

James F. Crow and the art of teaching and mentoring, pp. 1129–1133

Daniel L. Hartl

Crow is widely admired for his major contributions to the conceptual foundations of modern genetics and his role as an inspirational teacher and mentor. This Perspectives is a memoir of student life in Crow's laboratory, written by a former undergraduate student in his genetics course who became his protégé. The essay recounts Crow's teaching and mentoring style and conveys the excitement of being in a laboratory that included Motoo Kimura, Yuichiro Hiraizumi, Terumi Mukai, Takeo Maruyama, and Rayla Greenberg Temin during a golden age of genetics at the University of Wisconsin.

A general definition of the heritable variation that determines the potential of a population to respond to selection, pp. 1347–1359

Piter Bijma

Response of a population to selection is the product of strength of selection and heritable variation. But that ignores the social organization of life, and models that account for social organization lack a general measure of heritable variation. This article proposes a general definition of the heritable variation that determines the potential of a population to respond to selection. It shows that heritable variance relevant for response is the variance among individuals in the heritable quantity that determines the mean trait value of a population, rather than the classical additive genetic variance.

Dynamics of homology searching during gene conversion in *Saccharomyces cerevisiae* revealed by donor competition, pp. 1225–1233

Eric Coïc, Joshua Martin, Taehyun Ryu, Sue Yen Tay, Jané Kondev, and James E. Haber

How do the ends of DNA caused by a double-strand break (DSB) search the entire genome for homologous templates that can be used to repair the break? Results of competitions between two donors during yeast mating-type switching described in this article imply that there are several encounters between the DNA ends and homologous templates before recombination is consummated.

Trisomic and allelic differences influence phenotypic variability during development of Down syndrome mice, 1487–1495

Samantha L. Deitz and Randall J. Roper

The phenotypes of individuals with Down syndrome (DS) vary significantly. To understand this, the authors of this article examined developmental phenotypes of the Ts1Rhr DS mouse model. Their results suggest that trisomic and nontrisomic genes and their natural variation are important in the manifestation and severity of phenotypes associated with DS.

Next-generation mapping of complex traits with phenotype-based selection and introgression, pp. 1203–1209

Eric J. Earley and Corbin D. Jones

This article shows how new sequencing technology combined with selective phenotypic introgression can be used to

efficiently identify genomic regions underlying a complex trait. This approach, which is applicable to many systems, does not rely on laborious marker development or genotyping.

Environment-sensitive epigenetics and the heritability of complex diseases, pp. 1377–1387

Robert E. Furrow, Freddy B. Christiansen, and Marcus W. Feldman

Genome-wide association studies have so far failed to explain the observed heritability of complex human diseases. This study suggests that epigenetic variation, inherited both directly and through shared environmental influences on epigenetic states, may make a key contribution to phenotypic heritability.

Interactions among flower-size QTLs of *Mimulus guttatus* are abundant but highly variable in nature, pp. 1461–1471

John K. Kelly and Julius P. Mojica

Epistasis—the interaction between genes in determining phenotype—is well documented in molecular studies, but we remain largely ignorant about the extent of epistasis in complex trait variation. This study of the interactions among flower-size QTLs of the yellow monkeyflower reveals that interactions among QTLs are abundant. However, the nature of interactions (whether positive or negative) is highly variable among locus pairs.

The maize high-lysine mutant *opaque7* is defective in an acyl-CoA synthetase-like protein, pp. 1271–1280

Mihai Miclaus, Yongrui Wu, Jian-Hong Xu, Hugo K. Dooner, and Joachim Messing

***Opaque7* encodes an acyl-activating enzyme-like protein that affects storage protein synthesis in maize endosperm, pp. 1281–1295**

Gang Wang, Xiaoling Sun, Guifeng Wang, Fei Wang, Qiang Gao, Xin Sun, Yuanping Tang, Chong Chang, Jinsheng Lai, Lihuang Zhu, Zhengkai Xu, and Rentao Song

The main source of amino acids in food and livestock feed are maize seeds because they are sinks for amino acids produced during photosynthesis. But seed storage zein proteins are low in lysine, an essential amino acid. If zein proteins are reduced, lysine-rich proteins are elevated. This disturbs a proteinaceous matrix that engulfs the starch granules, producing an opaque seed, providing a phenotype to discover genes affecting seed protein balance. Here, unexpectedly, a protein acylation activity is shown to affect this balance.

A general mechanistic model for admixture histories of hybrid populations, pp. 1413–1426

Paul Verdu and Noah A. Rosenberg

Admixed populations have been used for inferring migrations, detecting natural selection, and finding disease genes. These investigators develop a flexible mechanistic model of admixture as a function of simple parameters describing the admixture process. Their approach will be helpful for investigating admixed populations and for developing tools for reconstructing their history.