ISSUE HIGHLIGHTS

GENETICS, Vol. 215, June 2020, Copyright © 2020

Silencing of Mutator elements in maize involves distinct populations of small RNAs and distinct patterns of DNA methylation, pp. 379–391
Diane Burgess, Hong Li, Meixia Zhao, Song Yol Kim, and Damon Lisch

Small RNA-mediated de novo silencing of AcDcs transposons is initiated by alternative transposition in maize, pp. 393–406
Dafang Wang, Jianbo Zhang, Tao Zuo, Meixia Zhao, Damon Lisch, and Thomas Peterson

Transposable elements (TEs) are a ubiquitous feature of plant genomes. Because of their threat to genome integrity, most TEs are epigenetically silenced. However, even closely related plant species often have dramatically different populations of TEs, suggesting periodic rounds of activity and silencing. Here, Burgess et al. show that de novo methylation of an active MuDR element in maize involves two distinct pathways, one of which is directly implicated in causing epigenetic silencing and one of which is the result of that silencing. In a companion article, Wang et al. show that silencing of a second maize TE, Ac, involves a strikingly similar process. In both cases, a hairpin transcript from a rearranged element is processed into small RNAs that can then trigger heritable silencing of an otherwise active element.

The dynamics of P granule liquid droplets are regulated by the Caenorhabditis elegans germline RNA helicase GLH-1 via its ATP hydrolysis cycle, pp. 421–434
Wenjian Chabbing Hong Hu, Charles E. Long, Jordan S. Brown, Sierra Schwabach, Xiaoyan Song, Ying Zhang, Edwin Munro, Karen Bennett, Donglei Zhang, and Heng-Chi Lee

Germ granules, also known as P granules in Caenorhabditis elegans, are phase-separated cellular bodies that are frequently found at the perinuclear region of germ cell nuclei in various animals. However, how the dynamics and localization of P granules are regulated remains largely unknown. Here we provided evidence that the VASA-like RNA helicase GLH-1 couples its RNA binding and release to promote the formation and disassembly of P granules, respectively. In addition, the FGG repeats in GLH-1 promote its localization at the nuclear periphery. Together, Chen et al. results highlight the versatile roles of an RNA helicase in controlling the formation of germ granules in space and time.

Detecting shared genetic architecture among multiple phenotypes by hierarchical clustering of gene-level association statistics, pp. 511–529
Melissa R. McGuil, Samuel Partillo Smith, Bijnor Sandsted, and Sohini Ramachandran

McGuil et al. present a new method, Ward clustering to identify Internal Node branched dwellers using Gene Scores (WINGS), for identifying shared genetic architecture among multiple phenotypes. Past research, from these authors and others, has shown that gene-level tests of association produce biologically interpretable characterization of a phenotype's genetic architecture. The objective of WINGS is to identify clusters of phenotypes sharing multiple genes enriched for mutations in cases. The authors validate WINGS using extensive simulation studies and apply WINGS to case-control and quantitative phenotypes in European-ancestry UK Biobank individuals. They identify eight prioritized phenotype clusters and recover multiple published gene-level associations within these clusters.

Cuticle collagen expression is regulated in response to environmental stimuli by the GATA transcription factor ELT-3 in Caenorhabditis elegans, pp. 483–495

Mesihi et al. find that environmental factors, including diet, starvation, and population density can differentially influence the penetration of collagen mutant phenotypes. Factors that decrease the penetrance of dominant rol-6 mutants, increase rolling in dominant mutants of the collagen gene sqt-3 and vice versa, demonstrating that the effects they observe are collagen-specific. Their data suggest that cuticle composition is modified in response to environment by transcriptional regulation of collagen expression. They find that ELT-3 acts to regulate the expression of lon-3, dpy-13, sqt-1 and rol-1, which are altered in response to environment.

Private genomes and public SNPs: homomorphic encryption of genotypes and phenotypes for shared quantitative genetics, pp. 359–372
Richard Mott, Christian Fischer, Pjotr Prins, and Robert William Davies

Mott et al. show that association between a quantitative trait and genotype can be performed using data that has been processed by first rotating it into a high-dimensional space. The resulting encrypted phenotypes and genotypes have little resemblance with the original data, thereby combining genetic analysis with genetic privacy.

Oocyte elimination through DNA damage signaling from CHK1/CHK2 to p53 and p63, pp. 373–378
Viv D. Rinaldi, Jordana C. Bloom, and John C. Schimenti

Unrepaired DNA damage in mouse oocytes leads to apoptosis, in part via CHK2 signaling to TRP53 and TRP63. Here, Rinaldi, Bloom, and Schimenti provide evidence that CHK1 can also be involved, especially in the absence of CHK2. Additionally, they find that all damage signaling in oocytes is transduced by upstream kinases to TRP53 and TRP63.

Analysis of haplotypic variation and deletion polymorphisms point to multiple archaic introgression events, including from Altai Neanderthal lineage, pp. 497–509
Oegus Taskent, Yin Lung Lin, Ioannis Patramanis, Pavlos Pavlidis, and Omer Gokcenan

Although analysis of modern and ancient genomes showed that Neanderthals contributed genetic material to the ancestors of extant human populations, when and where Neanderthals interacted with modern human populations remain exciting questions in the field. Here, Taskent et al. take advantage of recently available Neanderthal genomes and combined best single nucleotide and copy number variations to ask whether different Neanderthal lineages contributed to extant human populations. Their results suggest that different Neanderthal populations contributed to geographically diverse modern human populations at different times in history.

Golgi outposts locally regulate microtubule orientation in neurons but are not required for the overall polarity of the dendritic cytoskeleton, pp. 435–447
Shua Z. Yang and Jill Wildonger

Golgi are emerging as key regulators of axon-tosomal microtubule networks. In neurons, the role of dendrite-specific Golgi outposts in creating or maintaining the unique organization of the dendritic cytoskeleton is an open question. Using genetic approaches in a Drosophila model, Yang and Wildonger show that outposts are not essential for dendritic microtubule polarity. However, inducing the formation of ectopic multi-compartment outposts alters microtubule polarity in dendrites. Combined, their data indicate that the compartmental organization of Golgi outposts must be tightly controlled to generate proper microtubule polarity in dendrites.

This Month’s Perspectives

Ehab Lamm, Oren Harman, and Sophie Juliana Veigl

The story of genetics typically omits the original discovery of the molecular nature of DNA: Friedrich Miescher’s 1869 discovery of the substance he christened “nuclein”. The article explains how he came to be forgotten, highlighting factors that affect contemporary science as well. Miescher made two other observations that were remarkably prescient: that nuclein had an acidic and a protein component (in other words, that it was what we now call “chromatin”) and that stereo-chemistry could be the basis of hereditary transmission. This makes his contribution highly relevant to present day concerns.

In CBE — Life Sciences Education (LSE)

Peer leader reflections on promoting discussion in peer group-learning sessions: reflective and practiced advice through collaborative annual peer-advice books, CBE—Life Sciences Education 9 Jan. 2020; https://doi.org/10.1187/cbe.19-05-0091
Gabriela Satenberg, Michelle Repice, Claudia Hendrick, Stephen Mererink, and Regina Frey

This article presents detailed information collected from years of students’ reflections on their experiences as Peer Leaders. As part of a Peer-led team learning (PLTL) program for general chemistry, students wrote advice books for future team leaders. The authors categorized almost 2,000 entries into themes, further describing each theme with categories and examples. The main themes were “environment” (e.g. leader attitude, social and physical environment and group expectations), “group dynamics” (e.g. group functioning, balancing personalities, and promoting equal participation), and “motivation” (e.g. pacing, questioning, motivating). These themes reveal student thinking, especially regarding the importance of a supportive near-peer community, and provide a valuable resource for training new generations of peer leaders.