

Techniques

Wu, M. C., Chu, L. A., Hsiao, P. Y., Lin, Y. Y., Chi, C. C., Liu, T. H., ... & Chiang, A. S. (2014). Optogenetic control of selective neural activity in multiple freely moving *Drosophila* adults. *Proceedings of the National Academy of Sciences*, 111(14), 5367-5372.

Xue, W., Chen, S., Yin, H., Tammela, T., Papagiannakopoulos, T., Joshi, N. S., ... & Jacks, T. (2014). CRISPR-mediated direct mutation of cancer genes in the mouse liver. *Nature*. *CRISPR plasmids targeting Pten and p53, alone and in combination, are delivered by hydrodynamic injection to the liver; the CRISPR-mediated mutations phenocopy the effects of deletions using Cre-LoxP technology, allowing the direct mutation of tumour suppressor genes and oncogenes in the liver using the CRISPR/Cas system, which presents a new approach for rapid development of liver cancer models and functional genomics.*

Evolution

Evolution of multicellularity

Levin, T. C., Greaney, A. J., Wetzel, L., & King, N. (2014). The rosetteless gene controls development in the choanoflagellate *S. rosetta*. *eLife*, 3. *A genetic screen has revealed one of the molecules that allow choanoflagellates, the closest unicellular relative of animals, to form colonies, which could help researchers to answer questions about the earliest days of animal evolution.*

Hammerschmidt, K., Rose, C. J., Kerr, B., & Rainey, P. B. (2014). [Life cycles, fitness decoupling and the evolution of multicellularity](#). *Nature*, 515(7525), 75-79. *Simple cooperating groups of bacteria reproduced either by embracing or purging cheating types; those that embraced cheats adopted a life cycle of alternating phenotypic states, underpinned by a developmental switch that allowed the fitness of collectives to decouple from the fitness of constituent cells*

Large-scale Evolution (Bilateria, insects, sex chromosomes)

Fortunato, S. A., Adamski, M., Ramos, O. M., Leininger, S., Liu, J., Ferrier, D. E., & Adamska, M. (2014). [Calcisponges have a ParaHox gene and dynamic expression of dispersed NK homeobox genes](#). *Nature*, 514(7524), 620-623.

Misof, B., Liu, S., Meusemann, K., Peters, R. S., Donath, A., Mayer, C., ... & Ott, M. (2014). Phylogenomics resolves the timing and pattern of insect evolution. *Science*, 346(6210), 763-767. *Insects are the most speciose group of animals, but the phylogenetic relationships of many major lineages remain unresolved. We inferred the phylogeny of insects from 1478 protein-coding genes. Phylogenomic analyses of nucleotide and amino acid sequences, with site-specific nucleotide or domain-specific amino acid substitution models, produced statistically robust and congruent results resolving previously controversial phylogenetic relationships. We dated the origin of insects to the Early Ordovician [~479 million years ago (Ma)], of insect flight to the Early Devonian (~406 Ma), of major extant lineages to the Mississippian (~345 Ma), and the major diversification of holometabolous insects to the Early Cretaceous. Our phylogenomic study provides a comprehensive reliable scaffold for future comparative analyses of evolutionary innovations among insects.*

Soh, Y. S., Alföldi, J., Pyntikova, T., Brown, L. G., Graves, T., Minx, P. J., ... & Page, D. C. (2014). [Sequencing the Mouse Y Chromosome Reveals Convergent Gene Acquisition and Amplification on Both Sex Chromosomes](#). *Cell*.

We sequenced the MSY (male-specific region of the Y chromosome) of the C57BL/6J strain of the laboratory mouse Mus musculus. In contrast to theories that Y chromosomes are heterochromatic and gene poor, the mouse MSY is 99.9% euchromatic and contains about 700 protein-coding genes.

Short-term evolution

Stuart, Y. E., Campbell, T. S., Hohenlohe, P. A., Reynolds, R. G., Revell, L. J., & Losos, J. B. (2014). Rapid evolution of a native species following invasion by a congener. *Science*, 346(6208), 463-466.

On small islands in Florida, we found that the lizard Anolis carolinensis moved to higher perches following invasion by Anolis sagrei and, in response, adaptively evolved larger toepads after only 20 generations. These results illustrate that interspecific interactions between closely related species can drive evolutionary change on observable time scales.

Faria, N. R., Rambaut, A., Suchard, M. A., Baele, G., Bedford, T., Ward, M. J., ... & Lemey, P. (2014). The early spread and epidemic ignition of HIV-1 in human populations. *science*, 346(6205), 56-61.

The early history of HIV centered on Kinshasa before accelerating in 1960 as a result of seismic social change after independence.

Fu, Q., Li, H., Moorjani, P., Jay, F., Slepchenko, S. M., Bondarev, A. A., ... & Pääbo, S. (2014). Genome sequence of a 45,000-year-old modern human from western Siberia. *Nature*, 514(7523), 445-449.

A modern human fossil femur found in 2008 on the banks of the river Irtysh in western Siberia was dated at some 45,000 years old. The genome from this individual — a male who lived at about the time of the separation of the populations in western and eastern Eurasia — has now been sequenced. Analyses reveal a level of Neanderthal ancestry similar to that found in present-day Eurasians, and suggest that interbreeding between modern humans and Neanderthals occurred 50,000 to 60,000 years ago, coinciding with the expansion of modern humans into Europe, and possibly Asia.

Hudson, N. J., Baker, M. L., Hart, N. S., Wynne, J. W., Gu, Q., Huang, Z., ... & Reverter, A. (2014). Sensory Rewiring in an Echolocator: Genome-Wide Modification of Retinogenic and Auditory Genes in the Bat Myotis davidii. *G3: Genes| Genomes| Genetics*, 4(10), 1825-1835.

Ffrench-Constant, R. H. (2014). Genomics: Of monarchs and migration. *Nature*, 514(7522), 314-315.

The genomes of 101 monarch butterflies from migratory and resident populations have been sequenced, revealing genes and molecular pathways that underlie insect migration and colouration.

Repeated evolution

Pankey, M. S., Minin, V. N., Imholte, G. C., Suchard, M. A., & Oakley, T. H. (2014). Predictable transcriptome evolution in the convergent and complex bioluminescent organs of squid. *Proceedings of the National Academy of Sciences*, 111(44), E4736-E4742.

Sicard, A., Thamm, A., Marona, C., Lee, Y. W., Wahl, V., Stinchcombe, J. R., ... & Lenhard, M. (2014). Repeated Evolutionary Changes of Leaf Morphology Caused by Mutations to a Homeobox Gene. *Current Biology*, 24(16), 1880-1886.

Hotspot gene for leaf shape, which is also involved in a plasticity response (change in leaf change due to temperature).

Evolution of symbionts and metabolic dependence

Van Leuven, J. T., Meister, R. C., Simon, C., & McCutcheon, J. P. (2014). [Sympatric Speciation in a Bacterial Endosymbiont Results in Two Genomes with the Functionality of One](#). *Cell*, 158(6), 1270-1280.

Hillesland, K. L., Lim, S., Flowers, J. J., Turkarslan, S., Pinel, N., Zane, G. M., ... & Stahl, D. A. (2014). Erosion of functional independence early in the evolution of a microbial mutualism.

Proceedings of the National Academy of Sciences, 111(41), 14822-14827.

Coding versus cis-regulatory evolution, input/output genes

Jasper, W. C., Linksvayer, T. A., Atallah, J., Friedman, D., Chiu, J. C., & Johnson, B. R. (2014). Large scale coding sequence change underlies the evolution of post-developmental novelty in honey bees. *Molecular biology and evolution*, msu292.

Here we conduct ten RNA-Seq experiments across both novel and conserved tissues in the honey bee to determine to what extent post-developmental novelty is based on changes to the coding regions of genes. We make several discoveries. First, we show that with respect to novel physiological functions in the adult animal, positively selected tissue-specific genes of high expression underlie novelty by conferring specialized cellular functions. Such genes are often, but not always taxonomically restricted genes (TRGs). We further show that positively selected genes, whether TRGs or conserved genes, are the least connected genes within gene expression networks. Overall, this work suggests that the evo-devo paradigm is limited, and that the evolution of novelty, post-development, follows additional rules. Specifically, evo-devo stresses that high network connectedness (repeated use of the same gene in many contexts) constrains coding sequence change as it would lead to negative pleiotropic effects. Here we show that in the adult animal, the converse is true: genes with low network connectedness (TRGs and tissue-specific conserved genes) underlie novel phenotypes by rapidly changing coding sequence to perform new specialized functions.

Lorenz, K., & Cohen, B. A. (2014). Causal variation in yeast sporulation tends to reside in a pathway bottleneck. *PLoS genetics*, 10(9), e1004634.

Genetics

Mutations, mosaicism - in cancer and other diseases

McFarland, C., Mirny, L., & Korolev, K. S. (2014). A tug-of-war between driver and passenger mutations in cancer and other adaptive processes. *arXiv preprint arXiv:1402.6354*.

New traits required for cancer progression are acquired by driver mutations in a few key genes. Most mutations, however, are unimportant for progression and can be damaging to cancer cells, termed "passengers." The role these damaging passengers play in cancer and other adaptive processes is unknown. Here we show that driver mutations engage in a tug-of-war with damaging passengers. This tug-of-war explains many phenomena in oncology, suggesting how to develop new therapies and target existing therapies to exploit damaging passengers.

de Bruin, E. C., McGranahan, N., Mitter, R., Salm, M., Wedge, D. C., Yates, L., ... & Swanton, C. (2014). Spatial and temporal diversity in genomic instability processes defines lung cancer evolution. *Science*, 346(6206), 251-256.

Zhang, J., Fujimoto, J., Zhang, J., Wedge, D. C., Song, X., Zhang, J., ... & Futreal, P. A. (2014). Intratumor heterogeneity in localized lung adenocarcinomas delineated by multiregion sequencing. *Science*, 346(6206), 256-259.

Two papers. Different regions of a human lung tumor harbor different mutations, possibly explaining why the disease is so tough to treat.

Hamdan, F. F., Srour, M., Capo-Chichi, J. M., Daoud, H., Nassif, C., Patry, L., ... & Michaud, J. L. (2014). De Novo Mutations in Moderate or Severe Intellectual Disability. *PLoS genetics*, 10(10), e1004772.

We sequenced the exomes of 41 probands and their parents, and confirmed 81 DNMs affecting the coding sequence or consensus splice sites (1.98 DNMs/proband). We observed a significant excess of de novo single nucleotide substitutions and loss-of-function mutations in these cases compared to control subjects, suggesting that at least a subset of these variations are pathogenic.

Genomics

Weirauch, M. T., Yang, A., Albu, M., Cote, A. G., Montenegro-Montero, A., Drewe, P., ... & Hughes, T. R. (2014). Determination and inference of eukaryotic transcription factor sequence specificity. *Cell*, 158(6), 1431-1443.

Gut bacteria, symbiosis and other interactions between species

Goodrich, J. K., Waters, J. L., Poole, A. C., Sutter, J. L., Koren, O., Blekhman, R., ... & Ley, R. E. (2014). [Human Genetics Shape the Gut Microbiome](#). *Cell*, 159(4), 789-799.

Here, we compared microbiotas across >1,000 fecal samples obtained from the TwinsUK population, including 416 twin pairs. We identified many microbial taxa whose abundances were influenced by host genetics. The most heritable taxon, the family Christensenellaceae, formed a co-occurrence network with other heritable Bacteria and with methanogenic Archaea. Furthermore, Christensenellaceae and its partners were enriched in individuals with low body mass index (BMI). An obese-associated microbiome was amended with Christensenella minuta, a cultured member of the Christensenellaceae, and transplanted to germ-free mice. C. minuta amendment reduced weight gain and altered the microbiome of recipient mice. Our findings indicate that host genetics influence the composition of the human gut microbiome and can do so in ways that impact host metabolism.

Vigneron, A., Masson, F., Vallier, A., Balmand, S., Rey, M., Vincent-Monégat, C., ... & Heddi, A. (2014). Insects Recycle Endosymbionts when the Benefit Is Over. *Current Biology*.

By investigating the cereal weevil Sitophilus association with the Sodalis pierantonius endosymbiont [8, 12], we discover that endosymbiont populations intensively multiply in young adults, before being rapidly eliminated within few days. We show that young adults strongly depend on endosymbionts and that endosymbiont proliferation after metamorphosis matches a drastic host physiological need for the tyrosine (Tyr) and phenylalanine (Phe) amino acids to rapidly build their protective exoskeleton. Tyr and Phe are precursors of the dihydroxyphenylalanine (DOPA) molecule that is an essential component for the cuticle synthesis. Once the cuticle is achieved, DOPA reaches high amounts in insects, which triggers endosymbiont elimination. This elimination relies on

apoptosis and autophagy activation, allowing digestion and recycling of the endosymbiont material. Thus, the weevil-endosymbiont association reveals an adaptive interplay between metabolic and cellular functions that minimizes the cost of symbiosis and speeds up the exoskeleton formation during a critical phase when emerging adults are especially vulnerable.

Cinkornpumin, J. K., Wisidagama, D. R., Rapoport, V., Go, J. L., Dieterich, C., Wang, X., ... & Hong, R. L. (2014). A host beetle pheromone regulates development and behavior in the nematode *Pristionchus pacificus*. *eLife*, 3.

Physiology

Drosophila physiology

Katayama, N., Abbott, J. K., Kjærandsen, J., Takahashi, Y., & Svensson, E. I. (2014). Sexual selection on wing interference patterns in *Drosophila melanogaster*. *Proceedings of the National Academy of Sciences*, 111(42), 15144-15148.

Oh, Y., Yoon, S. E., Zhang, Q., Chae, H. S., Daubnerová, I., Shafer, O. T., ... & Kim, Y. J. (2014). A Homeostatic Sleep-Stabilizing Pathway in *Drosophila* Composed of the Sex Peptide Receptor and Its Ligand, the Myoinhibitory Peptide. *PLoS biology*, 12(10), e1001974.

Researchers have observed that mating reduces the daytime sleep of female flies and shown that the seminal fluid protein Sex Peptide (SP), a ligand of the Sex Peptide Receptor (SPR) that is transferred to females during copulation, is responsible for this reduction of siesta sleep. Here, we investigated further the role of SPR in sleep regulation in Drosophila. We show that SPR is required for sleep stabilization in both sexes and that in mutant flies lacking SPR or its ligand myoinhibitory peptide (MIP) sleep is fragmented independently of reproduction. Unlike SP, MIP is expressed in the brain of both sexes and acts on SPR to silence specific neurons that keep flies awake, stabilizing sleep. Hence, our results reveal that SPR interacts with two distinct ligands to control different behaviors: SP for reproduction and MIP for sleep.

Chanut-Delalande, H., Hashimoto, Y., Pelissier-Monier, A., Spokony, R., Dib, A., Kondo, T., ... & Payre, F. (2014). Pri peptides are mediators of ecdysone for the temporal control of development. *Nature cell biology*, 16(11), 1035-1044.

Fagegaltier, D., König, A., Gordon, A., Lai, E. C., Gingeras, T. R., Hannon, G. J., & Shcherbata, H. R. (2014). A genome-wide survey of sexually dimorphic expression of *Drosophila* miRNAs identifies the steroid hormone-induced miRNA let-7 as a regulator of sexual identity. *Genetics*, 198(2), 647-668.

Rice, W. R. (2014). An X-Linked Sex Ratio Distorter in *Drosophila simulans* That Kills or Incapacitates Both Noncarrier Sperm and Sons. *G3: Genes| Genomes| Genetics*, 4(10), 1837-1848.

Annelid physiology

Tosches, M. A., Bucher, D., Vopalensky, P., & Arendt, D. (2014). Melatonin Signaling Controls Circadian Swimming Behavior in Marine Zooplankton. *Cell*, 159(1), 46-57.

They show that melatonin signaling regulates circadian swimming in annelid worms by rhythmically activating cholinergic neurons. This suggests an evolutionary connection between melatonin signaling in invertebrates and sleep regulation in vertebrates.

Sterol biochemistry and thermal resistance

Caspeta, L., Chen, Y., Ghiaci, P., Feizi, A., Buskov, S., Hallström, B. M., ... & Nielsen, J. (2014). Altered sterol composition renders yeast thermotolerant. *Science*, 346(6205), 75-78.

Cell and Developmental Biology

Developmental noise

Kiviet, D. J., Nghe, P., Walker, N., Boulineau, S., Sunderlikova, V., & Tans, S. J. (2014). Stochasticity of metabolism and growth at the single-cell level. *Nature*.

We show that expression fluctuations of catabolically active enzymes can propagate and cause growth fluctuations, with transmission depending on the limitation of the enzyme to growth. Conversely, growth fluctuations propagate back to perturb expression. Accordingly, enzymes were found to transmit noise to other unrelated genes via growth.

Development of Drosophila sensory organs

Y Jiang, W Boll, M Noll - *Developmental Biology*, 2014. Pox neuro control of cell lineages that give rise to larval poly-innervated external sensory organs in *Drosophila*. *In Press*.

Left-right asymmetry

Hüsken, U., Stickney, H. L., Gestri, G., Bianco, I. H., Faro, A., Young, R. M., ... & Carl, M. (2014). Tcf712 Is Required for Left-Right Asymmetric Differentiation of Habenular Neurons. *Current Biology*.

In a forward genetic screen for mutations that result in loss of habenular asymmetry, we identified two mutant alleles of tcf712, a gene that encodes a transcriptional regulator of Wnt signaling. In tcf712 mutants, most neurons on both sides differentiate with dHbl identity. Consequently, the habenulae develop symmetrically, with both sides adopting a pronounced leftward character. Tcf712 acts cell autonomously in nascent equipotential neurons, and on the right side, it promotes dHbm and suppresses dHbl differentiation. On the left, the parapineal prevents this Tcf712-dependent process, thereby promoting dHbl differentiation.

Science and Society

Carroll, S. P., Jørgensen, P. S., Kinnison, M. T., Bergstrom, C. T., Denison, R. F., Gluckman, P., ... & Tabashnik, B. E. (2014). Applying evolutionary biology to address global challenges. *Science*, 346(6207), 1245993.

Krueger, A. B., & Stone, A. A. (2014). Progress in measuring subjective well-being. *Science*, 346(6205), 42-43.