EARLYTROP: A PROGRAM TO ADAPT 100% TROPICAL MAIZE GERMPLASM TO SHORT-SEASON ENVIRONMENTS

Marcelo Javier Carena*

AgResearch Ltd. Science Team Leader, Grasslands Research Centre, Palmerston North 4442, New Zealand. Most work performed as Professor and Leader of the North Dakota Maize Breeding and Genetics Program at North Dakota State University, Fargo, ND, USA
Corresponding author: Marcelo Javier Carena (marcelocarena2@gmail.com).

Abstract: Tropical maize germplasm can contribute useful and unique genes. It can provide greater resistance to pests and diseases, better quality crops, and trait genes and combinations not often present in commercially available northern U.S. temperate hybrids. Uniform farmer fields with genetically identical hybrids have a high risk of genetic vulnerabilities due to disease epidemics and abiotic stresses, especially after the recent major industry mergers. The EarlyTROP program was created with the long-term goal to increase the genetic diversity of short-season maize carrying 100% tropical germplasm. Five tropical maize populations were assessed for adaptation to ND short-season environments: NDSHLC (an improved composite from highland Mexico), BS16 (an improved strain of ETO from Colombia), BS28 (an improved strain of Tuxpeño from Mexico), BS29 (an improved strain of Suwan-1 from Thailand), and BS39 (an improved strain of Tusón mainly from Brazil and Cuba). The program conducted three cycles of stratified mass selection for days to silking near Casselton and Prosper, ND for all varieties except for NDSHLC, which had six selection cycles of stratified mass selection. Selected populations (NDHighland, NDEto, NDTuxpeño, NDSuwan-1, and NDTusón), and 31 checks including standard known and commercialized population and single-cross hybrids were evaluated across 12 short-season environmend. Stratified mass selection was a cost-effective and successful breeding procedure for adapting tropical populations to short-season environments without exceptions. NDTuxpeño is ready to be used in very short-season areas. It has shown to be the driest population of the experiment with 17.6% grain moisture at harvest time, statistically lower than 18 checks. Thus, confirming its adaptation to short-season environments. NDHighland, NDEto, NDSuwan-1, and NDTusón also showed evidence of adaptation. Adapted varieties represent unique new options for maize breeders to expand the genetic base of their current breeding programs. This gene pool, not present in current U.S. genome sequences or short-season areas, will offer unique early maturing competitive genes and products not available in the northern U.S. industry.

Keywords: Zea mays L., tropical maize, short-seasons, genetic diversity, EarlyTROP, adaptation.

Abbreviations: CIMMYT, international maize and wheat improvement center; GEM, germplasm enhancement maize program; FS, full-sib recurrent selection; FR, full-sib reciprocal recurrent selection; GCA, general combining ability; ISU, Iowa State University; LAMP, Latin American maize program; M, stratified mass selection; ND, North Dakota; NDSU, North Dakota State University; QPM, quality protein maize; SCA, specific combining ability; PVP, plant variety protection.

Introduction

Plant genetic resources are the future of agriculture for genetic adaptability to climate changes. Unique genes from genetically broad-based germplasm are the raw materials to produce new and better varieties. Sustainable maize (*Zea mays* L.) breeding requires the most efficient use of resources to develop the next generation of hybrids and genetic diversity is one of the key factors needed for sustainable maize production. Sustainable breeding is a viable scientific alternative to maintain enough food supply under the environmental challenges facing our planet, maximizing biodiversity and minimizing waste and pollution (Carena, 2017).

Germplasm carrying unique genes can break environmental margins (Carena, 2011). However, Brown (1953) pointed out that farmers utilized only 2% of the world's maize germplasm after hybrids dominated the maize production market. Utilization of maize genetic diversity was even reduced further (Hallauer et al., 2010). The U.S. Academy of Sciences encouraged the use of genetically diverse germplasm after the Southern Corn Leaf Blight epidemic (*Bipolaris maydis*) in the 1970s. But even with LAMP and GEM efforts (Pollak, 2003; Carena, 2003; Carena, 2017; Carena and Sharma, 2016), the excessive use of ex-PVP genetic materials (Bari et al., 2016) and the recent company mergers have increased the number of genetically narrow identical hybrids with just different single-gene transgenic events. These factors increase the probability of extensive epidemics and crop failures while affecting sustainability on farms (Davies et al., 2020).

Tropical germplasm can contribute useful and unique genes for economically and environmentally important traits. Continuous exposure of tropical maize to major pests (Holley and Goodman 1988) has proven useful for building up resistance to new diseases. It has also shown above average grain quality traits (Carena et al., 2009a,b; Sharma and Carena, 2012; Carena and Dong, 2017) and grain yield heterosis expression (Mungoma and Pollak, 1988; Crossa et al., 1990; Echandi and Hallauer, 1996; Hallauer, 2005; Laude and Carena, 2014). However, long-term program efforts focused on the incorporation of exotic germplasm to broaden the genetic basis of breeding programs, are still scarce (Hallauer and Sears, 1972; Goodman, 1999; Pollak, 2003; Carena et al., 2009a,b; Sharma and Carena, 2012; Carena 2013a,b,c; Carena and Sharma, 2016).

Breeders have taken advantage of applying several selection strategies in order to improve different genetic backgrounds for different traits. Early breeders utilized the mass selection method for centuries. This method of selection is the main cause of maize domestication and diversification (Hallauer et al., 2010). The success of this method, however, is dependent on the genetic complexity of the trait. The use of mass selection has been successful for highly heritable traits but less successful for genetically complex traits such as grain yield. Sprague (1955) indicated that the ineffectiveness of mass selection was not because of the method per se, but due to poor isolation, lack of environmental control, lack of parental control, genotype x environment interacttions, and poor plot techniques.

Therefore, in addition to the genetic complexity of the trait under selection, proper isolation techniques, adequate sample sizes, and experimental precision were essential. Following Sprague (1955) ideas, Gardner (1961) obtained encouraging results after growing populations in isolation utilizing a grid 'stratified' system to minimize environmental effects. Breeders have refined selection strategies in order to overcome the limitations of mass selection, especially with progeny testing in low heritable traits. Still, when properly conducted for genetically simple traits, stratified mass selection has maximum efficiency, explained by low cost and reduced time, and success across genotypes without exceptions (Hallauer and Carena, 2009).

Thus, stratified mass selection allows the highest genetic gain in time for genetically simple traits that are easy to measure and lack significant environmental influence. One of the major advantages of this method is that it allows largest sample sizes for an effective direct selection response per year. Moreover, mass selection can be an effective method to improve traits under minimum resources. The estimated cost of population adaptation per year was $2,000 (Hallauer and Carena, 2014). Stratified mass selection (Gardner, 1961) has proven useful in adapting exotic germplasm to target temperate environments (Hallauer and Sears, 1972; Goodman, 1999; Hallauer, 1999; Carena et al., 2008; Hallauer and Carena, 2009, Hallauer et al., 2010; Hallauer and Carena, 2016).

Stratified mass selection for earliness, as primary selection target, has shown to be a cost-effective methodology to adapt mid-season temperate maize to short-season environments (Carena et al., 2008). Tropical genetic materials have been effectively adapted to mid-season temperate environments (Hallauer and Carena, 2014, 2016) and their agronomic performance has been comparable to adapted populations. The methodology has shown to be effective across genetic backgrounds. Flowering date is a genetically simple trait that has been amenable to significant change with adequate sample sizes.

EarlyTROP is a maize breeding program created with the goal to increase the genetic diversity of short-season maize with 100% tropical germplasm. The objective of this research was to adapt new 100% tropical maize germplasm to short-season environments and make it available for the first time to short-season maize breeders. New germplasm will be essential to develop the future generation of sustainable maize populations, lines, and hybrids adapted to climate changes and lower environmental footprint.

Material and methods

Genetic materials included elite 100% tropical genetically broad-based populations. NDSHLC was created recombining four tropical highland populations [POP800(FS)C5, POP85(FS)C4, POP902(FS)C2, and POP903(FS)C2] under intra-population FS in CIMMYT, Mexico

(Eno and Carena, 2008). BS16 is an improved strain of ETO composite from Colombia, BS28 derived from an improved strain of Tuxpeño from Mexico, BS29 represents an improved strain of Suwan-1 from Thailand, and BS39 belongs to an improved strain of Tusón mainly from Brazil and Cuba. Genetic background information on BS16, BS28, BS29, and BS39 was described in Hallauer and Smith (1979), Hallauer (1994), and Hallauer and Carena (2016). CIMMYT provided highland improved populations from Mexico and ISU provided the rest of the elite populations.

Nursery seed increases

A sample of each tropical population was planted in the Fargo maize breeding nursery, ND. Plants of all populations were phenotypically non-adapted, tall (>4.5 m), and flowered during late August while flowering time in Fargo short-seasons is normally during early July. During pollination, we used plants only once either as a male or as a female so that gametes were represented equally, thus, the number of needed pollinations decreased significantly. We harvested a balanced set of 100 ears from each population the day before hard frost. Harvested ears were dried to form three balanced bulks per population. We saved two bulks in cold storage, and the third bulk was the source for the original populations used for selection.

Selection for adaptation

Stratified mass selection (Gardner, 1961) for earliness started near Prosper and Casselton towns in ND. Casselton represents a Fargo (Epiaquert) soil type located at 46°53' N, 97 18' W, with an elevation of 288 m. Prosper represents a Perella-Bearden (Endoaquolls and Calciaquolls) soil type located at 47°0' N, 97 7' W, with an elevation of 284 m.

Isolated dry land fields of approximately ½ Ha was utilized for each population. Fields were at least 800 m from other maize grown in the surrounding areas to avoid pollen contamination and were treated with two pre-emergence herbicides and fertilized with 225 kg.ha^{-1} of N, 55 kg.ha^{-1} of P, and 55 kg.ha^{-1} of K. Approximately, 30,000 seeds were planted for each selection cycle across all populations. Final stands were no less than 22,500 plants. We selected the first 350

to 400 earliest silking plants with equal representation from field grids while checking for silk emergence daily.

We tagged the earliest silking plants in each grid at the ear node indicating the date of silk emergence. All competitive plants were included for selection except those that were stalk or root lodged. In all cases, date of silk emergence was the primary trait considered, but selection also considered lower plant and ear height, no lodging, and absence of leaf diseases at time of silking. Additional selection for disease resistance and fast dry down was conducted at harvest time and very late in the season when possible.

Nursery and isolation fields were always left untouched after harvest for observation purposes even after field trials across locations were harvested. Within isolation fields, ears on tagged plants were harvested, dried, and shelled in balanced bulks. As done with the original seed increases, two bulks were saved in cold storage and a third one was used to plant the isolated fields the following year for the next cycle of selection. The process was repeated to complete three cycles of stratified mass selection for earlier silk expression for BS16, BS28, BS29, and BS39, and six cycles of stratified mass selection for NDSHLC. Seed of advanced selection cycles and checks were produced in the Fargo nursery population maintenance section for field trials and further genetic improvement through recurrent selection.

Field trials, data collection, traits evaluated, and experimental design

We evaluated NDHighland, NDEto, NDTuxpeño, NDSuwan-1, and NDTusón populations together with 31 checks in field trials arranged in a partially balanced lattice experimental design across 12 northern U.S. locations representing northern North Dakota and Minnesota in 2016. Data were collected based on means representing 24 observation plots per entry. Fields were planted and harvested with equipment adapted for small experimental plots.

Agronomic data were collected for each plot at each location and converted to grain yield ($t.ha^{-1}$, adjusted on a 15.5% grain moisture basis),

grain moisture at harvest (%), and stand ($M.ha^{-1}$). Days to anthesis (days) data were collected when at least 50% of the plants in the plot were shedding pollen with anthers emerged while days to silking (days) was noted when at least 50% of the plants in the plot were showing visible silks. Data on root and stalk lodging resistance were collected within the week before actual harvest. Root lodging (%) was measured as percentage of plants leaning greater than 30° from vertical with intact stalks. Stalk lodging (%) data were measured as the percentage of plants broken below the ear.

Checks included 22 populations (Carena, 2005) and nine standard known short-season single-cross and population hybrid checks representing a range of relative maturities (75-95RM) and a range of tropical germplasm percentages (12.5%, 25%, and 100%), a few already commercialized. We utilized standard checks as experiment controls for the newly created germplasms (Table 1). The 22 populations included two groups of 11 populations representing two heterotic groups.

The Stiff-Stalk (SS) group included:

NDSSR	North Dakota Synthetic for Strength on Roots
NDSS	North Dakota Stiff Stalk Synthetic under FR
NDBSSS	an adapted short-season version of BSSS after four cycles of M
NDEarlyGEM3	an adapted GEM version with germplasm from Cuba under FS and FR
NDEarlyGEM55	an adapted GEM version for drought and cold tolerance
NDS7378, NDS7300, and NDS7317	three adapted short-season population versions of B73
NDBS13	an adapted short-season strain of BS13 after inbred progeny recurrent selection and six cycles of M
NDEarlyQPM	a short-season Stiff Stalk Quality Protein Maize Synthetic from the EarlyQPM program (Carena and Dong, 2017)
NDSSTR	a synthetic of short-season lines with top GCA and SCA with non-Stiff Stalk industry testers

The non-Stiff-Stalk (non-SS) group included:

NDL	North Dakota Lancaster under FR,
NDEarlyGEM2	an adapted GEM version with germplasm from Uruguay,
NDS1778 and NDS1700	two adapted short-season population versions of Mo17,
NDEarlyQPM1, NDEarlyQPM2, NDEarlyQPMPt, NDEarlyQPMLys, NDEarlyQPMMet, NDEarlyQPMCys	six short-season synthetics from the EarlyQPM program, and
NDLTR	a synthetic of short-season lines with top GCA and SCA with SS industry testers.

Experimental checks included mostly unreleased synthetic varieties representing different maize breeding programs including the ND EarlyGEM (Carena, 2003), and NDEarlyQPM programs (Dong et al., 2012), currently under the NDSU Dept. Plant Sciences cold storage system. All genetic materials should be available under agreements with NDSU Agriculture Experiment Station for unreleased genetic materials and with the NDSU Research Foundation for released genotypes.

Standard single-cross and population hybrid checks represented the average of top public and public x private NDSU maize breeding hybrids available to industry. Some public x public hybrids proved commercially viable in short-season world areas for the dairy industry. Public x private hybrids were possible under exclusive licenses with foundation seed companies, including one derived from a female NDSU inbred line with record seed yields for hybrid seed production. NDSU signed three comercialization agreements since 2013. U.S. and Canada seed industry and cooperatives requested four commercialization agreements on our standard checks since 2017.

Statistical analyses

Individual analyses of variance (ANOVAs) were computed using SAS (SAS INSTITUTE, 1990) for traits within locations. Data were summarized on excel files and then imported to SAS for analyses. ANOVAs for each location were produced using the PROC LATTICE procedure. For each trait, the relative efficiency

of the lattice design with the randomized complete block design (RCBD) was calculated. If the relative efficiency was higher than 105%, adjusted means by incomeplete blocks were utilized in order to combine data across locations. If the efficiency was lower than 105%, then unadjusted means were used. For high efficiency traits, the effective error was the denominator in the F-test instead of the RCBD error mean square.

Traits with homogeneous variance were the only ones used for the combined analyses and adjusted and unadjusted means from each trait were utilized. Combined analyses of variance across locations were computed using individual observations for each trait. Expected mean squares were calculated following the rules of Schultz (1955) and were based on a mixed linear model that considered locations and replications as random effects and entries as fixed effects. Combined error mean squares (pooled error) were calculated by pooling the correspondent individual error mean squares weighed by their corresponding degrees of freedom. Mean comparisons were assessed with Fisher's protected least significant difference (FLSD) since it has shown to be an adequate test for detection of differences (Carmer and Swanson, 1971). Data averaged over replications and locations were presented.

Results and discussion

Earliness has been the focus on selection for adaptation in maize (Hallauer and Sears, 1972; Troyer and Brown, 1976; Carena et al., 2008; Hallauer and Carena, 2009). Hallauer and Sears (1972) first successfully reported mass selection for early silking in a program for integrating exotic maize germplasm. Since then stratified mass selection for earliness has been a very successful (Hallauer and Carena, 2009) and cost effective (Hallauer and Carena, 2016) breeding methodology to adapt temperate and tropical genetic materials to mid- and late season environments. This is the first report of adaptation of 100% tropical genetic materials to short season environments.

Record grain yields occurred in most regions of the northern U.S. in 2016. Table 1 shows that yields of populations and population hybrids have expressed their genetic potential (Carena, 2017) with significant ($P \leq 0.05$)

differences were detected among entries evaluated. Tropical genetic materials have shown to be competitive to either be used directly or as new sources of inbred lines. Data have shown an average grain yield of 8.93 t.ha^{-1}, grain moisture at harvest of 19.5%, and stalk lodging of 1.4%

for tropical germplasm after selection for adaptation. Data for NDHighland, NDEto, NDSuwan-1, and NDTusón were not statistically different to those for experimental or standard checks on economic and adaptation traits (Table 1).

Table 1. Average of six traits for NDHighland, NDEto, NDTuxpeño, NDSuwan-1, and NDTusón compared with experimental synthetic varieties and populations under recurrent selection and external standard adapted checks evaluated at 12 short-season environments.

Entries	Tropical %	Grain Yield t.ha^{-1}	Grain Test weight Kg.l^{-1}	Grain Moisture %	Stand M.ha^{-1}	Lodging Root %	Lodging Stalk %
NDTusón [a]	100	9.27	68.9	20.8	71.2	6.3	3.6
NDTuxpeño [b]	100	8.98	72.0	17.6	71.6	0.0	0.0
NDSuwan1 [b]	100	9.68	67.7	21.9	70.7	6.1	1.7
NDEto [c]	100	8.57	70.5	18.8	68.6	2.4	0.7
NDHighland [d]	100	8.13	70.8	18.2	69.0	1.5	1.0
MEAN (5)		8.93	70.0	19.5	70.2	3.2	1.4
NDSSR	0	7.92	68.4	24.7	70.1	0.0	0.0
NDBS13	0	8.12	69.2	19.4	70.4	6.2	5.6
NDSS	0	9.42	70.1	18.1	70.8	2.1	1.6
NDBSSS	0	7.88	68.6	21.1	69.6	7.5	8.0
NDEARLYGEM3	12.5	9.21	71.4	18.8	70.3	3.1	3.8
NDEARLYGEM55	12.5	8.91	72.2	19.1	70.7	2.6	3.7
NDS7378	0	7.59	68.1	22.3	70.1	4.8	7.9
NDS7300	0	9.11	68.6	20.2	69.9	1.5	2.3
NDS7317	0	9.19	68.4	21.3	70.9	1.0	2.1
NDSSTR	0	9.36	69.7	19.3	70.6	0.4	0.7
NDEARLYQPM	25	7.88	72.3	23.2	70.4	3.1	4.7
MEAN (11)		8.59	69.7	20.7	70.3	2.9	3.7
NDLTR	0	9.58	70.1	19.2	71.9	0.8	2.3
NDL	0	9.87	69.8	17.9	72.8	3.2	0.8
NDEARLYGEM2	0	9.17	71.3	22.2	70.6	4.2	3.9
NDS1778	0	7.89	67.9	23.0	72.3	10.8	6.9
NDS1700	0	9.02	68.6	22.7	70.9	9.3	3.4
NDEARLYQPM1	25	8.79	71.1	22.5	69.7	2.3	4.2
NDEARLYQPM2	25	8.58	71.8	22.3	70.2	2.6	4.8
NDEARLYQPMPt	25	8.19	71.7	21.8	69.8	5.5	5.1
NDEARLYQPMLys	25	8.43	71.9	23.1	68.9	4.3	4.4
NDEARLYQPMMet	25	8.02	70.6	22.7	68.1	9.9	5.8
NDEARLYQPMCys	0	7.92	70.1	22.8	70.2	8.9	3.9
MEAN (11)		8.68	70.4	21.8	70.5	5.6	4.1
POPULATION HYBRIDS (5)	0	11.63	69.8	18.6	71.3	3.4	1.6
SINGLE-CROSS HYBRIDS (4)	0	12.22	67.9	19.2	71.8	2.3	1.2
LSD (0.05)*	0	0.98	5.82	2.13	5.92	7.9	3.2

a) Hallauer and Carena (2014); b) Hallauer (1994); c) Hallauer and Smith (1979); d) Carena (2016).
* Comparisons among entries.

Adaptation to short season environments was confirmed by grain moisture at harvest values as selected strains showed a reduction of 18.1% to 22.4% when compared to their original

un-adapted strains. After three and six cycles of selection, selected strains silked 2 to 3 weeks earlier than the original strains acquired. These results agree to the scientific justification provi-

ded for BS39 tropical adaptation to Iowa environments (Hallauer and Carena, 2016) and it is better than expected for selection studies focused on earliness (Hallauer and Carena, 2009). The same authors showed scientific evidence on important adaptation traits such as grain moisture at harvest and lodging resistance.

Stratified mass selection has shown to be a very cost-effective methodology to adapt not only temperate maize germplasm (Eno and Carena, 2008; Hallauer and Carena, 2014) but also 100% tropical maize germplasm to short season environments. NDTuxpeño has shown the most successful example of adaptation, showing significant differences for grain moisture at harvest with other genetic backgrounds (Table 1). In addition, NDTuxpeño was the earliest maturing genotype of the whole NDSU maize-breeding nursery, representing genetic materials with <75RM. Time of silk expression, after three and six cycles of selection, was equal or earlier than other short-season temperate cultivars adapted to short-season environments. Improvement in earliness led to positive changes in plant height, ear height, and lodging resistance.

NDSHLC, BS16, BS28, BS29, and BS39 tropical germplasms were adapted to short-season environments. Adapted versions are unique sources of new early maturing inbred lines carrying unique and valuable alleles available for sequencing. This research supports other studies utilizing mass selection for adaptation in exotic elite populations to develop the next generation of hybrids carrying diverse genetics.

The adaptation of unique tropical genes to short-season environments has positive implications for farmers and industry in the long-term. The genetic diversity from tropical maize contributes useful and unique genes allowing a combination of desirable traits, a unique combination of agronomic and quality traits often not available in industry hybrids. NDHighland, NDEto, NDSuwan-1, and NDTusón, and NDTuxpeño are genetically diverse germplasms ready to be used directly or improved by intra- or inter-population recurrent selection programs. As improved 100% tropical germplasm they can be used to develop unique short season inbred lines and hybrids not available commercially (Bari and Carena, 2014; 2016). They are

excellent options for short-season maize breeders with an interest in expanding the genetic base of their current breeding programs. The NDSU maize breeding program has worked toward increasing the genetic diversity from tropical and temperate regions while improving earliness, fast dry down, cold and drought tolerance, low fertilizer and seed use, disease resistance, and ethanol and feedstock quality. With significant genetic diversity and sampling, top yielding hybrids with lowest grain moisture at harvest have demonstrated to be easier to achieve, a sustainable combination for shorter season environments that reduces risk (Yang et al., 2010).

Adaptation and improvement of short-season tropical maize will serve as new sources of unique hybrid combinations that supplement the narrow genetic diversity present in most industry hybrids. This gene pool will offer unique early maturing competitive genes and products not available in the short-season maize hybrid industry and the maize genome sequences available. These elite and uniquely diverse products will not only be tolerant to climate changes with better abiotic and disease resistance and less input needs but also will provide the stability of maize production and sustainable profitability (Carena, 2017).

Conclusion

For the first time, 100% tropical maize has been adapted to short-season increasing the genetic diversity of maize ahead of climate changes. This research clearly shows statistical evidence on adaptation traits as it did for Hallauer and Carena (2016) when adapting tropical maize to Iowa environments. In this case we have evidence, with similar data, for adapting not only BS39 tropical germplasm to temperate short-season environments but also for NDSHLC, BS16, BS28, and BS29 additional tropical improved genetic resources. Maximizing their genetic improvement is the next step recommended before the development of the next generation of short-season elite populations, inbred lines, and hybrids with 100% tropical genetic background.

Continuity of public maize breeding programs seems essential to reduce the vulnerability of maize production and increase its adaptation to climate changes and lower environmental

footprint. Keeping maize breeding programs strong will be essential for providing sustainable options to the future generation of farmers and ranchers with environmental requirement needs. These programs need full support for infrastructure, especially excellent cold storage facilities to avoid the risk for reduced viability of unique products, in this case, 100% tropical germplasm adapted to short-season environments. We encourage department head administrators to preserve these unique genetic resources for future generations.

Germplasm maintenance and availability

The EarlyTROP maize breeding program produced two balanced bulks of NDHighland, NDEto, NDTuxpeño, NDSuwan-1, and NDTusón maize germplasms for further selection studies and for cold storage. In addition, the NDSU maize-breeding program produced one unbalanced large bulk of each new variety for distribution and should be available at Wiidakas Laboratory, NDSU. Under agreement, NDSU has transferred ownership of short-season materials to the NDSU Research Foundation (NDSURF). However, since these varieties were still experimental, requests of NDHighland, NDEto, NDTuxpeño, NDSuwan-1, and NDTusón should be made directly to the head of NDSU Department of Plant Sciences. Material Transfer, Population, and Commercialization Agreements might need to be signed with the NDSURF Executive Director before seed lots are sent. With the maize breeding unit currently vacant, the Head of the NDSU Department of Plant Sciences is responsible for maintaining breeder seed of these unique tropical short-season germplasm versions.

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