New Insights into Ancient Grain

RICHARD BLAUSTEIN

Genetics reveals fresh understanding of corn’s potential to adapt.

Maize, commonly called corn in the United States and Canada, is perhaps the most enigmatic of the major food staples. Although scientists have been able to narrate the domestication and diffusion of wheat, anthropologists, archaeologists, biologists, geneticists, and linguists continue to grapple with gaps in the history of maize. In fact, it was only in the twenty-first century that geneticists were able to definitively prove the contested notion that teosinte, a wild grass native to Mesoamerica, is the singular ancestor for maize in all its varieties. Still unresolved is the reason indigenous peoples were attracted to wild teosinte thousands of years ago. Many historical questions remain, and while scientists work on these, others in the biological and social sciences focus on the contemporary market-based and cultural concerns related to maize.

Maize is both an ancient crop and modernly ubiquitous. Today, in the United States, some 99 million acres are planted in maize, nearly twice the amount that was planted in 1969. Maize is a staple food for humans, animals, and farm-raised fish; a source for biofuels; and a key ingredient in industrial food processing, with high-fructose corn syrup attracting attention for its link to diabetes and obesity. The widespread use of maize has helped fuel interest in its genetics.

In 2009, the genome of one variety of maize was made public for the first time, and in 2012, two National Science Foundation (NSF)–supported genomic studies shed light on the diversity, domestication, and improvement of maize varieties. These and other ongoing studies underscore the plant’s vast genetic diversity, setting it apart from other agricultural staples.

“Something we have understood for a while is that, at the DNA level, for any two varieties of maize, they are far [more] different from each other than humans are from chimpanzees,” says US Department of Agriculture’s Agricultural Research Service (USDA-ARS) geneticist Edward Buckler, who also teaches at Cornell University and was a leader and coauthor on both of the NSF-supported studies. Geneticist Doreen Ware, also with USDA-ARS and based in Cold Spring Harbor Laboratory in New York, led the NSF study commonly referred to as HapMap2, and she adds, “It is really amazing when you look at two corn specimens that look so much alike that they can be so different at the genome level.”

Buckler underscores that maize genetic diversity, which includes the regions between genes that regulate genetic activity, is perhaps the central conveyance of recent studies. “We know that in the genome, only about half the DNA is in the same place between two varieties of maize. The genome is incredibly diverse,” Buckler says. “So maize is at the high end of
diversity of most plants... It is that diversity which enabled the domestication from teosinte to what we have today.”

In addition to addressing the historical questions of maize, scientists point to this increasingly understood genetic diversity as promising for growing ecologically sustainable and high-yield maize harvests. Others maintain that genetic research for maize yields is necessary but caution that with expected population growth and environmental stresses, such as the drought in the Midwest that diminished the maize harvest in 2012, genetic breakthroughs alone will not be able to meet the expected demand. Still others, most notably in Mexico, are concerned that business and government will not properly steward biotechnology for maize and that this will undercut the conservation of culturally valued varieties that are genetically diverse and a part of local livelihoods and culture. Researchers call for more public dialogue and participation in order for maize to be managed to maximally contribute to twenty-first century sustainability.

The maize genome
The two NSF-supported papers, “Maize HapMap2 identifies extant variation from a genome in flux” and “Comparative population genomics of maize domestication and improvement,” were published in Nature Genetics in 2012. The first study has emerged as a template for other investigations because it provides the most recent HapMap, which Buckler explains, “is a catalog of genetic variation across a series of individuals.” In the second paper, Buckler points out that “we are determining [that] there are some big important genes that are involved in maize domestication.” Buckler explains that these genes are responsive to selection pressures, which led to domesticated maize’s becoming genetically different from teosinte.

HapMap2 builds on many investigations—in particular, the 2009 maize genome study, referred to as B73, which was focused on a single maize variety. Ware points out that “the foundational single genome reference, B73, set up the course for understanding genomic variation, which was surveyed as part of HapMap1 and HapMap2.” She adds that “HapMap2 changed from HapMap1 in the breadth and depth of the data sets... In the second HapMap, we could look at the whole genomes and increase the number of genomes from different varieties from 25 to 103.” The 103 varieties in HapMap2 included varieties of domesticated maize, teosinte, and the related plant species of Tripsacum. HapMap2 also sampled a very high number of the varieties’ single-nucleotide polymorphism samples (55 million SNPs, as they are called), which are important genetic components linked to variation.

University of North Carolina at Wilmington student Carletha Blanding, who analyzed maize genomic data sets in her thesis, holds a flask containing maize kernels. Photograph: Jaime Moncrief.
first genome sequencing. “Making the genome sequence public, something we can all freely access, was key…. We can use that public genome sequence to look at diversity, see where things are different and where they are the same, how that has changed through time and how that has interacted with the human history for maize…. It is a way of sharing information we did not have before.”

About HapMap2, Stapleton says, “a maize HapMap, like the human HapMap, tells us about the range of diversity in the species or the organism. We see that the diversity of maize is astounding; it has genetic mechanisms that increase the difference between different types.” She adds that HapMap is “extremely handy for associating ways that features of the plant… are related to the differences in the DNA…. We can use this HapMap information to increase the resolution and the quality of our analysis—for example, how the offspring adapt to a new environment (my interest) or how a leaf shape is different.”

**New genetics and the elusive questions**

In addition to agriculture, the new maize genomics aids with understanding how and why maize was originally domesticated and its phenomenal diffusion in the Western Hemisphere.

University of British Columbia archaeologist Michael Blake and Texas Wesleyan University ethno­botanist Bruce Benz have worked on maize origin and diffusion questions for decades and, since 2007, have collaborated on the Ancient Maize Map, which links archaic maize finds with dates, locations, and descriptions. Investigating these archaic questions for maize illuminates key transitions in human history, such as from hunter–gatherers to sedentary agriculturists, then to a largely urban society. Blake and Benz believe that the new genomic advances for maize will shed light on how maize was spread and also on the original attraction to maize. “One of the great discoveries coming out of the genomics work published during the past decade is that maize is now pretty much definitively shown to have derived from one or two subspecies of teosinte: *Zea mays*, with subspecies *parviglumis* and subspecies *mexicana*—primarily *parviglumis* but with some introgression from *mexicana,*” Blake states. “The exciting genetic work, and including the published work funded by [the] NSF, reveals the genetic relationships among all modern domesticated maize varieties and between these and their wild teosinte ancestors.”

Benz agrees and calls attention to important work in forensic genetics that is being done at McMaster University, in Canada, and at the Max Planck Institute for Evolutionary Anthropology, in Germany. This research enables maize DNA sequencing to be derived from previously unpromising samples. Benz also highlights the long-standing work of John Doebley, at the University of Wisconsin–Madison, and others who have made crucial contributions to understanding maize origins and diffusion. “In the last 3 or 4 years, they have really been able to disentangle some very difficult-to-answer questions with sophisticated analyses and massive data sets,” Benz says.

Blake and Benz stress that challenging and fundamental questions persist. “Thanks to genetics, we now know where maize comes from,” Blake explains, “but we still don’t have clear and sufficient evidence to show how people were manipulating and growing teosinte in its natural range in the Rio Balsas region of Western Mexico and then moving it from there into new environments far removed from its natural habitat.”

Blake believes that new genetic advances could offer breakthroughs.

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**Two archaic specimens:** (a) fruitcases of maize’s teosinte source, *Zea mays* subspecies *parviglumis,* and (b) an ancient cob found in the San Marcos cave, Tehuacan Valley, Puebla, Mexico. Photographs: Bruce Benz.
University of Illinois geneticist Stephen Moose is in fact working on maize and environmental stresses and looks to new genetic understandings, such as HapMap2, for possibilities. In addition to researching hybrid vigor and its genetic connection, Moose is particularly interested in reducing excessive nitrogen on farms from fertilizer, which has deleterious runoff effects—most famously, the dead zones in the Gulf of Mexico. Nitrogen-based fertilizer is the source of atmosphere-borne nitrous oxide, a very potent greenhouse gas. The fertilizer also requires a huge amount of fuel to produce and alters the natural nitrogen cycle of the Earth.

“We are trying to get at gene function... of important traits, and the one we are particularly interested in is nitrogen-use efficiency,” Moose explains. “There are economic and environmental benefits [of] reducing nitrogen, and we really have not tried to do this in the last century. Most of the effort was to push yield up under high-nitrogen conditions. When we did this, we lost some of the good genes for productivity under low-nitrogen conditions.”

Cassman points out that “the rate of gain in yields of maize has fallen way behind” what it needs to be for the expected population growth. In addition, Cassman emphasizes that we must make do with the total amount of current farmland because “expansion beyond that is going to go into rainforests and wetlands, and we are learning that these ecosystems are the climate regulators of the planet... If we start losing large swaths of rainforest and wetlands, we are in real trouble.”

According to Cassman, genetics will nonetheless play an important role, especially for helping breeders keep up with the pathogens and insects that adapt to and afflict agriculture. “Genetics in support of crop breeding [is] also critical to chip away at improving overall tolerance to abiotic stresses—to drought, other climate stresses, salinity, soil acidity, and so forth... [Although] there are no quantum leaps here, small gains over time are significant... What we can do is some fine-tuning of the genetics of a crop for a given environment.”

Innovation and demands: Local and global

In the United States, the agricultural sector is especially interested in the new possibilities from advanced maize genomics. Ware explains that “we are starting to understand where genes could have consequences and how there are lots of opportunities for leveraging the genes for the future.... A very large portion of that opportunity is where the diversity has not been optimized. If you can unlock that, we will have a much larger set of diversity than we have had before to potentially improve maize.”

University of Nebraska agronomist Kenneth Cassman is skeptical that maize genomics can meet the high hopes, given the environmental and growing population stresses expected this century. “Of all the major food crops, the increase in the demand for maize is going to be faster than the increased demand for other cereals because of the increased demand for livestock,” Cassman says. “The US role in the global food supply is going to increase... in large part because of its ability to be the low-cost, high-yield maize and soybean producer, with the smallest negative environmental footprint from production of those crops. Having said that, there are real challenges.”

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conditions… The HapMap and other resources help us identify those lost alleles, lost genes, and [to] bring them back in.”

Importantly, this maize improvement approach is not transgenesis, in which genetic material is inserted from other species into the targeted agricultural plant. Moose’s nitrogen investigation instead looks to the diversity of the maize genome. “The question,” Moose says, “is how do we make the parts work together now that we have the foundation of genomic structure and variation of maize. There is a lot of natural variation that can be optimized. For a lot of the sustainability traits like drought and nitrogen tolerance and pest resistance, nature does give us what we need; we just have to find it.”

Mexico: Place of origins, diversity, and concerns
In Mexico, where an advocacy movement arose to protest transgenic maize, small farmers and many other Mexicans urge conservation and protection of maize landraces, the regional varieties that have come about over long periods of time as a result of both natural and cultural influences. The North American Free Trade Agreement (NAFTA) mandated changes in the Mexican agricultural sector that serve to promote both high-tech farming of maize and maize imports from the United States, which is also of concern. Despite NAFTA, Mexico, which has the most varieties of maize and teosinte, still produces maize on a large scale. Maize remains a staple of the Mexican diet, and 2.5 million farmers raise maize on less than 5 hectares. Moreover, Mexican heritage is associated with maize origins and archaic uses and remnants, and maize depictions are found in Amerindian archaeology. Now, in addition to their concerns about transgenic maize and NAFTA, Mexican researchers and farmers are worried about how climate change will affect landraces.

Agroecologist Hugo Perales, of El Colegio de la Frontera Sur, in the state of Chiapas, works on maize for all of Mexico and focuses on Chiapas farming. In Chiapas, three landraces make up 90 percent of the maize farmed: the Oloton–highland variant, the Comiteco–midelevation, and the Tuxpeno–lowlands landraces. These landraces, which also have varieties within their respective groups, have adapted over time to their local environments with distinct phenotypes. Perales points out that the higher you go, the more the landraces predominate on the farms.

Landraces are part of culture and lifestyle for Chiapans, and farm families often work at other jobs while maintaining small farms. According to Perales, Chiapans, like other Mexicans, grow maize because “it is more about something they feel they
Perales is proactively investigating Chiapas varieties and their responses to climate change pressures. The local landraces are adapted to very restricted regions and climate change could cause disequilibrium in Chiapas farming systems. In what they are calling reciprocal gardens, Perales and his university colleagues and students are planting different landrace varieties at different altitudes, checking for adaptation resiliency. “When we cross highland maize with [midelevation] or with lowland varieties, the cross is better than original varieties when [they are] planted in foreign environments,” comments Perales. “Maybe we could find avenues for climate change adaptation, utilizing our own materials. I am a little unsure [whether] genomics would take a prominent place here, but maybe genomics could indicate genes associated with this phenomenon and then we could use it in a scientific environment.” Where genomics might help, Perales notes, is in better understanding of landraces. “We would like to know more about variation in landraces.... We would like to advance our understanding of how the genomic side is linked to the phenotypical side under [the] farmer and natural selection.”

Perales maintains that transgenic maize is certainly not the answer for the challenges posed by climate change. In addition to transgenics’ being designed for less-varied ecologies and can undercut the way farmers preserve and exchange seeds and also safeguard diversity. “Losing traditional seeds could be extremely damaging to poor farmers,” he says, “and these [seeds] could be difficult to replace if [they are] generalized to communities and regions. These seeds are the product of an uninterrupted evolutionary process and [are], for us, something very valuable.”

Perales’s work with landraces is important, Bruce Benz points out, because “without the landraces, we are not going to be able to look for genetic resources [for]... the challenges that agriculture is going to go through, especially how maize is going to cope with changing climate. Hugo, a brilliant ecologist, is asking the right questions about the maize genome’s adaptability to changing environments.”

Maize and the future

Although challenges remain, scientists agree that new genomics will offer promising avenues for understanding maize. How to communicate with the public or inform policymakers is, however, another challenge. “There is a tremendous amount of things we can do with genomics and diversity, and I believe the public really needs to start asking what kind of agriculture we want and what the trade-offs [are that] we are interested in,” Buckler reflects. “Once we make this decision, we need to fund the research to meet this societal goal. For example, I have been interested in looking at [whether we] could have a perennial variety of maize rather than an annual variety. We know [that] we have natural variation out there to do that.... We need more communication between society and the scientific community to set common goals.”

For Stapleton, too, communication is key. “Maize is really important in our economy and diet. Because of its importance, it is often controversial. We care a lot about maize in its countries of origin, places where it has a long cultural history, and we care a lot about it here, “ she says. “My students and I want to understand the genetic mechanisms of maize’s stress responses and to share our knowledge so that what we learn is used for everyone’s benefit. I would like to see us all—both the public and the scientific community—spend our time on important questions whose answers matter [for] a sustainable Earth system.”

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