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INVESTIGATIONS

- 1141–1151 The Genetic Basis of Baculum Size and Shape Variation in Mice**
Nicholas G. Schultz, Jesse Ingels, Andrew Hillhouse, Keegan Wardwell, Peter L. Chang, James M. Cheverud, Cathleen Lutz, Lu Lu, Robert W. Williams, and Matthew D. Dean
- Rapid divergence of male genital morphology is a ubiquitous evolutionary pattern. Here, Schultz *et al.* develop novel morphometric methods to measure the baculum (a bone in the penis of many mammals) in three dimensions and then map variance in size and shape across a family of recombinant inbred lines of mice. The authors found loci that explain a large proportion of the variance and independently influence size and shape. With further bioinformatic and RNA expression analyses, they narrowed these loci to several promising candidate genes. Their study provides insight into the evolution of male genitalia.
- 1153–1163 Does 3D Phenotyping Yield Substantial Insights in the Genetics of the Mouse Mandible Shape?**
Nicolas Navarro and A. Murat Maga
- Despite the increasing availability of 3D technologies, 2D imaging techniques seem still at first an appealing compromise for large-scale phenotyping protocols. By quantifying the 3D shape of the mouse mandible in detail and mapping associated genetic loci, the authors of this study show a fairly robust knowledge on its genetic architecture built over a few decades and initially based on 2D imaging techniques. Nonetheless, despite inherent difficulties and workload, 3D data may clearly provide some new insights on the genetics of shape even for organs that seem at first embedded in a 2D plane.
- 1165–1177 Genomic Bayesian Prediction Model for Count Data with Genotype \times Environment Interaction**
Abelardo Montesinos-López, Osva A. Montesinos-López, José Crossa, Juan Burgueño, Kent M. Eskridge, Esteban Falconi-Castillo, Xinyao He, Pawan Singh, and Karen Cichy
- In this study, Montesinos-López *et al.* propose a Bayesian mixed negative binomial (BMNB) genomic regression model for counts that takes into account genotype by environment (G \times E) interaction. The authors also provide all the full conditional distributions to implement a Gibbs sampler. They evaluated the proposed model using a simulated data set and a real wheat data set from the International Maize and Wheat Improvement Center (CIMMYT) and collaborators. Results indicate that the authors' BMNB model is a viable alternative for analyzing count data.
- 1179–1189 Sequence of the *Gonium pectorale* Mating Locus Reveals a Complex and Dynamic History of Changes in Volvocine Algal Mating Haplotypes**
Takashi Hamaji, Yuko Mogi, Patrick J. Ferris, Toshiyuki Mori, Shinya Miyagishima, Yukihiro Kabeya, Yoshiki Nishimura, Atsushi Toyoda, Hideki Noguchi, Asao Fujiyama, Bradley J. S. C. Olson, Tara N. Marriage, Ichiro Nishii, James G. Umen, and Hisayoshi Nozaki
- Volvocine algae represent an extreme expansion of mating loci (*MT*) between isogamous *Chlamydomonas* and oogamous *Volvox*. To characterize the evolutionary history of volvocine *MT* in which recombination is suppressed, the authors sequenced the third *MT* from isogamous *Gonium pectorale*. *Gonium MT* shows maintenance of key mating determinant gene homologs *MID* and *FUS1* and lower divergence in gametologs, whereas there was a mass exodus of other gametologs from *MT* to all over the genome. Overall, these findings suggest the volvocine *MT* locus does not simply accumulate mutations but also experiences dynamic and continuous structural reorganization to make its history more complex.

- 1191–1200 **Comparative and Transcriptome Analyses Uncover Key Aspects of Coding- and Long Noncoding RNAs in Flatworm Mitochondrial Genomes**
Eric Ross, David Blair, Carlos Guerrero-Hernández, and Alejandro Sánchez Alvarado
 Although the traditional approach to the annotation of mitochondrial genomes has been successful in bringing order to the wealth of mitochondrial genome sequences available, this strategy is not without limitations. Here, the authors report a novel approach to annotate mitochondrial genomes that has allowed them to discover evidence for an alternative start codon, an extended *cox1* gene, a previously undescribed conserved open reading frame, long non-coding RNAs and a highly conserved gene order across the large evolutionary distances represented within planarians.
- 1201–1215 **Massive Amplification at an Unselected Locus Accompanies Complex Chromosomal Rearrangements in Yeast**
Agnès Thierry, Varun Khanna, and Bernard Dujon
 In this study, the authors report the complete molecular characterization of extensive chromosomal rearrangements associated with very-high order amplification at an unselected locus in yeast and propose a mechanism underlying such catastrophic events.
- 1217–1226 **The Genetic Linkage Map of the Medicinal Mushroom *Agaricus subrufescens* Reveals Highly Conserved Macrosynteny with the Congeneric Species *Agaricus bisporus***
Marie Foulongne-Oriol, Manuela Rocha de Brito, Delphine Cabannes, Aurélien Clément, Cathy Spataro, Magalie Moinard, Eustáquio Souza Dias, Philippe Callac, and Jean-Michel Savoie
 Foulongne-Oriol *et al.* developed the first genetic linkage map for the medicinal mushroom *Agaricus subrufescens*, providing a framework for future genetic or genomic studies in this emerging crop species. Through a comparative mapping approach, they have proved the high level of macrosynteny with the genome of the model mushroom *A. bisporus*. Their results were discussed in the light of *Agaricus* species evolution process. Beyond evolutive considerations, the conserved synteny allows a potential transferability of the genetic information between these two agronomic mushroom species to be imagined.
- 1227–1237 **Staufen Negatively Modulates MicroRNA Activity in *Caenorhabditis elegans***
Zhiji Ren, Isana Veksler-Lublinsky, David Morrissey, and Victor Ambros
 Establishing and maintaining proper gene expression requires various regulatory mechanisms including post-transcriptional regulation by microRNAs and RNA-binding proteins. The double-stranded RNA-binding protein Staufen was known to exert both positive and negative regulation on gene expression. The authors of this study report genetic analysis showing that Staufen can negatively modulate the efficacy of microRNAs in *Caenorhabditis elegans*, suggesting a role for Staufen's translational activator function in buffering microRNA-based inhibition of mRNA activity in developmental, physiological and environmental contexts. Staufen and microRNAs are evolutionarily conserved, and therefore, this study presents implications for similar integration of these two pathways in other animals.
- 1239–1249 **Comparative Transcriptomics Indicates a Role for *SHORT VEGETATIVE PHASE (SVP)* Genes in *Mimulus guttatus* Vernalization Response**
Jill C. Preston, Jinshun Zhong, Meghan McKeown, Meghan den Bakker, and Jannice Friedman
 The use of winter chilling (vernalization) as a cue to ready plants for spring flowering has evolved repeatedly in angiosperms, probably as an adaptation to seasonal temperate environments. Flowering time genetic pathways are generally conserved, suggesting that genetic changes underlying convergent evolution of vernalization might be similar. To test this, Preston *et al.* used global and targeted gene expression to identify the genes underlying population variation in vernalization responsiveness in *Mimulus guttatus*. They identified 414 genes whose expression matched predictions for vernalization genes; follow-up analyses supported the novel recruitment of *SHORT VEGETATIVE PHASE* genes in the evolution of this important flowering trait.
- 1251–1266 **Latitudinal Clines of the Human Vitamin D Receptor and Skin Color Genes**
Dov Tiosano, Laura Audi, Sharlee Climer, Weixiong Zhang, Alan R. Templeton, Monica Fernández-Cancio, Ruth Gershoni-Baruch, José Miguel Sánchez-Muro, Mohamed El Kholly, and Zèev Hochberg
 Tiosano *et al.* introduce a linkage disequilibrium measure and multi-locus network construction algorithm for allele-specific associations and show that it is a practical population genomics tool. They present novel results about skin color adaptation in human populations and identify multi-locus responses. In addition, they show that these multi-locus responses are likely due to a mixture of parallel adaptation and coadaptation.

- 1267–1275 **Transcriptomic Analysis Identifies Candidate Genes and Gene Sets Controlling the Response of Porcine Peripheral Blood Mononuclear Cells to Poly I:C Stimulation**
Jiyang Wang, Yanping Wang, Huaizhong Wang, Haifei Wang, Jian-Feng Liu, Ying Wu, and Jianfeng Guo
 To gain deep knowledge of the host transcriptional response of pigs to Polyinosinic:polycytidylic acid (poly I:C), a synthetic analog of dsRNA virus, the authors of this study cultured and stimulated peripheral blood mononuclear cells (PBMC) of piglets of one modern commercial breed (Landrace) and one Chinese indigenous breed (Dapulian) with poly I:C and comparatively analyzed their transcriptional profiling using RNA sequencing. Their results identified some significantly differentially expressed (DE) genes and enriched gene sets in Dapulian and Landrace. Most of the DE genes and gene sets were immune-related and may play crucial roles in the immune response of host to poly I:C stimulation.
- 1277–1285 **Chicken gga-miR-103-3p Targets CCNE1 and TFDP2 and Inhibits MDCC-MSB1 Cell Migration**
Bo Han, Ling Lian, Xin Li, Chunfang Zhao, Lujiang Qu, Changjun Liu, Jiuzhou Song, and Ning Yang
 In this study, gga-miR-103-3p was found down-regulated in MDV-infected tissues, and it inhibited cell migration in MDCC-MSB1 cell line. Two target genes *CCNE1* and *TFDP2* were identified to be the mRNA targets of gga-miR-103-3p. The effective binding sites of gga-miR-103-3p in 3'-UTR of *CCNE1* and *TFDP2* mRNA were confirmed. Gga-miR-103-3p could suppress the *CCNE1* gene expression at both mRNA and protein levels, while the *TFDP2* gene was regulated by gga-miR-103-3p at the protein level but not at the mRNA level. Gga-miR-103-3p working together with its targets may play a potential role in MDV tumorigenesis.
- 1287–1296 **Conflation of Short Identity-by-Descent Segments Bias Their Inferred Length Distribution**
Charleston W. K. Chiang, Peter Ralph, and John Novembre
 Identity-by-descent (IBD) is a fundamental concept in genetics and is utilized in many applications, including long-range phasing, imputation, genetic mapping, detection of natural selection, and demographic inferences. Moreover, in the age of direct-to-consumer genetics, companies like Ancestry.com or 23andme routinely utilize IBD sharing to identify relatives. However, the authors of this study show that popular IBD detection programs oftentimes identify long stretches of IBD segments that are in fact due to confluences of shorter, but independent, segments. They then show that inferences such as mutation rate estimation based on this errant distribution of IBD segment lengths will also be in error.
- 1297–1304 **Mapping Challenging Mutations by Whole-Genome Sequencing**
Harold E. Smith, Amy S. Fabritius, Aimee Jaramillo-Lambert, and Andy Golden
 Mutagenesis and phenotypic screening in model organisms is an experimental geneticist's stock-in-trade for determining gene function. Such screens can recover alleles—dominant and semi-dominant mutations, multigenic traits, and terminally arrested phenotypes—that make gene identification challenging. The authors of this study demonstrate the utility of whole-genome sequencing for the identification of mutations in those categories that are difficult to map by other methods.
- 1305–1312 **Characterization of Chicken MMP13 Expression and Genetic Effect on Egg Production Traits of Its Promoter Polymorphisms**
Zhenjie Yuan, Yuxia Chen, Qiuyue Chen, Miao Guo, Li Kang, Guiyu Zhu, and Yunliang Jiang
 Chicken ovarian follicle growth requires constant remodeling of extracellular matrix performed by MMPs. MMP13 is up-regulated in sexually mature chicken ovaries. In this study, the authors found that the expression of MMP13 in chicken ovary and ovarian follicles is critical for ovary development, follicle growth and ovulation. They identified a critical promoter region controlling chicken MMP13 transcription as well as six SNPs and found that hens with the A⁻¹³⁵⁶-C⁻¹⁰⁷⁹/A⁻¹³⁵⁶-C⁻¹⁰⁷⁹ genotype had an earlier age at first laying than those with the G⁻¹³⁵⁶-T⁻¹⁰⁷⁹/G⁻¹³⁵⁶-T⁻¹⁰⁷⁹ genotype ($P < 0.05$), which could be used as molecular markers in chicken breeding.
- 1313–1326 **Genomic Selection in Multi-environment Crop Trials**
Helena Oakey, Brian Cullis, Robin Thompson, Jordi Comadran, Claire Halpin, and Robbie Waugh
 Genomic selection is a technique used in livestock breeding in which the breeding value of an animal is predicted from the genetic markers it carries. However, using genomic selection for crop breeding presents challenges for statistical modelling that are not found in animal studies. Oakey *et al.* devised a new genomic selection approach for crops that solves these problems. Their model performed better than current models at predicting the trait of plant height in barley, even when fewer markers were used. This approach could increase confidence in the selection of the best lines for breeding and reduce costs by using fewer markers.

- 1327–1343 **The SEB-1 Transcription Factor Binds to the STRE Motif in *Neurospora crassa* and Regulates a Variety of Cellular Processes Including the Stress Response and Reserve Carbohydrate Metabolism**
Fernanda Zanolli Freitas, Stela Virgilio, Fernanda Barbosa Cupertino, David John Kowbel, Mariana Fioramonte, Fabio Cesar Gozzo, N. Louise Glass, and Maria Célia Bertolini
- All living cells respond to environmental conditions by integrating sensing and signal transduction pathways, which impact their gene expression. The SEB-1 transcription factor was identified here as a *Neurospora crassa* protein that binds to STRE, a DNA motif present in the promoters of stress-responsive genes. This transcription factor is described as involved in stress response; however, its requirement for resistance to different stress may vary among filamentous fungi. Using RNA-seq to determine the global gene expression of the $\Delta seb-1$ strain under heat stress, the authors demonstrated that SEB-1 might connect the heat stress response to a broad range of cellular mechanisms.
- 1345–1355 **Patterns of Transcriptional Response to 1,25-Dihydroxyvitamin D3 and Bacterial Lipopolysaccharide in Primary Human Monocytes**
Silvia N. Kariuki, John D. Blischak, Shigeki Nakagome, David B. Witonsky, and Anna Di Rienzo
- Epidemiological studies have linked insufficiency in vitamin D levels with risk of various immune-mediated diseases, but the underlying mechanisms are poorly understood. Inter-individual variation in the modulatory role played by vitamin D in the immune system could contribute to variation in disease risk. The authors of this study profiled gene expression patterns in monocytes treated with vitamin D and bacterial lipopolysaccharide, a potent stimulus of the immune system. They identified biological pathways that are crucial in mediating the immunomodulatory role of vitamin D and could provide mechanistic clues underlying the links between insufficient vitamin D levels and increased disease risk.
- 1357–1364 **Gene Regulatory Evolution During Speciation in a Songbird**
John H. Davidson and Christopher N. Balakrishnan
- Birds are important for the study of speciation because of unique features like female heterogamety, a highly conserved karyotype, and the slow evolution of reproductive incompatibilities. This study for the first time examined gene expression divergence between two bird subspecies and their hybrids. In doing so, the study broadly describes how gene expression diverges during speciation and how gene expression is altered in hybrid birds. By focusing on an understudied taxon, this study contributes to a broader understanding of the mechanisms of speciation.
- 1365–1371 **The *HIST1* Locus Escapes Reprogramming in Cloned Bovine Embryos**
Byungkuk Min, Sunwha Cho, Jung Sun Park, Kyuheum Jeon, and Yong-Kook Kang
- Reprogramming errors in SCNT embryos and the genetic mechanisms behind them have not been revealed. *HIST1* histone genes are specifically underrepresented in bovine SCNT blastocysts. *HIST1* locus is resistant to reprogramming in SCNT embryos by epigenetic mechanism. The authors' efforts to find reprogramming resistant regions will help elucidate local and global reprogramming events in SCNT embryos.
- 1373–1381 **Preparing for Winter: The Transcriptomic Response Associated with Different Day Lengths in *Drosophila montana***
Darren J. Parker, Michael G. Ritchie, and Maaria Kankare
- Many organisms use day length to track changes in season and make changes to their physiology. Here, the authors used a northern Finnish population of *Drosophila montana* to identify genes that change in expression when *D. montana* is maintained in different light dark cycles. Overall, many genes changed in expression in response to decreased day length, including genes involved in neuron development and metabolism, consistent with an increase in cold tolerance previously observed to occur in these flies. The authors also identified many genes associated with reproduction, suggesting that *D. montana* use changes in day length to cue changes in their reproduction.
- 1383–1390 **The *Arabidopsis* Auxin Receptor F-Box Proteins AFB4 and AFB5 Are Required for Response to the Synthetic Auxin Picloram**
Michael J. Prigge, Kathleen Greenham, Yi Zhang, Aaron Santner, Cristina Castillejo, Andrew M. Mutka, Ronan C. O'Malley, Joseph R. Ecker, Barbara N. Kunkel, and Mark Estelle
- The plant hormone auxin acts by promoting the degradation of transcriptional repressors. This requires a family of E3 ligases called SCF^{TIR1/AFB}. Auxin interacts directly with the F-box protein subunits of the SCF. This study demonstrates that two of these F-box proteins, AFB4 and AFB5, are auxin receptors but have a unique specificity.

- 1391–1408 **Multiple Targets on the Gln3 Transcription Activator Are Cumulatively Required for Control of Its Cytoplasmic Sequestration**
Rajendra Rai, Jennifer J. Tate, and Terrance G. Cooper
 Nitrogen-responsive transcription activator Gln3 becomes nuclear in response to nitrogen limitation/short-term starvation, long-term nitrogen starvation, and methionine sulfoximine (Msx) or rapamycin treatment. The authors of this study previously identified unique Gln3 sites, one required for rapamycin-responsiveness and another for Gln3-mTor1 interaction. Here, they identified a serine/threonine-rich region (Gln3₄₇₇₋₄₉₃) required for effective cytoplasmic Gln3 sequestration in excess nitrogen. Serine to alanine substitutions in Gln3₄₇₇₋₄₉₃ partially abolish cytoplasmic Gln3 sequestration but have no effect on Gln3-Myc^{13'}'s responses to rapamycin or Msx. A Gln3₄₇₇₋₄₉₃, Tor1-interaction site double mutant completely abolishes cytoplasmic Gln3 sequestration, demonstrating Gln3 regulation is achieved by the cumulative action of multiple, distinct regulatory pathways.
- 1409–1416 **Genetic Background, Maternal Age, and Interaction Effects Mediate Rates of Crossing Over in *Drosophila melanogaster* Females**
Chad M. Hunter, Matthew C. Robinson, David L. Aylor, and Nadia D. Singh
 Rates of meiotic recombination have long been known to vary in response to environmental and genetic factors. By analyzing rates of recombination over the lifetime of female fruit flies, the authors of this study found that both age and genetic background significantly contribute to observed variation in recombination frequency, as do genotype-age interactions. Their results highlight the complexity of recombination rate variation and reveal a new role of genotype by environmental interactions in mediating recombination rate.
- 1417–1426 **A High-Density SNP Genetic Linkage Map and QTL Analysis of Growth-Related Traits in a Hybrid Family of Oysters (*Crassostrea gigas* × *Crassostrea angulata*) Using Genotyping-by-Sequencing**
Jinpeng Wang, Li Li, and Guofan Zhang
 Oysters are one of the most important aquaculture species in the world. In the present study, a second-generation genetic linkage map representing the densest genetic map for the oyster was constructed. In total, 1695 genotyping-by-sequencing generated markers were mapped with the average interval of 0.8 cM for the hybridized family of *Crassostrea gigas* and *C. angulata*. 27 QTLs for five growth-related traits were detected, and 38 genes were annotated in the QTL regions, two of which were growth-related as supported by previous studies. This provides valuable genetic resources and the basis for marker-assisted selection for both oysters.
- 1427–1437 **Quantitative Assessment of Eye Phenotypes for Functional Genetic Studies Using *Drosophila melanogaster***
Janani Iyer, Qingyu Wang, Thanh Le, Lucilla Pizzo, Sebastian Grönke, Surendra S. Ambegaokar, Yuzuru Imai, Ashutosh Srivastava, Beatriz Llamusi Troisi, Graeme Mardon, Ruben Artero, George R. Jackson, Adrian M. Isaacs, Linda Partridge, Bingwei Lu, Justin P. Kumar, and Santhosh Girirajan
 The authors of this study present a quantitative tool, Flynotyper, for assessment of eye phenotypes for functional studies in *Drosophila melanogaster*. Using proof-of-principle experiments, they quantified dosage sensitivity of 12 neurodevelopmental genes, accurately validated their method across different imaging platforms and genotypes from six independent studies, and demonstrated the utility of their tool by analyzing novel modifiers of sine oculis (so) obtained from two genome-wide deficiency screens and classifying them into enhancers and suppressors based on their effect on so-associated eye phenotypes. Their method will complement existing assays for eye phenotypes and increase the accuracy of studies that use fly eyes for functional evaluation.
- 1439–1447 **The Sorghum Gene for Leaf Color Changes upon Wounding (*P*) Encodes a Flavanone 4-Reductase in the 3-Deoxyanthocyanidin Biosynthesis Pathway**
Hiroyuki Kawahigashi, Shigemitsu Kasuga, Yuji Sawada, Jun-ichi Yonemaru, Tsuyu Ando, Hiroyuki Kanamori, Jianzhong Wu, Hiroshi Mizuno, Mitsuru Momma, Zui Fujimoto, Masami Yokota Hirai, and Takashi Matsumoto
 3-deoxyanthocyanidins are important phytoalexins produced as a defense system sorghum. In this study, the authors identified the *P* gene, Sb06g029550, as a flavanone 4-reductase that converts flavanone to flavan-4-ol in the 3-deoxyanthocyanidin synthesis pathway induced by wounding and pathogen attack. The molecular differentiation of dihydroflavonol 4-reductase and flavanone 4-reductase and the acquaintance of 3-deoxyanthocyanidin synthesis pathway in sorghum during the evolution of defense system are quite interesting. By loss of function of the gene, the sorghum plants results in producing flavones and shows tan color. Tan color crops were favored and positively selected by humans during the domestication process of crops.

- 1449–1457 **Organ Length Control by an ADAMTS Extracellular Protease in *Caenorhabditis elegans***
Yukimasa Shibata, Yuri Kawakado, Noriyoshi Hori, Kota Tanaka, Ryo Inoue, Tomomi Takano, Yukihiko Kubota, and Kiyoji Nishiwaki
- Precise control of organ length is a key feature in animal development. Although intracellular mechanisms regulating organ length are the major focus of recent studies, the extracellular molecular mechanisms that control organ length remain poorly understood. Members of the ADAMTS (a disintegrin and metalloprotease with thrombospondin motifs) family of secreted metalloproteinases have received considerable attention because defects in many of these proteins have been linked to hereditary diseases affecting the extracellular matrix. In the present study, the authors have showed that one of the ADAMTS family proteins acts in organ length regulation through remodeling of the basement membrane in *Caenorhabditis elegans*.
- 1459–1468 **Pollen Killer Gene S35 Function Requires Interaction with an Activator That Maps Close to S24, Another Pollen Killer Gene in Rice**
Takahiko Kubo, Atsushi Yoshimura, and Nori Kurata
- A pollen killer gene, S35, is one of the major loci responsible for hybrid male sterility between *Oryza sativa* ssp. *indica* and *japonica*. S35 has been proposed to interact with another pollen killer locus, S24, to induce pollen sterility. To examine this genetic interaction, the authors further dissected and characterized these loci. The results showed that S35 causes pollen sterility independently of S24 gene but is dependent on a novel gene close to S24. This study demonstrates that hybrid male sterility in rice is caused by several pollen killer networks with multiple factors positively and negatively regulating pollen killer genes.

MUTANT SCREEN REPORTS

- 1469–1474 **Novel Interactome of *Saccharomyces cerevisiae* Myosin Type II Identified by a Modified Integrated Membrane Yeast Two-Hybrid (iMYTH) Screen**
Ednalise Santiago, Pearl Akamine, Jamie Snider, Victoria Wong, Matthew Jessulat, Viktor Deineko, Alla Gagarinova, Hiroyuki Aoki, Zoran Minic, Sadhna Phanse, Andrea San Antonio, Luis A. Cubano, Brian C. Raymond, Mohan Babu, Igor Stagljar, and Jose R. Rodriguez-Medina
- The goal of this study was to expand the map of the Myo1p interactome and shed light on the functional properties of the Myo1p tail domain. The integrated split-ubiquitin membrane yeast two-hybrid (iMYTH) system, Tandem MS and co-IP methodologies were employed. Thirty novel protein-protein interactions were identified by iMYTH. Eight of the 30 novel proteins interactions with Myo1p were confirmed by AP-MS or co-IP.
- 1475–1487 **A Forward Genetic Screen for Molecules Involved in Pheromone-Induced Dauer Formation in *Caenorhabditis elegans***
Scott J. Neal, JiSoo Park, Danielle DiTirro, Jason Yoon, Mayumi Shibuya, Woochan Choi, Frank C. Schroeder, Rebecca A. Butcher, Kyuhyung Kim, and Piali Sengupta
- Animals produce and respond to complex blends of pheromones that elicit diverse behavioral and/or developmental responses in the receivers. This manuscript reports the results of a genetic screen designed to identify genes required for the sensation and signaling of pheromone cues in a developmental decision in *Caenorhabditis elegans*. This approach led to the identification and characterization of new molecules and neurons involved in this process. Mutants isolated in this screen will provide insights into the mechanisms underlying pheromone-mediated signaling.

- 1489 **CORRIGENDUM**