December 28

Genomic features of bacterial adaptation to plants

Asaf Levy, Isai Salas Gonzalez,[…]Jeffery L. Dangl
Nature Genetics **50**, 138–150 (2017) doi:10.1038/s41588-017-0012-9

Plants intimately associate with diverse bacteria. Plant-associated bacteria have ostensibly evolved genes that enable them to adapt to plant environments. However, the identities of such genes are mostly unknown, and their functions are poorly characterized. We sequenced 484 genomes of bacterial isolates from roots of Brassicaceae, poplar, and maize. We then compared 3,837 bacterial genomes to identify thousands of plant-associated gene clusters. Genomes of plant-associated bacteria encode more carbohydrate metabolism functions and fewer mobile elements than related non-plant-associated genomes do. We experimentally validated candidates from two sets of plant-associated genes: one involved in plant colonization, and the other serving in microbe–microbe competition between plant-associated bacteria. We also identified 64 plant-associated protein domains that potentially mimic plant domains; some are shared with plant-associated fungi and oomycetes. This work expands the genome-based understanding of plant–microbe interactions and provides potential leads for efficient and sustainable agriculture through microbiome engineering.

Whole-genome resequencing of 292 pigeonpea accessions identifies genomic regions associated with domestication and agronomic traits

Rajeev K Varshney& Swapan K Datta   *Nature Genetics* **49**, 1082–1088 (2017) doi:10.1038/ng.3872

Pigeonpea (*Cajanus cajan*), a tropical grain legume with low input requirements, is expected to continue to have an important role in supplying food and nutritional security in developing countries in Asia, Africa and the tropical Americas. From whole-genome resequencing of 292 *Cajanus* accessions encompassing breeding lines, landraces and wild species, we characterize genome-wide variation. On the basis of a scan for selective sweeps, we find several genomic regions that were likely targets of domestication and breeding. Using genome-wide association analysis, we identify associations between several candidate genes and agronomically important traits. Candidate genes for these traits in pigeonpea have sequence similarity to genes functionally characterized in other plants for flowering time control, seed development and pod dehiscence. Our findings will allow acceleration of genetic gains for key traits to improve yield and sustainability in pigeonpea.

Genomic analyses in cotton identify signatures of selection and loci associated with fiber quality and yield traits

Lei Fang……… & Tianzhen Zhang   *Nature Genetics* **49**, 1089–1098 (2017) doi:10.1038/ng.3887

Upland cotton (*Gossypium hirsutum*) is the most important natural fiber crop in the world. The overall genetic diversity among cultivated species of cotton and the genetic changes that occurred during their improvement are poorly understood. Here we report a comprehensive genomic assessment of modern improved upland cotton based on the genome-wide resequencing of 318 landraces and modern improved cultivars or lines. We detected more associated loci for lint yield than for fiber quality, which suggests that lint yield has stronger selection signatures than other traits. We found that two ethylene-pathway-related genes were associated with increased lint yield in improved cultivars. We evaluated the population frequency of each elite allele in historically released cultivar groups and found that 54.8% of the elite genome-wide association study (GWAS) alleles detected were transferred from three founder landraces: Deltapine 15, Stoneville 2B and Uganda Mian. Our results provide a genomic basis for improving cotton cultivars and for further evolutionary analysis of polyploid crops.

High-quality *de novo* assembly of the apple genome and methylome dynamics of early fruit development

Nicolas Daccord …..& Etienne Bucher *Nature Genetics* **49**, 1099–1106 (2017) doi:10.1038/ng.3886

Using the latest sequencing and optical mapping technologies, we have produced a high-quality *de novo* assembly of the apple (*Malus domestica* Borkh.) genome. Repeat sequences, which represented over half of the assembly, provided an unprecedented opportunity to investigate the uncharacterized regions of a tree genome; we identified a new hyper-repetitive retrotransposon sequence that was over-represented in heterochromatic regions and estimated that a major burst of different transposable elements (TEs) occurred 21 million years ago. Notably, the timing of this TE burst coincided with the uplift of the Tian Shan mountains, which is thought to be the center of the location where the apple originated, suggesting that TEs and associated processes may have contributed to the diversification of the apple ancestor and possibly to its divergence from pear. Finally, genome-wide DNA methylation data suggest that epigenetic marks may contribute to agronomically relevant aspects, such as apple fruit development.

Signatures of adaptation in the weedy rice genome
Lin-Feng Li, Ya-Ling Li, Yulin Jia, Ana L Caicedo & Kenneth M Olsen *Nature Genetics* **49**, 811–814 (2017) doi:10.1038/ng.3825

Crop domestication provided the calories that fueled the rise of civilization[1,2,3]. For many crop species, domestication was accompanied by the evolution of weedy crop relatives, which aggressively outcompete crops and reduce harvests[4,5,6]. Understanding the genetic mechanisms that underlie the evolution of weedy crop relatives is critical for agricultural weed management and food security. Here we use whole-genome sequences to examine the origin and adaptation of the two major strains of weedy rice found in the United States. We find that de-domestication from cultivated ancestors has had a major role in their evolution, with relatively few genetic changes required for the emergence of weediness traits. Weed strains likely evolved both early and late in the history of rice cultivation and represent an under-recognized component of the domestication process. Genomic regions identified here that show evidence of selection can be considered candidates for future genetic and functional analyses for rice improvement.

Reconstructing the genome of the most recent common ancestor of flowering plants
Florent Murat……. & Jérôme Salse *Nature Genetics* **49**, 490–496 (2017) doi:10.1038/ng.3813

We describe here the reconstruction of the genome of the most recent common ancestor (MRCA) of modern monocots and eudicots, accounting for 95% of extant angiosperms, with its potential repertoire of 22,899 ancestral genes conserved in present-day crops. The MRCA provides a starting point for deciphering the reticulated evolutionary plasticity between species (rapidly versus slowly evolving lineages), subgenomes (pre- versus post-duplication blocks), genomic compartments (stable versus labile loci), genes (ancestral versus species-specific genes) and functions (gained versus lost ontologies), the key mutational forces driving the success of polyploidy in crops. The estimation of the timing of angiosperm evolution, based on MRCA genes, suggested that this group emerged 214 million years ago during the late Triassic era, before the oldest recorded fossil. Finally, the MRCA constitutes a unique resource for scientists to dissect major agronomic traits in translational genomics studies extending from model species to crops.

Genomic analysis of 6,000-year-old cultivated grain illuminates the domestication history of barley
Martin Mascher…………. & Nils Stein *Nature Genetics* **48**, 1089–1093 (2016) doi:10.1038/ng.3611

The cereal grass barley was domesticated about 10,000 years before the present in the Fertile Crescent and became a founder crop of Neolithic agriculture[1]. Here we report the genome sequences of five 6,000-year-old barley grains excavated at a cave in the Judean Desert close to the Dead Sea. Comparison to whole-exome sequence data from a diversity panel of present-day barley accessions showed the close affinity of ancient samples to extant landraces from the Southern Levant and Egypt, consistent with a proposed origin of domesticated barley in the Upper Jordan Valley. Our findings suggest that barley landraces grown in present-day Israel have not experienced major lineage turnover over the past six millennia, although there is evidence for gene flow between cultivated and sympatric wild populations. We demonstrate the usefulness of ancient genomes from desiccated archaeobotanical remains in informing research into the origin, early domestication and subsequent migration of crop species.

Genome-wide association study using whole-genome sequencing rapidly identifies new genes influencing agronomic traits in rice

Kenji Yano ……. & Makoto Matsuoka *Nature Genetics* **48**, 927–934 (2016) doi:10.1038/ng.3596

A genome-wide association study (GWAS) can be a powerful tool for the identification of genes associated with agronomic traits in crop species, but it is often hindered by population structure and the large extent of linkage disequilibrium. In this study, we identified agronomically important genes in rice using GWAS based on whole-genome sequencing, followed by the screening of candidate genes based on the estimated effect of nucleotide polymorphisms. Using this approach, we identified four new genes associated with agronomic traits. Some genes were undetectable by standard SNP analysis, but we detected them using gene-based association analysis. This study provides fundamental insights relevant to the rapid identification of genes associated with agronomic traits using GWAS and will accelerate future efforts aimed at crop improvement.

The genome sequences of *Arachis duranensis* and *Arachis ipaensis*, the diploid ancestors of cultivated peanut
David John Bertioli […] Peggy Ozias-Akins *Nature Genetics* **48**, 438–446 (2016) doi:10.1038/ng.3517

Cultivated peanut (*Arachis hypogaea*) is an allotetraploid with closely related subgenomes of a total size of ~2.7 Gb. This makes the assembly of chromosomal pseudomolecules very challenging. As a foundation to understanding the genome of cultivated peanut, we report the genome sequences of its diploid ancestors (*Arachis duranensis* and *Arachis ipaensis*). We show that these genomes are similar to cultivated peanut's A and B subgenomes and use them to identify candidate disease resistance genes, to guide tetraploid transcript assemblies and to detect genetic exchange between cultivated peanut's subgenomes. On the basis of remarkably high DNA identity of the *A. ipaensis* genome and the B subgenome of cultivated peanut and biogeographic evidence, we conclude that *A. ipaensis* may be a direct descendant of the same population that contributed the B subgenome to cultivated peanut.

OsSPL13 **controls grain size in cultivated rice**

Lizhen Si [...] Bin Han ***Nature Genetics*** **48, 447–456 (2016) doi:10.1038/ng.3518**

Although genetic diversity has a cardinal role in domestication, abundant natural allelic variations across the rice genome that cause agronomically important differences between diverse varieties have not been fully explored. Here we implement an approach integrating genome-wide association testing with functional analysis on grain size in a diverse rice population. We report that a major quantitative trait locus, *GLW7*, encoding the plant-specific transcription factor OsSPL13, positively regulates cell size in the grain hull, resulting in enhanced rice grain length and yield. We determine that a tandem-repeat sequence in the 5′ UTR of *OsSPL13* alters its expression by affecting transcription and translation and that high expression of *OsSPL13* is associated with large grains in tropical *japonica* rice. Further analysis indicates that the large-grain allele of *GLW7* in tropical *japonica* rice was introgressed from *indica* varieties under artificial selection. Our study demonstrates that new genes can be effectively identified on the basis of genome-wide association data.

Nature Communications

Improved split fluorescent proteins for endogenous protein labeling

Siyu Feng, …. & Bo Huang

Nature Communications **8**, Article number: 370 (2017)

Self-complementing split fluorescent proteins (FPs) have been widely used for protein labeling, visualization of subcellular protein localization, and detection of cell–cell contact. To expand this toolset, we have developed a screening strategy for the direct engineering of self-complementing split FPs. Via this strategy, we have generated a yellow–green split-mNeonGreen$2_{1–10/11}$ that improves the ratio of complemented signal to the background of $FP_{1–10}$-expressing cells compared to the commonly used split $GFP_{1–10/11}$; as well as a 10-fold brighter red-colored split-sfCherry$2_{1–10/11}$. Based on split sfCherry2, we have engineered a photoactivatable variant that enables single-molecule localization-based super-resolution microscopy. We have demonstrated dual-color endogenous protein tagging with sfCherry2_{11} and GFP_{11}, revealing that endoplasmic reticulum translocon complex Sec61B has reduced abundance in certain peripheral tubules. These new split FPs not only offer multiple colors for imaging interaction networks of endogenous proteins, but also hold the potential to provide orthogonal handles for biochemical isolation of native protein complexes.

Genetically encoded biosensors for visualizing live-cell biochemical activity at super-resolution

Gary C H Mo …. & Jin Zhang *Nature Methods* **14**, 427–434 (2017) doi:10.1038/nmeth.4221

Compartmentalized biochemical activities are essential to all cellular processes, but there is no generalizable method to visualize dynamic protein activities in living cells at a resolution commensurate with cellular compartmentalization. Here, we introduce a new class of fluorescent biosensors that detect biochemical activities in living cells at a resolution up to threefold better than the diffraction limit. These 'FLINC' biosensors use binding-induced changes in protein fluorescence dynamics to translate kinase activities or protein–protein interactions into changes in fluorescence fluctuations, which are quantifiable through stochastic optical fluctuation imaging. A protein kinase A (PKA) biosensor allowed us to resolve minute PKA activity microdomains on the plasma membranes of living cells and to uncover the role of clustered anchoring proteins in organizing these activity microdomains. Together, these findings suggest that biochemical activities of the cell are spatially organized into an activity architecture whose structural and functional characteristics can be revealed by these new biosensors.

Points of Significance: Interpreting P *values - pp213 - 214*

Naomi Altman & Martin Krzywinski doi:10.1038/nmeth.4210

A *P* value measures a sample's compatibility with a hypothesis, not the truth of the hypothesis.

Abstract - Points of Significance: Interpreting P values | Full Text - Points of Significance Interpreting P values | PDF (209 KB)

Responsible referencing - p209
doi:10.1038/nmeth.4219
Careful construction of reference lists is the responsibility of every scientist.
Abstract - Responsible referencing | Full Text - Responsible referencing | PDF (53 KB)

mScarlet: a bright monomeric red fluorescent protein for cellular imaging
Daphne S Bindels …… & Theodorus W J Gadella Jr *Nature Methods* **14**, 53–56 (2017) doi:10.1038/nmeth.4074
We report the engineering of mScarlet, a truly monomeric red fluorescent protein with record brightness, quantum yield (70%) and fluorescence lifetime (3.9 ns). We developed mScarlet starting with a consensus synthetic template and using improved spectroscopic screening techniques; mScarlet's crystal structure reveals a planar and rigidified chromophore. mScarlet outperforms existing red fluorescent proteins as a fusion tag, and it is especially useful as a Förster resonance energy transfer (FRET) acceptor in ratiometric imaging.

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Plant adaptations to the combination of drought and high temperatures (pages 2–12)
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Decreasing fructose 1,6-bisphosphate aldolase activity reduces plant growth and tolerance to chilling stress in tomato seedlings
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Nitric oxide as a signaling molecule in brassinosteroid-mediated virus resistance to Cucumber mosaic virus in Arabidopsis thaliana
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Prominent alterations of wild barley leaf transcriptome in response to individual and combined drought acclimation and heat shock conditions
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Nitrogen - essential macronutrient and signal controlling flowering time
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Small heat shock proteins and the postharvest chilling tolerance of tomato fruit (pages 148–160)
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What is hot in plant mitochondria?
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Per Gardeström and Abir U. Igamberdiev
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Visualization of Nicotine Adenine Dinucleotide Redox Homeostasis with Genetically Encoded Fluorescent Sensors
Yuzheng Zhao, Zhuo Zhang, Yejun Zou, and Yi Yang

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