Footprints of Hopi History

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ONE ASPECT OF LIFE most important to Hopi people is their relationship to corn (maize) and corn farming (Wall and Masayesva 2004). According to traditional knowledge, this relationship is tied to the origin of Hopi people. When the Hopi emerged into the Fourth World, they approached Màasaw, their guardian spirit, for guidance. Màasaw presented them with a planting stick, a bag of seeds, a gourd of water, and a small ear of blue corn and thereby gave the Hopi the option to pursue this new way of life as farmers. The Hopi accepted this challenge and since then corn has been woven into almost every aspect of Hopi traditional life. In addition to providing sustenance, corn is woven into Hopi life metaphorically (Washburn 2012). It is also an important part of Hopi ceremonial life in which, among other ritual uses, it is integral to rites that mark childbirth and the naming of babies, initiations that signal the transition from childhood to adult life, and the transition that marks the end of life.

Màasaw set the Hopi on a path of life that is not easy: direct precipitation farming in the arid lands of the present day southwestern United States. Perhaps even more important than the agricultural and ceremonial practices, the corn-farming life offered by Màasaw taught Hopi people the values that they refer to as hopivotkwani, which loosely translates as “the Hopi way” or “the Hopi path.” These values include those that the Hopi hold most dear: hard work, compassion, cooperation, reciprocity, a desire to live in balance and be stewards of the world that sustains all life, and perhaps foremost humility.

Given the importance of corn and corn farming to the Hopi, it is not surprising that the Hopi Cultural Preservation Office (HCPO) encouraged the Crow Canyon Archaeological Center to expand its Goodman Point Archaeological Project.
(GPAP) research to include more studies of Ancestral Pueblo agriculture. Crow Canyon archaeologists, along with members of the National Park Service, presented the GPAP research design to the HCPO staff at their offices in Kiqotsmovi, Arizona, in September 2004. At the end of a thorough discussion of the research design, Crow Canyon archaeologists asked if there were research questions not included in the research design that would be of interest to the Hopi. The staff quickly answered that they would like to see additional studies of Ancestral Pueblo agriculture and that they were especially interested in learning whether agricultural practices maintained at Hopi today would work in the Mesa Verde region of southwestern Colorado, which they view as part of their ancestral homeland.

To move forward on the Hopi request, Crow Canyon sought and obtained funding for a meeting to discuss how to best pursue studies of Ancestral Pueblo agricultural practices in the Mesa Verde region (figure 10.1). Held in 2005 at Crow Canyon, this two-day planning meeting was attended by traditional Pueblo farmers from Hopi, Jemez, Ohkay Owingeh, and Tesuque; by anthropologists who study Ancestral Pueblo agriculture and modern Pueblo agriculture; and by Crow Canyon staff. Hopi

![FIGURE 10.1 Map of the central Mesa Verde region and the Crow Canyon Archaeological Center (courtesy Crow Canyon Archaeological Center).](image)
attendees included members of the HCPO staff and the Hopi Cultural Resources Advisory Task Team (CRA TT), a group of cultural advisors who represent the diverse villages that comprise the Hopi nation today (figure 10.2).

At the conclusion of our meeting, the group decided to implement an experimental farming program. The group felt it best to focus on direct-precipitation farming, or what is commonly known as dry farming, because it is likely that this was the main type of farming practiced by Ancestral Pueblo farmers in the Mesa Verde region. The group agreed that the Hopi would take the lead as the traditional farming experts, since they still practice direct-precipitation farming. The experimental farming program established at this meeting has come to be known as the Pueblo Farming Project (PFP; Bocinsky and Varien 2017b; Varien et al. 2011). The PFP is one of a growing list of experimental studies that examine Indigenous corn in the Southwest and adjacent regions (Adams 2015; Adams et al. 1999, 2006; Bellorado 2010; Bellorado and Anderson 2013; Dominguez and Kolm 2005).

The PFP required funding. In addition to financial support from Crow Canyon, the project has received funding from The Christensen Fund, the History Colorado State Historical Fund, the National Geographic Society Genographic Legacy Fund,

**FIGURE 10.2** Attendees of the initial meeting that created the Pueblo Farming Project (courtesy Crow Canyon Archaeological Center).
and the National Science Foundation, for which the PFP was one part of a larger research and education initiative known as the Village Ecodynamics Project (VEP). The PFP began in 2007, when Hopi farmers came to Crow Canyon to select the location for agricultural plots. Our plan was to integrate these gardens into Crow Canyon’s education programs; therefore, they needed to be located on the campus of the Crow Canyon Archaeological Center. Hopi farmers used their traditional ecological knowledge to select the locations for agricultural plots, including identifying native plants that indicate good areas for farming and assessing soils, especially in terms of their texture and moisture-holding capacity.

Beginning in 2008, Hopi farmers traveled to Crow Canyon’s campus twice a year: once in the spring for a planting meeting and again in the fall for a harvest meeting (figure 10.3). Each meeting includes discussion of the project goals, evaluation of the project’s progress, and development of a plan for proceeding with current and future initiatives. Of course, each meeting also includes work in the agricultural plots.

From the beginning, the PFP was designed to create both research and education products. All PFP activities have been documented using numerous techniques—audio and video recording, still photography, written records, and detailed metrics on the plants and their growing environments—producing rich data sets from which several research and educational products have been produced (Bocinsky and Varien 2017a). For example, one of the PFP research goals was to evaluate the effect of annual variation in temperature and precipitation on agricultural yields and to use this knowledge to evaluate the estimates of agricultural yields produced by the VEP computer model (Bocinsky and Varien 2017; Kohler and Varien 2012; Varien et al. 2011). There were also numerous educational goals. Hopi and Crow Canyon educators have worked together to produce lesson plans for fourth and eighth grade students on Hopi lifeways, the importance of corn to Hopi culture and identity, and the ecology and sustainability of Pueblo farming practices. Audio and video recordings have been edited into short film clips highlighting traditional corn roasting and the production of *piiki* bread, as well as a full-length film documenting the PFP from inception to DNA analysis. Finally, a website will document the relationship between the experimental garden yields, weather and soil characteristics, will make our ongoing analyses available to the public, and will provide an exploratory data analysis tool to students and researchers (Bocinsky and Varien 2017b).

**Hopi Corn DNA Project History**

Informal and formal discussions leading to the genetics components of the PFP took place at both Crow Canyon and Hopi beginning in 2005. Two initial concerns raised
Leigh Kuwanwiswma discussing traditional planting methods during the Pueblo Farming Project (courtesy Crow Canyon Archaeological Center).
by the Hopi farmers were maintaining the purity of the traditional corn varieties and protecting their intellectual property rights. At our meeting that preceded the first planting of the Crow Canyon gardens (May 27, 2008), the archaeologists suggested mixing several varieties of corn in the same garden and holding growing conditions constant to determine if yields varied by variety. The Hopi farmers objected to this strategy, explaining that they separate varieties to maintain their distinctive qualities. They countered with a proposal that only one variety of corn should be planted in each garden—but that the single variety of corn could be planted with cultigens, including beans, squash, and melons, and with wild plants like sunflowers and bee-weed, as long as those plants were located far enough from the corn that the plants didn’t compete with each other for soil moisture.

While the two alternatives were being considered, the Hopi farmers shared information about their stewardship of the corn—thousands of years of plant husbandry that has produced corn varieties that are morphologically distinct and adapted to very specific (and harsh) conditions. They talked of the many sources of contamination and their concerns that cross-pollination would dilute characteristics of the specific varieties to the point at which they would lose their ability to survive the varied conditions at Hopi. They also noted that modern hybrid corn did not produce viable seed and worried that this characteristic might be transferred to cross-pollinated corn.

Additionally, early discussions highlighted the mutual interest in origins that both the Hopi and Crow Canyon Center shared—origins of corn, technology, ritual, and people. In particular, we shared interests in people and corn: When did Ancestral Pueblo people first come to the northern Southwest? What spurred them to come to the northern Southwest? Who, if anyone, was here when they arrived? What happened socially and culturally once they arrived? We all had stories that proposed answers to these questions, but the stories differed and they focused on different agents of causality.

Our years of discussion, during which we bounced archaeological and Indigenous perspectives off of one another, resulted in a shared belief that a project that analyzed the DNA of Hopi corn varieties would provide information useful to both the Hopi Tribe and the Crow Canyon Archaeological Center. We decided to pursue the study in the hope that the DNA analysis might help prevent future contamination of Hopi corn strains, protect Hopi intellectual property rights, help answer questions about early Hopi migrations, and provide evidence for determinations of cultural affiliation between modern Hopi and the Ancestral Pueblo people pursuant to the Native American Graves Protection and Repatriation Act (NAGPRA). The HCPO believed that there was an urgent need to create a DNA baseline of Hopi corn varieties before they became further contaminated with non-Hopi corn and that this same baseline could contribute to answers to the other questions. Thus, the current collaboration was born.
ADDRESSING HOPI CONCERNS

All of our collaborative team, especially the Hopi members, had concerns regarding the DNA analysis of Hopi corn. Frank discussion of these concerns was an important part of designing and implementing this project. Most importantly, the genetic material in Hopi corn has developed as a result of the agricultural practices of Hopi farmers over a period of millennia. Therefore, the Hopi view the information encoded in the DNA of this corn as the intellectual property of all Hopi people—past, present, and future. We realized that analyzing the DNA of Hopi corn implies responsibility for safeguarding this intellectual property and doing right by the ancestors, the Hopi community today, and future generations of Hopi people.

Addressing these concerns remained difficult for our group because none of us—the HCPO staff, the CRATT members, nor the Crow Canyon staff—were experts in the DNA analysis of corn or the laws that govern intellectual property. With regard to the analysis itself, we did not and still do not possess an expert’s understanding of the nature of the data produced by these analyses or how those data might be used by others. In addition, there were no lawyers at the table so that we could not obtain expert opinions about the laws that govern the creation and use of the kinds of information that would result from these analyses and whether they could or could not be protected as intellectual property. We moved forward by informing ourselves about these issues as best we could and we used the information we gathered as we designed the project.

We came to believe that a way to address our concerns was to develop a close working relationship with the scientists who would conduct the analysis. To accomplish this goal we contacted Darrell Maddox, who lived in nearby Durango, Colorado, and had developed an interest in Crow Canyon’s mission. Darrell had just retired as president of Eurofins STA Laboratories, Inc. (ESTA), an independent laboratory founded in 1987 and located in Longmont, Colorado, that conducts DNA analysis of seeds and plants. He had since formed his own company, Endless Sky Partners, LLC (ELSP), to continue as a consultant in this field. Darrell participated in our corn DNA project in many ways: he came to a meeting at Crow Canyon and explained the basics of the DNA analysis to the HCPO staff, CRATT members, and Crow Canyon staff (and he helped us harvest the 2009 corn crop!). He also established a connection with his former company, ESTA, so that we would have a direct and personal relationship with the company that would conduct the DNA analysis. Darrell directly communicated our concerns about this project to the ESTA scientists and helped to develop the protocols that addressed these concerns.

In the end, we addressed our concerns by developing a written agreement that was signed by ELSP and ESTA and submitted to the Hopi Tribe via the HCPO.
This document was modeled after formal agreements developed by the Hopi Tribe and Crow Canyon when the PFP began. It specified Hopi concerns and defined the working relationship between Hopi and Crow Canyon. The corn DNA agreement that served as the foundation for this analysis acknowledged that ELSP and ESTA recognized the Hopi Tribe’s need to protect its corn seed legally and specified that ELSP and ESTA did not have the authority to do any analysis beyond the extraction of DNA. Further, the agreement specified that ELSP and ESTA recognized that the samples, data, and results that were the subject of these analyses were the sole and exclusive property of the Hopi Tribe. Finally, the agreement specified that the genetic material would be properly disposed of or returned to the Hopi at their request and that the results of the analysis would not be revealed to any third party.

**GENETIC STUDIES OF MAIZE**

The complete genome sequence of *Zea mays* (cv. B73) was first published in 2009 by the Maize Genome Sequencing Project (Schnable et al. 2009) funded by the National Science Foundation. Among the world’s major cereals, which include rice (*Oryza sativa*), sorghum (*Sorghum bicolor*), wheat (*Triticum* spp.), and barley (*Hordeum vulgare*), maize has the most thoroughly researched genetic system (Strable and Scanlon 2009) thanks to research that can be traced back to Mendel’s 1869 experiments in which he used maize to corroborate his renowned experiments on peas (Coe 2001; Rhoades 1984).

Many characteristics of the plant make it a model species for genetic research that explores a wide range of topics including genome evolution, developmental physiology, epigenetics, pest resistance, heterosis, quantitative inheritance, and comparative genomics (Strable and Scanlon 2009). It is also useful for studies of plant domestication; genetic research has played a pivotal role in understanding the evolution of maize from its wild progenitor, teosinte, and determining that, of the four species of teosinte, *Zea mays* ssp. *parviglumis* is the direct ancestor of maize (Doebley 2004). Genetic research helped to pin down the location of the domestication process to the Rio Balsas region of present-day Mexico (Matsuoka et al. 2002; Piperno and Flannery 2001; Ranere et al. 2009).

Genetic studies of maize have documented its extraordinary level of genotypic diversity. Remarkably, the nucleotide polymorphism observed in the genomes of any two modern maize inbred lines is equivalent to the sequence diversity between chimpanzees and humans (Buckler et al. 2006). Maize has about two billion bases of DNA, and mapping the maize genome has shown that some 32,000 genes are crammed onto just 10 chromosomes. Compare this to the human genome, which has about 20,000
genes dispersed among 23 chromosomes (Washington University School of Medicine 2009). At 2.3 Gbp, maize is a relatively large plant genome, although it is much smaller than that of plants such as wheat, and its genome is relatively repetitive, with 85 percent of the genome consisting of transposons and repetitive elements (Schnable et al. 2009).

METHODS

The field of maize genetic analysis provides the analytical tools used to analyze the nine Hopi corn varieties examined in this study. The seed from the nine varieties of Hopi corn were submitted to ESTA for analysis by the HCPPO. The nine varieties were blue (sakwapu), white (qötsaqa’ö), red (pala’qa’ö), magenta (wique’tö), yellow (takuri), purple (kokoma), blue-gray (masiqa’ö), speckled (pintoqaö), and sweet (tawak’tsi). The first four were analyzed during a pilot study, and the remaining five were analyzed after this pilot study yielded positive results.

The genetics of these Hopi varieties were compared to those of two modern corn inbreds known to geneticists as B/seven and Mo/one. Variety B/seven is the one analyzed to obtain the complete corn genome (Schnable et al. 2009). The genetic signatures of these modern varieties were compared to those of the Hopi varieties to interpret the results of this analysis.

Between thirty and sixty seeds of each variety were packaged and submitted for analysis. The seeds from each corn variety were planted and allowed to grow at the ESTA laboratory. The leaf material was the source of DNA analysis. Twenty plants of each variety were used for the analysis: plants 1 through 10 were combined for one sample, and plants 11 through 20 were combined for a second sample. Therefore, there were two analyses of each of the nine varieties of Hopi corn submitted for analysis. The analysis was replicated twice for each variety to verify the analytical procedures; drastic differences between replicated samples would indicate a possible mistake in samples processing and analysis. For this study, there was another reason to replicate the analysis of each variety: evaluating twenty seeds in two replications allowed the ESTA scientists to document as many alleles as possible in a given variety. There were slight allelic differences between the replicated samples for each of the nine varieties. However, the differences between replicated samples were so minor that the replication can be seen to demonstrate that there was no error when samples were analyzed and that the two replicated analyses can be interpreted as a single variety that is unique in its own way based on the genetic data.

To evaluate the similarity and difference among the nine varieties and to compare these varieties to the modern controls, ESTA analysts identified eighty microsatellite pairs, also known as simple sequence repeats (SSRs). These SSRs are short sequences
of base pairs of DNA repeated many times. The number of the repeating nucleotide sequences varies between members of a species, making SSRs extremely useful in genetic analyses. Although SSRs are good for overall diversity studies, they do not provide enough genomic coverage to map specific traits in outbred landraces (local cultivars improved by traditional agricultural methods) (Barrett and Cardon 2006).

Each of the eighteen samples (two samples for each of the nine varieties of Hopi corn) were screened for these eighty SSRs. Seventy-three of the eighty SSRs were informative for the four samples submitted for the pilot study, and seventy-seven were informative for the five samples submitted for the expanded study. The SSRs that were not informative—seven in the pilot study and three in the subsequent analysis—were monomorphic, meaning that these SSRs expressed the same allele/fragment size across all entries. These uninformative SSRs were excluded from the subsequent analyses. More important, in both analyses, allelic differences were detected for almost all SSRs among all entries. These particular SSRs provide excellent coverage of the entire corn genome.

Genotypic data were generated following established protocols using an ABI3730XL capillary sequencer. Included in the documentation provided by ETSA is the list of SSRs along with their respective linkage order by chromosome. Reported values in respective entry marker cells represent DNA fragment sizes in base pairs. When a single value is present, the respective entry is homozygous for the given locus. If separated by a slash (/) the entry is heterozygous. Different fragment sizes or the length polymorphisms among entries for a given marker indicate that those entries are genetically different. Included in the raw data provided by ESTA were diagrams with colored blocks that indicate SSR results for each entry. When two entries have the same color for a given marker, they represent the same alleles.

The values were analyzed using Nei and Li’s (1979) dissimilarity genetic distance algorithm, which is a well-accepted method for comparing genetic relationships based on DNA markers. Data were organized into a full-rank matrix where the values in the respective cells represent percent genetic dissimilarity rounded to whole numbers.

**RESULTS**

The primary goals of this project were to genotype nine varieties of Hopi corn and to determine the genetic relationships among each Hopi variety and the relationship of the Hopi corn to two modern inbred lines (control samples) that commonly serve as baseline standards in corn genotyping. Figure 10.4 presents the results of the DNA analysis as a tree diagram. The numbers at the bottom of the diagram represent percent genetic dissimilarity between entries. Entries that are the most similar are arranged closer together. Not included in this chapter is another figure created as basic
documentation for this project. It is a diagram that shows the SSR results for each entry as colored blocks. Entries that have the same color for a given marker represent the same alleles, while entries that have different colors for the same marker represent alleles that produced the dissimilarity between entries.

Two general results are noteworthy. First, the greatest dissimilarity is between the Hopi corn as a group and the modern control samples. On average, the Hopi samples were 65 percent different when compared to the controls, indicating that Hopi corn probably has a distinct genetic background, although comparison to other modern varieties is needed. This is not surprising because B73 and Mo17 are early inbreds developed by Pioneer Hybrid. Both are dent corn that was developed by crossing a Southern Dent, related to maize from southern Mexico, with a Northern Flint, derived from the maize of the Southwest U.S. (Doebley et al. 1986, 1988).

The second important general result is that there is considerable heterogeneity among the Hopi varieties. This heterogeneity can be measured by quantifying the

![Tree diagram based on Nei and Li's (1979) dissimilarity-genetic-distance algorithm, illustrating the results of the DNA analysis of Hopi corn (courtesy Crow Canyon Archaeological Center).](image)

**FIGURE 10.4** Tree diagram based on Nei and Li’s (1979) dissimilarity-genetic-distance algorithm, illustrating the results of the DNA analysis of Hopi corn (courtesy Crow Canyon Archaeological Center).
percentage of heterozygous loci for each entry when compared to all other entries. Among the eighteen entries for the nine varieties, heterozygous loci ranged from a low of 0 percent for Magenta-1 to a high of 68.8 percent for Speckled-1. To put this considerable heterogeneity into perspective, the heterozygous loci for the two modern controls were 2.5 percent for B73 and 3.75 percent for Mo17. One might think that the color differences among the Hopi corn varieties are just morphological, but this analysis dispels that notion. Instead, it shows that the different Hopi corn varieties, visually distinguished by color variations that are sometimes obvious and sometimes quite subtle, are in fact genetically distinct. This result supports the Hopi view and the view of other Pueblo groups that varieties of Hopi (and Pueblo) corn, distinguished by color, have distinct characteristics that were important to the survival of Pueblo people (Ford 1980). Each Hopi variety can be characterized as heterozygous when compared to the other varieties but homogenous in terms of the phenotypic similarity within each variety. This contrasts with the modern inbred lines that companies have developed to produce commercial hybrids; heterozygous loci on these inbred lines are so few (two of eighty for Mo17) that these hybrids could almost be characterized as homozygous.

Figure 10.4 shows that the Hopi varieties form two general groups. In one, blue and white corn are the most similar. The next variety to join this group is red. In the other group, speckled and yellow are the most similar. The next variety to join this group is purple, followed by blue-gray and then by Hopi sweet. The two groups come together at that point, and then magenta (colloquially known in Hopi as “greasy head”), which is the genetically most dissimilar, joins the remaining eight varieties. Blue and white are the two varieties that are most similar: 30 percent of their genetic makeup is dissimilar. Speckled and magenta are the most different: 50 percent of their genetic makeup is dissimilar.

Scientists at ESTA concluded that the Hopi corn varieties are maintained by open-pollination and that they are grown in areas that are physically isolated from one another. This conforms to Hopi agricultural practices. The DNA analysis of Hopi corn demonstrated the uniqueness of the nine Hopi varieties. Clearly, thousands of years of Hopi plant husbandry have created and preserved morphologically and genetically distinct corn varieties that are uniquely suited to the highly variable environmental conditions of the northern Southwest.

**DISCUSSION**

The DNA analysis demonstrated that all nine varieties sampled in this study were genetically distinct and concluded that this was a result of Hopi farmers planting only
one variety of corn in a field so that the distinctive characteristics of each variety were not mixed by cross-pollination. As Hopi and Crow Canyon team members discussed the analysis they realized that this result created a new question for consideration: if Hopi agricultural practices are designed to perpetuate the distinctiveness of each variety, how did new varieties come into existence?

We have discussed three hypotheses that address this question. The first is that new varieties developed in different locations and were then brought to Hopi through clan migrations. The second was that new varieties were created at Hopi through Hopi cultural and agricultural practices. The third was that new varieties came to Hopi through exchange with other Pueblo groups.

In discussing clan migrations, we realized that archaeologists and Hopi both have stories about how the origins of corn farming were related to migrations. These stories overlap in some respects but also diverge in important ways. Very simply stated, the archaeological story focuses on the Archaic, Basketmaker II, and Basketmaker III periods. Archaeologists have traced people and corn as they moved north out of Mexico into southern Arizona (figure 10.5) and eventually onto the Colorado Plateau. Once on the Colorado Plateau (figure 10.6), the corn-bearing immigrants, who have become known to archaeologists as Western Basketmaker II people, encountered Indigenous populations that by most archaeological reckonings were hunter-gatherers who did not have corn but adopted corn farming after it was introduced. This second group likely included at least two groups: hunter-gatherers who lived in the Western Basketmaker II area in northeastern Arizona and southeastern Utah and a different group of hunter-gatherers who lived in northeastern New Mexico and southwestern Colorado. The New Mexico-Colorado hunter-gatherers who adopted corn farming after it was introduced have become known to archaeologists as the Eastern Basketmaker II people. Western and Eastern Basketmaker II people eventually coalesced into a more homogenous group during the period archaeologists call Basketmaker III (figure 10.7), and in many ways this marks the beginning of a Pueblo tradition that spans the entire Ancestral Pueblo world, a tradition that integrates Pueblo people who have different histories and languages, one that has continued to the present.

The Hopi story starts with Hopi clans and their emergence into this, the Fourth World. It features the Motisinom—the “first people,” who originated in the north—people who inhabited what is North America today. A distinct group, the Nutungqsisinom, arrived later, migrating from the south and moving into the vast area occupied by the Motisinom. Clans from both of these groups eventually made their way to the Hopi Mesas, the center place known as Tuuwanasavi (figure 10.8), where they combined to form a single group that today are called Hopisinom (Bernardini 2011; Judge et al. 1991; Kuwanwisiwma 2004). At first glance, the Hopi and archaeological stories
converge, with one population indigenous to the Colorado Plateau (and perhaps the Great Basin) and the second population of later immigrants from points south.

Unlike the archaeological story, however, the Hopi story says that both the Motisinom and the Nutungqwsinom had corn. The Motisinom had blue corn that was well adapted to the cold arid conditions of the Colorado Plateau, while southern immigrants brought with them red corn that originated in the warmer and wetter climes to the south.

These two versions of Hopi migration were shared during many discussions over several years. As we accumulated a larger picture, we came to wonder whether the stories were variations on the same theme. In particular, Leigh Kuwanwiswma noted
that the blue and red corn varieties associated with the Motisinom and the Nutungqwsinom corresponded to the colors associated with the different directions recognized by the Hopi, blue with the northwest and red with the southeast. He suggested that the corn could be used as a surrogate for the people themselves: blue corn for the Motisinom and red corn for the Nutungqwsinom. We reasoned that, if this were true, we could use the corn genetics and the distributions of blue and red corn over time to reconstruct the migrations of the Motisinom and the Nutungqwsinom. Further,
this has led us to wonder to what degree clan migrations were a means by which other varieties of corn were first introduced to the Hopisinom. We hope to examine this question in our future collaborative research.

In our collective discussions we also speculated on whether other Hopi cultural practices—cultural dynamics that were internal to Hopi society—could have resulted in the development of new varieties of corn. As an example, the HCPO staff and CRATT members shared how at certain times Hopi katsinam distribute bags of seeds

FIGURE 10.8 The migrations of the Nutungqwsinom (people from the south [directional color red, bearers of red corn]) and Motisinom (people from the north [directional color blue, bearers of blue corn]) (Bernardini 2011:figure 10.1; courtesy Crow Canyon Archaeological Center).
to Hopi people; these bags include seeds from many different varieties of corn and from other cultigens. These seeds are planted in a single hole. Of course, this is the opposite of typical Hopi corn farming practices because different varieties of corn grow together in a single clump. The different varieties of corn cross-pollinate and produce multicolored ears of corn known to Hopi people as Kachina corn. It is possible that Hopi farmers in the distant past selected the new and unusually colored seed from these ears of Kachina corn and propagated them, eventually producing new and distinct varieties of corn.

Finally, the Hopi and the other Pueblo groups in the Southwest have detailed accounts of interacting over a period that probably spans millennia. It is entirely possible, even likely, that this interaction included the exchange of different varieties of corn. Distinct varieties of corn may have arrived at Hopi through exchanges in the distant past and may have been planted again and again in Hopi fields. Gradually, this corn would have become increasingly adapted to the local conditions of the Hopi area until it became thought of today as distinct varieties of Hopi corn. One possibility for future studies would be to compare the genetics of Hopi varieties in use today with the varieties in use at other Pueblos.

CONCLUSIONS

The staff at Crow Canyon conducts research and education programs about the lives of Ancestral Pueblo people and seeks to connect the distant past to the lives of Pueblo people living today. We know from a variety of studies that Ancestral Pueblo people derived the majority of their calories from corn, and we know that this crop was the centerpiece of their agricultural efforts (Coltrain et al. 2006; Matson 1991, 2016; Matson and Chisholm 1991). Although we were well aware of the importance of corn and corn farming to Ancestral Pueblo subsistence, the Crow Canyon staff had almost no practical knowledge of how farming was conducted in the past.

Thanks to the Pueblo Farming Project and the knowledge shared by the Hopi farmers, we now have a much better practical understanding of how direct-precipitation corn farming was accomplished. Perhaps more importantly, we learned that corn farming is much more than an activity that provides food and that instead corn and corn farming are central to how Hopi and other Pueblo people think of themselves as people and how they view their place in the world. We have also learned how collaborative research like the Pueblo Farming Project can lead to new research like the corn DNA project.

The Hopi perspective on the corn DNA project goes back to the mission of the HCPO, which has a constitutional and legal mandate to protect Hopi culture for
the future. The HCPO initiated the corn DNA project because, after careful deliberation, Hopi staff decided that analyzing the DNA of Hopi corn was vital to that cultural preservation effort. The Hopi also have a perspective on this project as collaborative research: they view the corn DNA study as an educational project in which Hopi and Crow Canyon learn from each other.

Although the Hopi viewed this project as a pioneering and innovative study, they entered into it not merely for the sake of using science to create new knowledge. Instead, they wanted to create knowledge that was consistent with their mandate of protecting Hopi culture for the future. The use of modern science to document the genetic distinctiveness of Hopi corn is seen as a progressive endeavor that is not entirely free from risk, but in the words of one CRATT member, “The DNA is information that the corn has to give to us, and we have to trust the corn. Corn has always taken care of us, and it will help us save our culture into the future.” In the end, the DNA analyses were scientific methods that were seen as justified because they could help the Hopi to achieve their larger goals. The baseline genetic data gathered by this project are seen as information gathered in order to benefit future generations of Hopi people.

This study also lays the groundwork for future collaborative research. First, we hope to expand the DNA analysis of modern Hopi corn to include all extant Hopi varieties and to sample varieties being used by different farmers whose fields are located throughout Hopi lands. Second, we hope to compare the DNA of Hopi corn with that of other Pueblo varieties and with that of corn grown by other Indigenous groups in the Southwest and adjacent areas. Third, we hope to conduct DNA analyses of ancient Pueblo corn recovered from Ancestral Pueblo archaeological sites and to compare this DNA to the DNA from modern Hopi corn. These future studies will require ongoing collaboration among Crow Canyon, the HCPO, other Indigenous groups, the institutions where samples are curated, and the scientists who conduct the DNA analysis. We look forward to working together to achieve our shared goals.

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