TOUCHING BASE

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Mutant of the Month

Photo courtesy of Martha James

As the days grow shorter and the nights get chilly, now is the time to savor those last few tastes of summer. And high on the list is local, sweet corn-on-the-cob. It is in this spirit that this month we bring you the *sugary1* (*su1*) mutant of maize. Kernels homozygous for the *su1* allele have a glassy, translucent and shrunken appearance, and they accumulate water-soluble sugars at the expense of complex starches. Pictured is a dried self-pollinated ear from a heterozygous *sugary1* plant; approximately 25% of the kernels have the mutant phenotype. The *sugary1* locus encodes an isoamylase-type debranching enzyme that hydrolyzes α-(1→6) glycosidic bonds and is involved in starch biosynthesis. Martha James and colleagues at Iowa State University identified the nucleotide changes responsible for the classic *sugary1* allele, which was one of the first loci described genetically and was reported in the scientific literature in 1901. They identified two missense mutations in the classic *sugary1* allele. The mutations reduce or eliminate the debranching activity, but how the reduction of this enzymatic activity leads to the *sugary1* chemical phenotype is not yet completely understood. Interestingly, as part of a study on signatures of selection in the maize starch pathway, Edward Buckler and colleagues subsequently reported that one of these *su1* nucleotide changes is present in every variety of North American sweet corn that they surveyed. A different genetic change in *su1* was identified in Central and South American sweet corn varieties, indicating that there are multiple, independent origins of sweet corn in the New World. ***EN***

Mouse knockouts on the march

The global initiative to generate a comprehensive collection of knockouts for every mouse gene is in full swing, with funding bodies from Europe, Canada and the US announcing plans to coordinate efforts to help move this ambitious project forward. The collaborative program, second only to the Human Genome Project in scale, will be guided by a steering committee comprised of scientific leaders from the three research projects (KOMP, EUCOMM and NorCOMM) and representatives from the three major funding bodies (the US National Institutes of Health, the European Commission and Genome Canada). The groups have agreed to make the resources generated from their efforts freely available to the scientific community and are encouraging other funding agencies and scientists engaged in similar projects to join the coordinated effort to generate a comprehensive community resource. A recent set of awards from the NIH, granted to teams based in the US, Canada and the UK, will help create 8,500 new knockout mouse lines, establish a new data coordination center and improve the efficiency of methods for creating knockout lines. The EUCOMM and NorCOMM efforts will focus on generating conditional knockout alleles, which will serve as a powerful complement to the constitutive knockout lines generated through KOMP. *KV*

Touching Base written by Emily Niemitz, Alan Packer and Kyle Vogan.

100th anniversary

"Like other new crafts, we have been compelled to adopt a terminology, which, if somewhat deterrent to the novice, is so necessary a tool to the craftsman that it must be endured. But though these attributes of scientific activity are in evidence, the science itself is still nameless, and we can only describe our pursuit by cumbrous and often misleading periphrasis. To meet this difficulty I suggest for the consideration of this Congress the term *Genetics*, which sufficiently indicates that our labours are devoted to the elucidation of the phenomena of heredity and variation...."

—William Bateson, in his inaugural address at the Third Conference on Hybridisation and Plant-Breeding, London, 1906

Repository for association studies

The trend in data reporting has been toward greater openness. Microarray data, sequence data and polymorphisms are all typically made publicly available upon publication, or in some cases upon generation. Earlier this year, a workshop was held to discuss a data release policy for The Cancer Genome Atlas, which for the first time would make de-identified individual genotype data and associated health data available to qualified researchers. The NIH has just issued a request for information on a similar policy proposed for all NIH-supported genome-wide association studies. Submissions to the repository would be accompanied by local institutional review board approval, and access to the data would be governed by an NIH Data Access Committee, which would ensure that such data are used solely for approved purposes. Interestingly, the proposed publication policy gives those contributing the data the exclusive right to publish analyses of the data sets for a period of nine months; this contrasts with sequence data, for which no such period is explicitly specified. Comments on the proposed policy may be sent to gwas@nih.gov. *AP*