GENETICS, Vol. 207, September 2017, Copyright © 2017

MicroRNAs that contribute to coordinating the immune response in *Drosophila melanogaster*, pp. 163–178

Magda L. Atilano, Marcus Glittenberg, Annabel Monteiro, Richard R. Copley, and Petros Ligoxygakis

Atilano *et al*. present a *Drosophila* post-infection survival screen that takes advantage of a library of miRNA mutant flies. Using genome wide microarray and bioinformatics surveys to pinpoint the NF-kB-regulated fraction of these miRNAs, they reveal a layer of miRNA-mediated immune regulation at the whole organism level.

Regulation of lysosomal function by the DAF-16 Forkhead transcription factor couples reproduction to aging in *Caenorhabditis elegans*, pp. 83–101

Kunal Baxi, Ata Ghavidel, Brandon Waddell, Troy A. Harkness, and Carlos E. de Carvalho

Reproduction and aging are intertwined. While lifespan and reproductive strategies vary greatly among animals, the progeny production period generally coincides with the stage in life when the organism is the fittest. Here Baxi *et al*. show that, in *Caenorhabditis elegans*, the active regulation of lysosomal pH in the soma by signals from the gonad is one mechanism to ensure that animals delay somatic decline until reproduction is complete.

A gene implicated in activation of retinoic acid receptor targets is a novel renal agenesis gene in humans, pp. 215–228

Patrick D. Brophy, Maria Rasmussen, Mrutyunjaya Parida, Greg Bonde, Benjamin W. Darbro, Xiaojing Hong, Jason C. Clarke, Kevin A. Peterson, James Denegre, Michael Schneider, Caroline R. Sussman, Lone Sunde, Dorte L. Lildballe, Jens Michael Hertz, Robert A. Cornell, Stephen A. Murray, and J. Robert Manak

Renal agenesis is a devastating birth defect, and although genes encoding retinoic acid signaling components have been shown to be important for renal development in mice, no human genes of this pathway have been implicated in renal agenesis until now. Here, *Brophy et al*. identify the first such gene, *GREB1L*, and provide validation for its involvement in renal agenesis through a novel approach that takes advantage of genome editing in F0 mice.

Contrasting determinants of mutation rates in germline and soma, pp. 255–267

Chen Chen, Hongjian Qi, Yufeng Shen, Joseph Pickrell, and Molly Przeworski

A number of genomic features influence regional mutation rates in germline and soma. To examine if some factors behave differently in the two tissue types, Chen *et al*. applied a multivariate regression model to exome data from germline and soma, including expression levels and other features as predictors. They also considered the mutational strand asymmetry in soma and germline and its correlation with expression levels. They find evidence that the balance of damage and repair during transcription may differ between germline and soma.

Remarkable evolutionary conservation of antiobesity ADIPOSE/WDTC1 homologs in animals and plants, pp. 153–162

Eric Ducos, Valentin Vergès, Thomas Dugé de Bernonville, Nathalie Blanc, Nathalie Giglioli-Guivarc'h, and Christelle Dutilleul

Ducos *et al*. report that the farnesylated protein ASG2 is the *Arabidopsis* ortholog of human WDCT1, which controls fat accumulation. Both proteins harbor WD40 domains, tetratricopeptide repeats, and a C-terminal, farnesylatable CaaX-box. ASG2 dysfunction leads to the production of "obese" seeds with enhanced fat content. Their results highlight a remarkable evolutionarily conserved role for WDTC1-like proteins in fat metabolism in both the plant and animal kingdoms.

Histone acetylation, not stoichiometry, regulates linker histone binding in *Saccharomyces cerevisiae*, pp. 347–355

Mackenzie B. D. Lawrence, Nicolas Coutin, Jennifer K. Choi, Benjamin J. E. Martin, Nicholas A. T. Irwin, Barry Young, Christopher Loewen, and LeAnn J. Howe

Linker histones play an important role in shaping chromatin structure, but the regulation of their interactions with chromatin is poorly understood. In this study, Lawrence *et al.* explore the regulation of linker histone binding in *Saccharomyces cerevisiae*, showing that core histone acetylation negatively regulates linker histone binding. These results provide important insight into how chromatin structure is regulated and maintained to both facilitate and repress transcription.

Benchmarking relatedness inference methods with genome-wide data from thousands of relatives, pp. 75–82

Monica D. Ramstetter, Thomas D. Dyer, Donna M. Lehman, Joanne E. Curran, Ravindranath Duggirala, John Blangero, Jason G. Mezey, and Amy L. Williams

Relatedness inference is an essential component of many genetic analyses and popular in consumer genetic testing. Ramstetter *et al*. evaluate twelve relatedness inference methods and show that all methods have high accuracy for first and second degree relatives but struggle to infer higher relatedness degrees. The methods typically infer unrelated individuals correctly, suggesting a low rate of false positives. Relatedness inference is likely to become more important as sample sizes increase and the proportion of samples with a relative in a given dataset grows.

A model for epigenetic inhibition via transvection in the mouse, pp. 129–138

Juan D. Rodriguez, Dexter A. Myrick, Ilaria Falciatori, Michael A. Christopher, Teresa W. Lee, Gregory J. Hannon, and David J. Katz

Transvection—a phenomenon in which the allele on one chromosome genetically interacts with its paired allele on the homologous chromosome—is one of the oldest and most mysterious genetic phenomena, but there are only two documented cases in mammals. Rodriguez *et al*. present an additional example of mammalian transvection initiated by a meiotically expressed *Cre* allele. They show that the transvection does not appear to be regulated by DNA methylation and is dependent upon parental history, suggesting an epigenetic phenomenon and providing a new model for studying the underlying mechanism in mammals.

This Month's Perspectives

Mendelism: new insights from Gregor Mendel's lectures in Brno, pp. 1–8

Hui Zhang, Wen Chen, and Kun Sun

After dissolving misinterpretation and prejudice of the newspaper report of Mendel's lectures, we found the lecture content can be recovered to more closely reveal the reality of Mendel's experimental work with the garden pea in Brno in 1856-1863, quite different from what Mendel presented in his published paper, which is always the exclusive source for understanding Mendel's work and exploring the origin of genetics. Indeed, to characterize the development feature of unit-characters in self-crosses and backcrosses of hybrids in successive generations, Mendel discovered the law of inheritance regarding behaviors of reproductive cells from one generation to the next generation.

This Month in the American Journal of Human Genetics

Sensitive monogenic noninvasive prenatal diagnosis by targeted haplotyping, Am. J. Hum. Gent. 101(3)

Carlo Vermeulen, Geert Geeven, Elzo de Wit, Marjon J.A.M. Verstegen, Rumo P.M. Jansen, Melissa van Kranenburg, Ewart de Bruijn, Sara L. Pulit, Evelien Kruisselbrink, Zahra Shahsavari, Davood Omrani, Fatemeh Zeinali, Hossein Najmabadi, Theodora Katsila, Christina Vrettou, George P. Patrinos, Joanne Traeger-Synodinos, Erik Splinter, Jeffrey M. Beekman, Sima Kheradmand Kia, Gerard J. te Meerman, Hans Kristian Ploos van Amstel, and Wouter de Laat

In screening pregnancies for genetic conditions, non-invasive prenatal testing is becoming popular because it uses maternal blood containing small amounts of circulating cell-free fetal DNA and is less invasive than procedures like amniocentesis. However, low fetal fraction of DNA within the cell-free DNA in blood makes distinguishing between the fetal and maternal alleles difficult. In this issue, Vermeulen *et al*. use a targeted locus amplification to phase haplotypes at a given genetic locus allowing clinicians to distinguish between maternal and fetal genotypes. This approach was validated for eighteen pregnancies evaluating variation in *CFTR*, *CYP21A2* and *HBB* and could predict the inherited fetal allele with 98% confidence at 8 weeks of pregnancy.