryotic species in the United Kingdom, thought to number about 66,000.
Nature | 3 min read

https://www.sciencemag.org/news/2018/11/poop-vault-human-feces-could-preserve-gut-biodiversity-and-help-treat-disease?utm_campaign=news_weekly_2018-11-02&et_rid=328058488&et_cid=2465523

Bacterial Heme-Based Sensors of Nitric Oxide

Dominique E. Williams, Lisa-Marie Nisbett, Bezalel Bacon, and Elizabeth Boon

Antioxidants & Redox Signaling, Vol. 29, No. 18, December 2018: 1872-1887.
Abstract | Full Text | PDF (720 KB) | PDF Plus (637 KB)

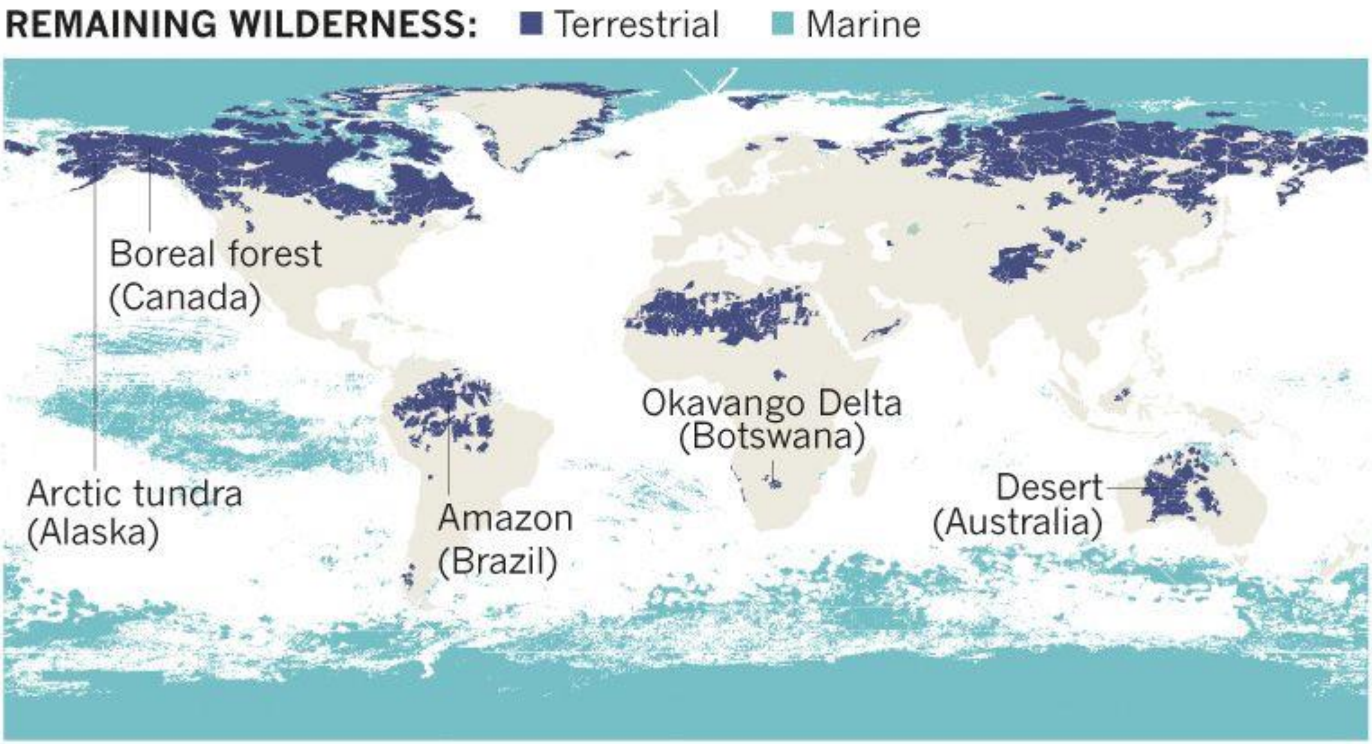
Cellular Ca2+ signals generate defined pH signatures in plants
Smrutisanjita Behera, Zhaolong Xu, Laura Luoni, Cristina Bonza, Fabrizio Gandolfo Doccula, Maria Ida DeMichelis, Richard J Morris, Markus Schwarzländer and Alex Costa
Plant Cell 2018 tpc.18.00655; Advance Publication October 29, 2018; doi:10.1105/tpc.18.00655 **OPEN**
http://www.plantcell.org/content/early/2018/10/29/tpc.18.00655.abstract
Calcium ions (Ca2+) play a key role in cell signaling across organisms. The question of how a simple ion can mediate specificity has spurred research into the role of Ca2+ signatures and their encoding and decoding machinery. Such studies have frequently focussed on Ca2+ alone and our understanding of how Ca2+ signalling is integrated with other responses remains poorly understood. Using in vivo imaging with different genetically-encoded fluorescent sensors in Arabidopsis cells we show that Ca2+ transients do not occur in isolation but are accompanied by pH changes in the cytosol. We estimate the degree of cytosolic acidification at up to 0.25 pH units in response to external ATP in seedling root tips. We validated this pH-Ca2+ link for distinct stimuli. Our data suggest that the association with pH may be a general feature of Ca2+ transients that depends on the transient characteristics and the intracellular compartment. These findings suggest a fundamental link between Ca2+ and pH dynamics in plant cells, generalizing previous observations of their association in growing pollen tubes and root hairs. Ca2+ signatures act in concert with pH signatures, possibly providing an additional layer of cellular signal transduction to tailor signal specificity.

WHAT'S LEFT?

Earth's remaining wilderness areas are becoming increasingly important buffers against changing conditions in the Anthropocene. Yet they aren't an explicit target in international policy frameworks.

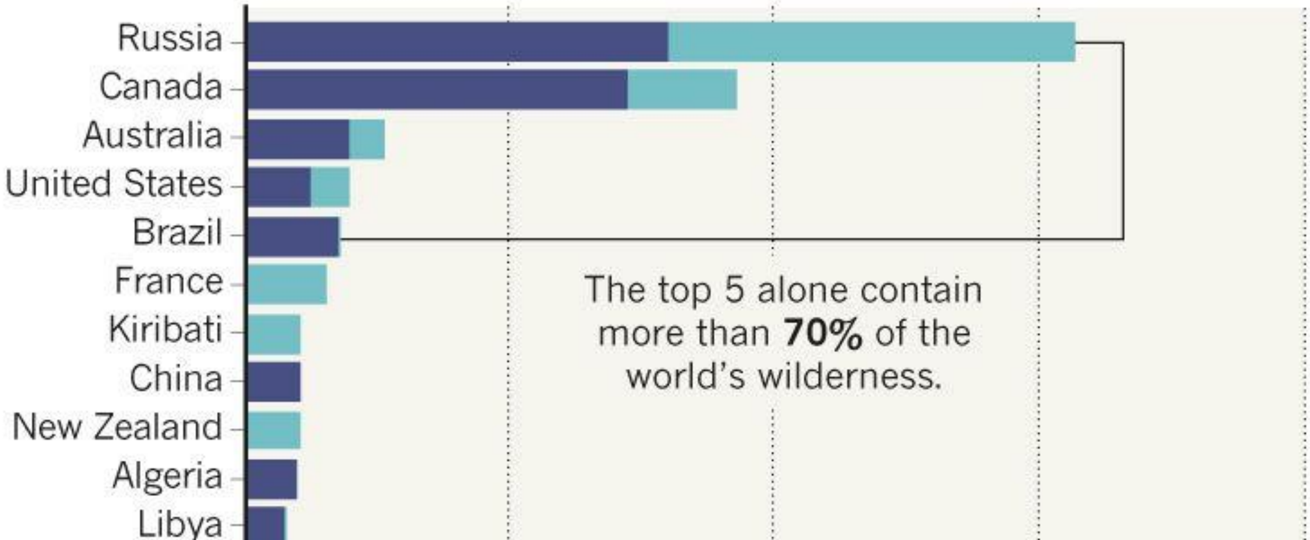
THE HUMAN FOOTPRINT

77% of land (excluding Antarctica) and 87% of the ocean has been modified by the direct effects of human activities.



THE WILDEST COUNTRIES

Twenty countries contain 94% of the world's wilderness, excluding Antarctica and the high seas.



The top 5 alone contain more than **70%** of the world's wilderness.

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https://www.nature.com/articles/s41594-018-0144-3

Data from meeting in Kyoto, August 2018

Satoshi Naito (Hokkaido University) presented data about an *S*-adenosyl methionine–mediated translation stalling mechanism of the 80S ribosome in *Arabidopsis thaliana*, which is critical for metabolite-controlled regulation of methionine synthesis in plants and, again, utilizes the constriction site with uL4 for pausing.

Data from Morimoto in *C. elegans* : Surprisingly, mutations in cytochrome oxidase that cause a reduction of respiration by 20–40% result in upregulated expression of cytoplasmic chaperones, which considerably increases the lifespan of animals.

Roland Beckmann (University of Munich) reported about the structural and molecular details by which Vms1, a Cdc48 adaptor protein with peptidyl-tRNA hydrolase activity, promotes peptidyl-tRNA hydrolysis, thereby serving as a release factor for ribosome-stalled nascent chains in yeast.

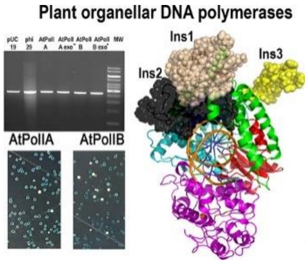
The concentration of proteasomes in the nucleus is five times higher than in the cytosol. This high concentration is reached by formation of ‘proteasome foci’. These clusters of proteasomes serve as transient and highly dynamic proteolysis centers that predominantly degrade proteins of the large ribosomal subunit. Keiji Tanaka (Tokyo Metropolitan Institute of Medical Science) provided deep insights into the function and architecture of these liquid-droplet-like nuclear subcompartments. Pedro Carvalho (University of Oxford) reported on a further function of nuclear proteasomes in the removal of non-assembled ER proteins of the inner nuclear membrane. A dedicated machinery, employing the specific factors Asi1, Asi2 and Asi3, recognizes these orphan subunits and promotes their proteolytic removal[8], thereby specifically recognizing features of transmembrane domains that presumably become occluded during membrane protein assembly.

movies shown by Toshiya Endo in which he used high-speed atomic-force microscopy to visualize the dynamic restructuring of the mitochondrial TOM complex.

The FEBS Journal Vol. 285, No. 21, November 2018 is now available online Plant organellar DNA polymerases paralogs exhibit dissimilar nucleotide incorporation fidelity

Víctor M. Ayala- García, Noe Baruch- Torres, Paola L. García- Medel, Luis G. Brieba

Pages: 4005-4018 | First Published: 27 August 2018



In flowering plants, organellar DNA polymerases are a duplicated gene product with high sequence identity. In the plant model Arabidopsis thaliana these gene products present an 8- fold difference in nucleotide incorporation fidelity. We hypothesize that the faithful polymerase is involved in organellar DNA replication.

J. Agronomy and Crop Science.
Australian rice varieties vary in grain yield response to heat stress during reproductive and grain filling stages
Fawad Ali, Daniel L.E. Waters, Ben Ovenden, Peter Bundock, Carolyn A. Raymond, Terry J. Rose
Version of Record online: 30 October 2018

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Cell

Microbial Interkingdom Interactions in Roots Promote *Arabidopsis* Survival Paloma Durán, Thorsten Thiergart, Ruben Garrido-Oter, Matthew Agler, ... Stéphane Hacquard Pages 973-983.e14

Structural Basis of Membrane Protein Chaperoning through the Mitochondrial Intermembrane Space Katharina Weinhäupl, Caroline Lindau, Audrey Hessel, Yong Wang, ... Paul Schanda Pages 1365-1379.e25

Visualizing Intracellular Organelle and Cytoskeletal Interactions at Nanoscale Resolution on Millisecond Timescales Yuting Guo, Di Li, Siwei Zhang, Yanrui Yang, ... Dong Li Pages 1430-1442.e17

Summary

In eukaryotic cells, organelles and the cytoskeleton undergo highly dynamic yet organized interactions capable of orchestrating complex cellular functions. Visualizing these interactions requires noninvasive, long-duration imaging of the intracellular environment at high spatiotemporal resolution and low background. To achieve these normally opposing goals, we developed grazing incidence structured illumination microscopy (GI-SIM) that is capable of imaging dynamic events near the basal cell cortex at 97-nm resolution and 266 frames/s over thousands of time points. We employed multi-color GI-SIM to characterize the fast dynamic interactions of diverse organelles and the cytoskeleton, shedding new light on the complex behaviors of these structures. Precise measurements of microtubule growth or shrinkage events helped distinguish among models of microtubule dynamic instability. Analysis of endoplasmic reticulum (ER) interactions with other organelles or microtubules uncovered new ER remodeling mechanisms, such as hitchhiking of the ER on motile organelles. Finally, ER-mitochondria contact sites were found to promote both mitochondrial fission and fusion.

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Physiologia Plantarum
Gene- edited plants on the plate: the ‘CRISPR cabbage story’
Stefan Jansson
Pages: 396-405 | First Published: 10 May 2018

Outlaws, old laws and no laws: the prospects of gene editing for agriculture in United States
Wayne Parrott
Pages: 406-411 | First Published: 10 May 2018

Plant Cell & Environment

Novel loci and a role for nitric oxide for seed dormancy and pre- harvest sprouting in barley
Manuela Nagel, Ahmad M. Alqudah, Marlène Bailly, Loïc Rajjou, Sibylle Pistrick, Gabriele Matzig, Andreas Börner, Ilse Kranner First Published: 22 November 2018

Arabidopsis HSP70- 16 is required for flower opening under normal or mild heat stress temperatures
Xu Chen, Lei Shi, Yuqin Chen, Lu Zhu, Dasheng Zhang, Shi Xiao, Asaph Aharoni, Jianxin Shi, Jie Xu

Plant Journal
Genome- Wide Association studies on the phyllosphere microbiome: embracing complexity in host- microbe interactions
Kathleen Beilsmith, Manus P.M. Thoen, Benjamin Brachi, Andrew D. Gloss, Mohammad H. Khan, Joy Bergelson
First Published: 22 November 2018

Trait discovery and editing in tomato
Christophe Rothan, Isidore Diouf, Mathilde Causse First Published: 11 November 2018

Nature Protocols.

CRISPR–Cas9-mediated genome editing in apple and grapevine **pp2844 - 2863**
Yuriko Osakabe, Zhenchang Liang, Chong Ren, Chikako Nishitani, Keishi Osakabe *et al.*
doi:10.1038/s41596-018-0067-9
This protocol provides approaches for applying the CRISPR–Cas9 system for genome editing in apple and grapevine plants, using both plasmid-mediated delivery of components and direct delivery of CRISPR–Cas9 ribonucleoproteins.

Speed breeding in growth chambers and glasshouses for crop breeding and model plant research **pp2944 - 2963**
Sreya Ghosh, Amy Watson, Oscar E. Gonzalez-Navarro, Ricardo H. Ramirez-Gonzalez, Luis Yanes *et al.*
doi:10.1038/s41596-018-0072-z

This protocol describes procedures for speed-breeding approaches using growth cabinets and LED-supplemented glasshouses. The approaches can be used to accelerate crop research and are compatible with a wide variety of crops.