Historical Minnesota Maize Inbreds: Relatedness, Diversity and Marker Associations for Flowering Time, Kernel Composition and Disease Resistance

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Abstract

Here I present three studies on the characterization and utilization of historical maize (*Zea maize* L.) inbreds for genomewide association mapping. In the first study, I characterized a collection of 284 maize inbreds, most of which were developed by the University of Minnesota between the 1910s and 1980s. My objective was to relate these inbreds to known heterotic patterns and identify unique groups of inbreds, if any, represented by the Minnesota germplasm. The inbreds were genotyped with 56,110 single nucleotide polymorphism markers. Model-based clustering identified five subpopulations, with the A321 subpopulation containing more than 60% of the Minnesota inbreds, some of which formed groups unique to the Minnesota inbreds. In the second study, I investigated the influence of the xenia effect on the evaluation of maize inbreds for kernel composition. My objective was to determine the influence of xenia on kernel composition traits among self- and open-pollinated plots of inbreds that were unadjusted and spatially and temporally adjusted. Pollination treatment was not significant for any kernel composition trait and simple and rank correlations were high between self- and open-pollinated treatments indicating that kernel oil, protein, and starch can be evaluated in open-pollinated plots without confounding differences among entries. In the third study, association mapping was used to identify major quantitative trait loci (QTL) for less-complex traits using historical inbreds. My objectives were to (i) characterize genomewide linkage disequilibrium and (ii) assess variation and map QTL for flowering time, kernel composition, and resistance to northern corn leaf blight (caused by *Setosphaeria turcica*) and Goss' wilt and blight (caused by *Clavibacter michiganensis* sups. *nebraskensis*). Linkage disequilibrium was high among all pairwise marker

combinations and among adjacent markers. The A321 subpopulation had inbreds with either or both the minimum and maximum inbred mean value for all traits except protein concentration. I identified 54 QTL across six traits, which accounted for 24% to 61% of the phenotypic variation for a given trait. To my knowledge, this was the first attempt to utilize high-density markers and association mapping to mine QTL among historical maize inbreds.

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Chapter 1: Population structure and SNP diversity of historical Minnesota maize inbreds

Introduction

The University of Minnesota maize (Zea mays L.) breeding program has developed more than 600 inbreds since the Saint Paul hybrid breeding program was established in 1915 (Johnson et al., 2000; Troyer and Mikel, 2010). At that time, inbreds were typically developed directly from established open-pollinated cultivars. Minnesota 13 (MN13), a popular open-pollinated cultivar, allowed for the northern expansion of maize production in the Upper Midwest because of its high yield, early maturity, and good agronomic qualities (Baker, 1984; Troyer and Hendrickson, 2007). Due to its great success in the region, MN13 became a prominent germplasm source within the University of Minnesota breeding program and was used, albeit to a lesser extent, by breeding programs throughout the United States (Johnson et al., 2000; Troyer and Hendrickson, 2007). The University of Minnesota breeding program also utilized other open-pollinated cultivars for inbred development, including Rustler White Dent, Northwestern Dent, and Reid's Yellow Dent.

Increased investment in inbred development by the U.S. hybrid seed industry in the 1960s and 1970s reduced the demand for publicly developed inbreds (Mikel and Dudley, 2006). In addition, inbred development from elite × elite crosses has reduced the use of older inbreds (Baker, 1984; Lu and Bernardo, 2001; MBS, 2009). In recent years, hundreds of proprietary maize inbreds that were previously protected by the U.S. Plant Variety Protection Act (PVPA) or by U.S. utility patents have become available (Mikel,

2006). Exotic germplasm can provide new genetic diversity but introgressing exotic germplasm into elite maize inbreds is often difficult and time consuming (Goodman, 2005). In contrast, older public and private inbreds developed in the U.S. Corn Belt do not suffer from the lack of adaptedness typical of exotic germplasm and are therefore more readily useful than exotic germplasm as a source of genetic diversity.

The MN13 genetic background has not been investigated thoroughly for its relationship to other genetic backgrounds in the U.S. hybrid maize germplasm. A few inbreds derived directly from MN13 were found to represent an independent cluster, separate from B73, Mo17, Oh43, Wf9, and Iodent-type inbreds (Hansey et al., 2011). Some work has been completed to characterize the relatedness of ex-PVPA inbreds using both pedigree and molecular marker approaches (Mikel, 2006; Nelson et al., 2008). An analysis of 92 ex-PVPA inbreds found that ex-PVPA germplasm is generally represented by six genetic backgrounds: B73, Mo17, PH207, A632, Oh43, and B37 (Nelson et al., 2008). The ex-PVPA inbreds that were investigated fit well within the heterotic patterns established by historical public germplasm with the exception of the PH207 (Iodent) background, which was mostly unique to Pioneer Hi-Bred breeding programs (Smith et al., 2004; Mikel and Dudley, 2006).

Marker characterization of relatedness and diversity among older inbreds and current heterotic patterns is critical for effective and efficient germplasm utilization. Our objectives were to (i) characterize the population structure and relatedness in the historical Minnesota maize inbred collection in comparison with inbreds of known heterotic groups, (ii) identify any unique germplasm groups among the historical Minnesota inbreds, and (iii) characterize the genetic diversity of the historical Minnesota

germplasm. Results from this study will help provide maize breeders with information necessary to effectively utilize historical genetic resources while maintaining heterotic patterns necessary in hybrid breeding.

Materials and Methods

Plant material

A collection of 284 inbreds was used in this study. The collection included 143 inbreds developed at the University of Minnesota (referred to as "A" inbreds), 26 inbreds developed by public breeding programs (referred to as "public" inbreds), and 115 inbreds previously protected under the PVPA (referred to as "ex-PVPA" inbreds; Supplemental Table S1). The ex-PVPA inbreds were developed by 12 different private breeding programs, several of which have since merged. Seed of the public, ex-PVPA, and a portion of the A inbreds were provided by the USDA North Central Regional Plant Introduction Station at Ames, IA. The remainder of the A inbreds were available from the University of Minnesota germplasm collection. Hundreds of additional A inbreds were not available due to old and poor quality seed (Supplemental Table S1). Seed stocks for most inbreds were increased in summer 2010 at St. Paul, MN and in winter 2010 at Molokai, HI.

Genotyping

The entire collection was grown in the field in summer 2011 at St. Paul. Leaf tissue samples were collected from a single plant of each inbred and were sent to DNA LandMarks (Saint-Jean-sur-Richelieu, Quebec) for DNA extraction and marker analysis. Three inbreds (A632, PH207, and LH59) were assayed in duplicate as technical

replicates. The MaizeSNP50 Beadchip (Illumina, San Diego, CA) was used to assay the 284 inbreds with 56,110 single nucleotide polymorphism (SNP) markers. To reduce the potential of including allele calling errors, markers with a minor allele frequency less than 7% and those with more than 10% missing data were removed prior to further analysis, leaving 43,252 high quality, polymorphic markers. Inbred BCC03 was removed from further analysis due to more than 15% missing marker data. The SNP filtering was completed using PLINK software (Purcell et al., 2007).

Population structure and cluster analysis

Model-based cluster analysis was conducted in STRUCTURE v.2.3.1 (Pritchard et al., 2000). To help meet the assumption in STRUCTURE that the markers are independent and in linkage equilibrium within subpopulations, we used a random subset of 3000 SNP markers instead of the entire set of SNP markers in the model-based cluster analysis. The value for the lambda parameter was inferred from the mean of five independent runs of STRUCTURE assuming K=1 subpopulations (Pritchard et al., 2010). The value for lambda was then set for all subsequent analyses. Five independent runs of STRUCTURE were conducted for each level of K=2-10 subpopulations, using 50,000 burn-in and model iterations. The analysis assumed admixture was present and linkage was absent. The most likely value of K was determined through an ad hoc statistic, ΔK, which is based on the rate of change in log likelihood estimates from STRUCTURE (Evanno et al., 2005). The independent runs for each level of K were integrated using CLUMPP v.1.1.2 (Jakobsson and Rosenberg, 2007), implementing the 'Greedy' algorithm. Inbreds were assigned to subpopulations based on the highest mean membership probability (which was at least 0.29 for all inbreds and $\geq$0.40 for all but 25

inbreds; Supplemental Table 1) of the combined data. Population substructure was also investigated by principal components analysis implemented in TASSEL using all polymorphic markers (Bradbury et al., 2007).

The level of population differentiation was determined by analysis of molecular variance (AMOVA) and by calculating pairwise F statistics (FST) between subpopulations through ARLEQUIN v. 3.5 (Excoffier and Lischer, 2010).

Hierarchical clustering was conducted among all inbreds in the collection and within the two subpopulations that contained most of the A inbreds (i.e., Oh43 and A321) to gain a better understanding of the relatedness of the historical Minnesota inbreds. Pairwise dissimilarity was calculated in TASSEL software v. 3 (Bradbury et al., 2007) as the proportion of SNPs that differed between two inbreds, with each of the possible marker genotypes at each SNP locus (i.e., MM, Mm, and mm) being treated as equally dissimilar to each other. Clustering was performed using the unweighted pair group method with arithmetic means (UPGMA) in TASSEL (Bradbury et al., 2007). Mean dissimilarity was calculated among inbreds within each developer group (A inbreds, public, and ex-PVPA), among inbreds within each subpopulation, and between pairs of inbreds that belonged to different subpopulations.

Genetic diversity

Genetic summary statistics, including major allele frequency, observed heterozygosity, gene diversity, and polymorphism information content (PIC) was calculated using R (R Development Core Team, 2012). Genotypic diversity statistics were calculated at three levels: the entire collection, by developer group, and by subpopulation. Gene diversity was calculated for each locus based on allele frequency,

population size, and inbreeding coefficient according to Weir (1996). The PIC values were calculated for each locus based on allele frequencies (Botstein et al., 1980).

Ascertainment bias

The influence of marker ascertainment bias was characterized by correlation analysis of the first five principal components estimated using three sets of SNPs: (i) 12,510 SNPs that were ascertained by polymorphism between B73 and Mo17 (SNPBM); (ii) the remaining 30,742 SNPs that were ascertained from other diverse sources (SNPDiverse); and (iii) all 43,252 SNPs (SNPAll; Ganal et al., 2011). Due to the different number of markers in each subset, principal component analysis was repeated 100 times using random samples of 12,510 SNPs from the SNPDiverse and SNPAll sets, and the mean correlation coefficient was calculated across repeats. The significance of differences between correlations was determined from 95% confidence intervals. This analysis was conducted in R (R Development Core Team, 2012).

Results

Population structure and differentiation

Model-based clustering divided the collection of 283 inbreds (inbred BCC03 was excluded due to poor marker data) into K=5 subpopulations represented by the most prominent inbred within each subpopulation, namely B73 (61 inbreds), Mo17 (29 inbreds), Oh43 (48 inbreds), A321 (116 inbreds), and PH207 (29 inbreds) (Fig. 1). The ΔK statistic peaked at K=5 (ΔK=46.7) and K=8 (ΔK=28.5), with all other levels of K having $\Delta K \leq 1.35$. The highest peak at K=5 indicated that five was the most likely number of subpopulations. In addition, previous knowledge of the germplasm and pedigree

backgrounds indicated that K=5 was a logical number of subpopulations. Most of the A inbreds were assigned to two subpopulations, A321 (87 A inbreds) and Oh43 (35 A inbreds); these two subpopulations accounted for 85% of the A inbreds used in this study (Table 1). The remainder of the A inbreds were distributed between the B73 (17 A inbreds) and the Mo17 (4 A inbreds) subpopulations. The PH207 subpopulation did not have any A inbreds or public inbreds. Ex-PVPA inbreds were distributed throughout all five subpopulations, with the B73 (37 ex-PVPA inbreds) subpopulation having the most and the Oh43 (9 ex-PVPA inbreds) having the fewest (Table 1).

Variation among subpopulations, among inbreds within subpopulations, and within inbreds were all significant ($P < 0.001$). Differences among subpopulations accounted for 16.5%, differences among inbreds within subpopulations accounted for 72.6%, and differences within inbreds (which had a mean observed heterozygosity of approximately 4%; Table 2) accounted for 10.9% of the molecular variation. Pairwise FST values between subpopulations ranged from 0.054 between the A321 and Oh43 subpopulations to 0.325 between the Mo17 and B73 subpopulations (Table 3). The mean pairwise FST value for the entire panel was 0.165. Similar results were found for pairwise mean dissimilarity, which ranged from 0.389 between the Oh43 and A321 subpopulations and the Oh43 and PH207 subpopulations to 0.458 between the B73 and Mo17 subpopulations (Table 3).

Principal components analysis

Principal components analysis supported the results from the model-based cluster analysis. The first five principal components (PC) explained 20.8% of the variation across the 43,252 SNP markers. A scatterplot of PC1 (8.5%) and PC2 (3.7%) formed a

triangular shape where PC1 differentiated the B73 and Mo17 subpopulations and PC2 differentiated the Mo17 and the PH207 subpopulations (Fig. 2). PC3 (3.4%) differentiated the Oh43 and A321 subpopulations from the PH207 and Mo17 subpopulations (Fig. 2). PC4 (2.8%) differentiated inbreds within the B73 subpopulation, separating those of B73-type from those of B14-type. PC5 (2.4%) differentiated the Oh43 subpopulation from the A321 subpopulation.

Hierarchical cluster analysis

The A321 subpopulation comprised 87 A inbreds, 12 public inbreds, and 17 ex-PVPA inbreds. Hierarchical cluster analysis indicated the presence of three distinct clusters along with a number of inbreds that did not fit within those clusters. Cluster A321-I was the largest of the three clusters; it had 39 inbreds, all of them being A inbreds, including A321 (Fig. 3). The second largest cluster, A321-II, had 33 inbreds. Cluster A321-II included a number of inbreds derived directly from or were very closely related to MN13 (e.g., A12, A116, C49, and Mt42; Fig. 3 and Supplemental Table S1). The third cluster, A321-III, had 20 inbreds, 17 of them being A inbreds.

The Oh43 subpopulation comprised 35 A inbreds, 4 public inbreds, and 9 ex-PVPA inbreds. Hierarchical cluster analysis among the inbreds in this subpopulation identified two distinct clusters, with a few additional lines that did not align with the two clusters (Fig. 4). Cluster Oh43-I had mostly A inbreds while cluster Oh43-II had a mixture of A inbreds (including A619), public inbreds (including Oh43 and H99), and ex-PVPA inbreds.

Genotypic diversity

Within each developer group, mean dissimilarity ranged from 0.385 (A inbreds and ex-PVPA inbreds) to 0.408 (public inbreds) (Table 2). Mean gene diversity within each developer group ranged from 0.360 (public inbreds) to 0.372 (A inbreds). The PIC values ranged from 0.289 (public inbreds) to 0.297 (A inbreds). Within each subpopulation, mean dissimilarity was lowest in the PH207 subpopulation (0.275) and highest in the A321 subpopulation (0.384). Similar trends were observed for gene diversity and PIC among subpopulations, with the PH207 subpopulation having the lowest values and the A321 subpopulation having the highest values for both diversity statistics (Table 2).

Ascertainment bias

The mean correlation of the first five principal components was 0.94 between the SNP_{BM} and $SNP_{Diverse}$ subsets, 0.96 between the SNP_{BM} and SNP_{All} sets, and 0.97 between the $SNP_{Diverse}$ and SNP_{All} sets. The mean correlation was 0.98 between two random $SNP_{Diverse}$ subsets. All four mean correlations were different from each other based on 95% confidence intervals.

Discussion

Three primary conclusions were drawn from this study. First, a majority of the A inbreds represent a genetic background different from the primary genetic backgrounds of U.S. Corn Belt inbreds. Second, subclusters containing only A inbreds, identified within the A321 and Oh43 subpopulations, represent groups of inbreds that are unique to the historical University of Minnesota germplasm. Third, the A inbred developer group

and the A321 and Oh43 subpopulations were found to have slightly higher genetic diversity compared to other developer groups and subpopulations.

Strong differentiation between the B73, Mo17, and PH207 subpopulations and weaker differentiation between the A321 and Oh43 subpopulations was indicated by model-based clustering (Pritchard et al., 2000), principal components analysis, and pairwise F_{ST}. The lack of strong differentiation between the A321 and Oh43 subpopulation compared to the three other subpopulations was not surprising as B73, Mo17, and PH207 represent the primary heterotic patterns in the U.S. hybrid maize industry, while a number of progenitors are shared among inbreds in the A321 and Oh43 subpopulations.

More than 60% (87 out of 143) of the A inbreds were assigned to the A321 subpopulation. Inbred A321 itself was developed in 1935, was one of the oldest A inbreds, and had the highest membership probability (0.9992) in the A321 subpopulation (Supplemental Table S1). In general, inbreds in the A321 subpopulation were derived from MN13, with some influence from Northwestern Dent and Reid's Yellow Dent open-pollinated cultivars (Supplemental Table S1). This result was consistent with the clustering of A inbreds included in the Wisconsin Diversity Set, as many of the A inbreds in that study also were assigned to the MN13 subpopulation (Hansey et al., 2011). The A321 subpopulation also had the highest mean dissimilarity, gene diversity, and PIC. A similar result was found in the Wisconsin Diversity Set where MN13 inbreds had higher gene diversity and PIC than all other subpopulations except the Tropical and Mixed subpopulations (Hansey et al., 2011).

On the other hand, the results regarding the higher genetic diversity within the A321 subpopulation than in the other subpopulations need to be interpreted with caution because of the larger number of inbreds in the A321 subpopulation (116 inbreds) than in each of the four other subpopulations (29 to 61 inbreds). The estimates of genetic diversity therefore may have been confounded with the effects of subpopulation size. Furthermore, the particular set of inbreds chosen for analysis could also influence the results. For example, B73 was developed at Iowa State University and it is conceivable that a similar analysis of a large collection of historical Iowa State University inbreds would lead to a large number of B73-type inbreds that are more diverse than those in the A321 subpopulation in this study.

MN13 has historically been utilized as a source of specific traits such as earliness, drought resistance, and disease resistance and it has not been used to form its own heterotic group as was done with other populations (Baker, 1984; Goodman, 2005; Troyer and Hendrickson, 2007). For example, A634 and A632 have been identified as highly influential lines in the hybrid seed industry; however, being backcrosses to B14, MN13 was only minimally represented in these inbreds. Pedigree information has indicated that MN13 was the third most utilized cultivar in maize hybrid development, representing 13% of the U.S. hybrid maize background (Troyer, 1999). Much of the initial selection in the University of Minnesota breeding program was for early maturity, high grain yield, prolific silking, and high grain protein content (Johnson et al., 2000; Troyer and Hendrickson, 2007). Many inbreds derived from MN13, including A109, A237, C49, Mt42, and ND203, have served the broad maize breeding community as a source of early maturing and high yielding parental inbreds (Rinke and Sentz, 1961;

Troyer and Hendrickson, 2007). Derivatives of MN13 were also sources of variation for secondary traits, including the inbred W153R as a source of resistance to northern corn leaf blight (*Setospharia turcica*) (Troyer and Hendrickson, 2007).

The A321-II cluster contains a number of influential inbreds derived from MN13, including A509, A654, C49, and W117 (Figure 3). C49, for example, was shown to be a major progenitor to modern germplasm, contributing to 151 of 305 proprietary inbreds registered between 2004 and 2008 (Troyer and Mikel, 2010). However, results from our study show that most of the inbreds closely related to C49 are A inbreds, with only a few public and ex-PVPA inbreds included. The A321-I cluster contains only A inbreds, many of which have not been utilized extensively in hybrid development. Therefore, inbreds in the A321-I cluster represent a unique group of A lines that could serve as a germplasm resource for modern maize breeding programs.

The Oh43 subpopulation mostly contains inbreds derived from MN13 and Richey Lancaster open-pollinated cultivars. This result was not surprising because one of the parents of Oh43 (W8) has MN13 in its pedigree (Troyer, 1999). Inbreds from the Oh43 subpopulation most closely related to MN13 include A7, A15, C14, and ND203, all of which were derived directly from MN13. In general, these inbreds clustered close to each other in the Oh43-I cluster. However, A15 did not group within the Oh43-1 cluster near other inbreds derived from MN13; we speculate that this separation may have been due to differences among MN13 germplasm sources (Figure 4; Supplemental Table S1). The Oh43-I cluster represents a group of A inbreds that are unique to the historical University of Minnesota germplasm, as all of the inbreds were either developed at Minnesota or directly from MN13.

The Iowa Stiff Stalk Synthetic (BSSS) and Lancaster Sure Crop heterotic pattern has historically been very important in U.S. hybrid maize breeding; development of A inbreds in these groups was limited, but highly successful. The B73 subpopulation contained 17 A inbreds, and most of these A inbreds were derived from early × late backcross populations that were developed to reduce the days to flowering in BSSS germplasm (Rinke and Sentz, 1961; Troyer and Mikel, 2010). Inbreds ND203 and Mt42, both derived directly from MN13, were used as the donor parents to reduce the flowering time of B14, resulting in the development of three highly utilized A inbreds (i.e., A632, A634, and A635) that were included in the B73 subpopulation. At the height of their use in 1975, inbred A632 comprised 15%, A634 comprised 8%, and A635 comprised 1% of the U.S. inbred seed demand (Troyer and Mikel, 2010).

The PH207 subpopulation did not contain any A or public inbreds, supporting previous reports showing that the Iodent background, represented here by PH207, was unique to Pioneer Hi-Bred and was unknown to public breeders (Mikel and Dudley, 2006; Nelson et al., 2008). This result was surprising because pedigree information shows that A78 (derived from Northwestern Dent) and A109, A237, and C49 (derived from MN13) were progenitors of PH207 (Troyer and Hendrickson, 2007). These inbreds likely contributed earliness to the Iodent genetic background but multiple generations of selection may have reduced the impact of MN13 on this genetic background (Troyer and Hendrickson, 2007).

Previous studies of diversity among maize inbreds indicated that marker ascertainment bias of SNPs on the MaizeSNP50 Beadchip tended to inflate the difference between B73 and Mo17 (Ganal et al., 2011; van Heerwaarden et al., 2012; Frascaroli et

al., 2013). This inflation resulted from the derivation of 26% of the SNP markers on the chip from polymorphism between B73 and Mo17, while the remaining markers were ascertained from more diverse sources (Ganal et al., 2011). While the mean correlation of principal components between biased (SNP_{BM}) and unbiased ($SNP_{Diverse}$) marker subsets (0.94) was significantly different from the mean correlation between random $SNP_{Diverse}$ samples (0.98), the difference between these mean correlations was small. A similar level of bias (r^2 = 0.96 versus 0.99) was previously found with the MaizeSNP50 Beadchip (van Heerwaarden et al., 2012). Furthermore, previous results indicated that ascertainment bias with the Maize SNP50 Beadchip was greater among European flint inbreds than among North American dent inbreds, and that such bias had little effect on the relative distances among inbreds within the flint subpopulation and within the dent subpopulation (Frascaroli et al., 2013). Our results suggest that while the ascertainment bias had little impact on the grouping of inbreds into subpopulations, the level of differentiation between the B73 and Mo17 subpopulations may have been inflated relative to the level of differentiation among the other subpopulations in this study.

We believe that as breeding tools such as doubled haploids and high-throughput SNP markers become routinely used, different breeding programs will become more and more differentiated not by breeding methodology but by the germplasm base available to the breeding organization. With the proper breeding tools, collections of historical inbreds are potential sources for increasing variation both within and between heterotic groups in an efficient manner. The introgression of highly diverse germplasm sources has been investigated through the Germplasm Enhancement of Maize program (Pollak, 2003; Goodman, 2005) and Early Germplasm Enhancement of Maize program (Sharma and

Carena, 2012). However, the lack of adaptedness of exotic germplasm makes introgressing exotic germplasm difficult (Hallauer and Sears, 1972; Goodman, 2005; Salhuana and Pollak, 2006). The utilization of older breeding germplasm, such as A inbreds or ex-PVPA inbreds, may provide sufficient diversity with less linkage drag of unfavorable alleles compared with tropical germplasm.

Furthermore, a recent survey has indicated a steep decline from 1984 to 2008 in the use of Mo17 germplasm (from 8.6 to 1.7%) and an increase in the use of Oh43 germplasm (from 1.5 to 3.9%) in commercial maize breeding programs (Mikel, 2011). The poor germination of Mo17 in cold soils may have contributed to this decrease in the use of Mo17 (Troyer, 2004), particularly as the U.S. Corn Belt has expanded to northern areas where soils are colder at planting. We speculate that the similarity of the A321 subpopulation to the Oh43 subpopulation would enhance the introgression of A inbreds in the A321 subgroup into current Oh43 germplasm.

Genomewide association analysis has been utilized in maize to identify alleles associated with traits of interest (Thornsberry et al., 2001; Zhu et al., 2009; Yan et al., 2011). We have initiated an association mapping project utilizing the collection of A inbreds and ex-PVPA inbreds in this study as the mapping panel, and we will describe the results of association mapping in a separate report.

Table 1: Number of maize inbreds assigned to each developer group and subpopulation as identified through model-based clustering of 283 maize inbreds with 3000 random single nucleotide polymorphism markers.

	Developer group			
Subpopulation	A lines	Public	ex-PVPA	Total
B73	17	7	37	61
Mo17	4	3	22	29
Oh43	35	4	9	48
A321	87	12	17	116
PH207	0	0	29	29
Total	143	26	114	283

Table 2: Genetic diversity summary statistics for 283 maize inbreds assayed with 43,252 single nucleotide polymorphism markers and divided by developer group and subpopulation. Subpopulations were defined by model-based cluster analysis of the inbreds based on 3000 random single nucleotide polymorphism markers.

	Number of inbreds	Major allele frequency	Observed heterozygosity	Mean allelic dissimilarity	Gene diversity	Polymorphism information content (PIC)
Complete collection	283	0.705	0.054	0.395	0.393	0.320
Developer group						
A inbreds	143	0.721	0.044	0.385	0.372	0.297
Public inbreds	26	0.727	0.042	0.408	0.360	0.289
ex-PVPA inbreds	114	0.723	0.046	0.385	0.368	0.294
Substructure group						
B73	61	0.718	0.049	0.289	0.371	0.297
Mo17	29	0.724	0.041	0.332	0.363	0.291
Oh43	48	0.723	0.040	0.354	0.366	0.293
A321	116	0.715	0.042	0.384	0.377	0.301
PH207	29	0.727	0.041	0.275	0.360	0.289

Table 3: Pairwise F_{ST} (above diagonal) and mean dissimilarity (below diagonal) values for *K*=5 subpopulations identified through model-based clustering in a collection of 283 maize inbred lines assayed with 43,252 single nucleotide polymorphism markers. All pairwise F_{ST} values were significant at $P < 0.001$.

	B73	Mo17	Oh43	A321	PH207
B73		0.325	0.226	0.178	0.301
Mo17	0.458		0.163	0.137	0.256
Oh43	0.416	0.409		0.054	0.186
A321	0.414	0.416	0.389		0.142
PH207	0.408	0.408	0.389	0.390	

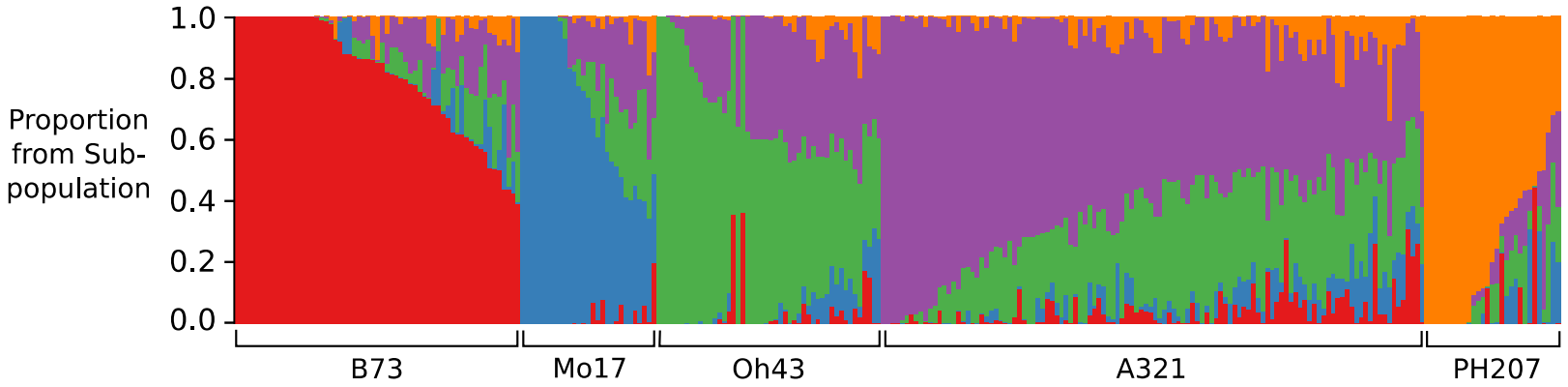

Figure 1: Population structure of 283 maize inbreds representing the B73, Mo17, Oh43, A321, and PH207 genetic backgrounds. Subpopulation assignments were based on maximum mean membership probabilities for each inbred. Membership probabilities were obtained from five runs of STRUCTURE software utilizing a random set of 3000 single nucleotide polymorphism markers.

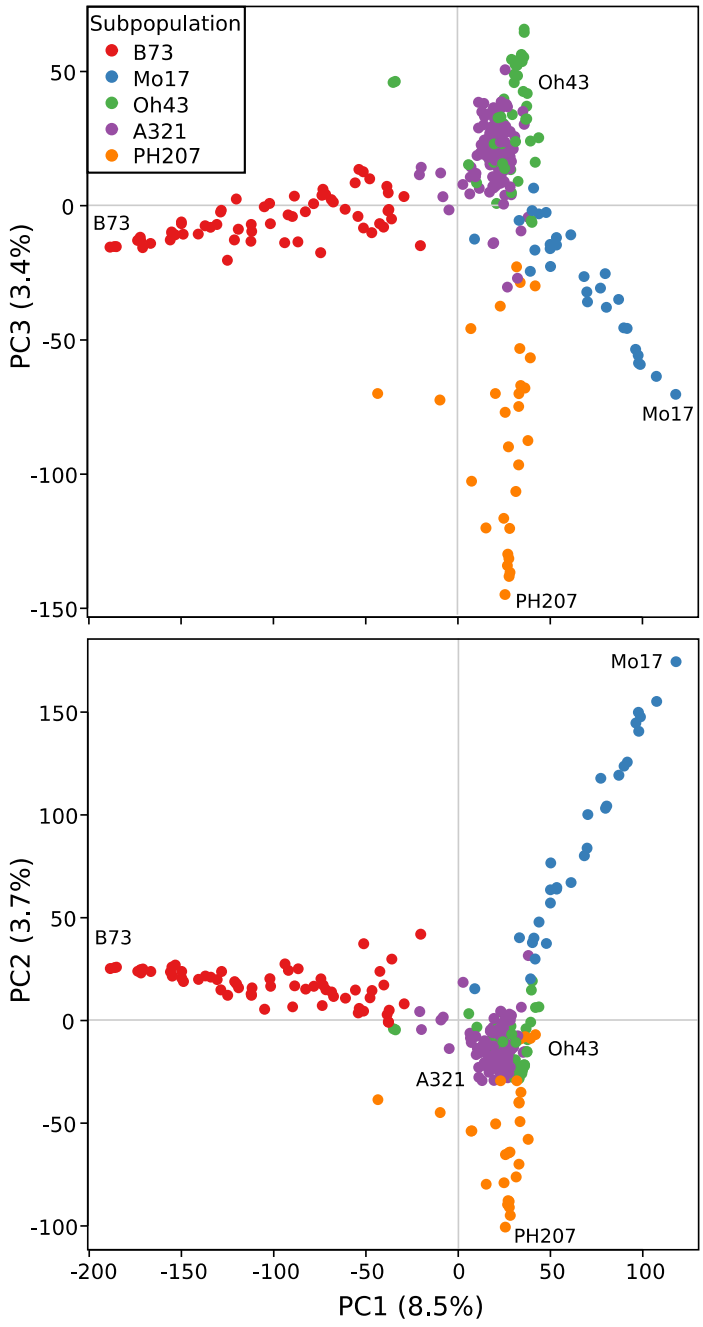

Figure 2: Principal components (PC) analysis of 283 maize inbreds genotyped with 43,252 single nucleotide polymorphism markers. The color of the points indicates the subpopulation membership as determined by model-based clustering; representative inbreds were labeled.

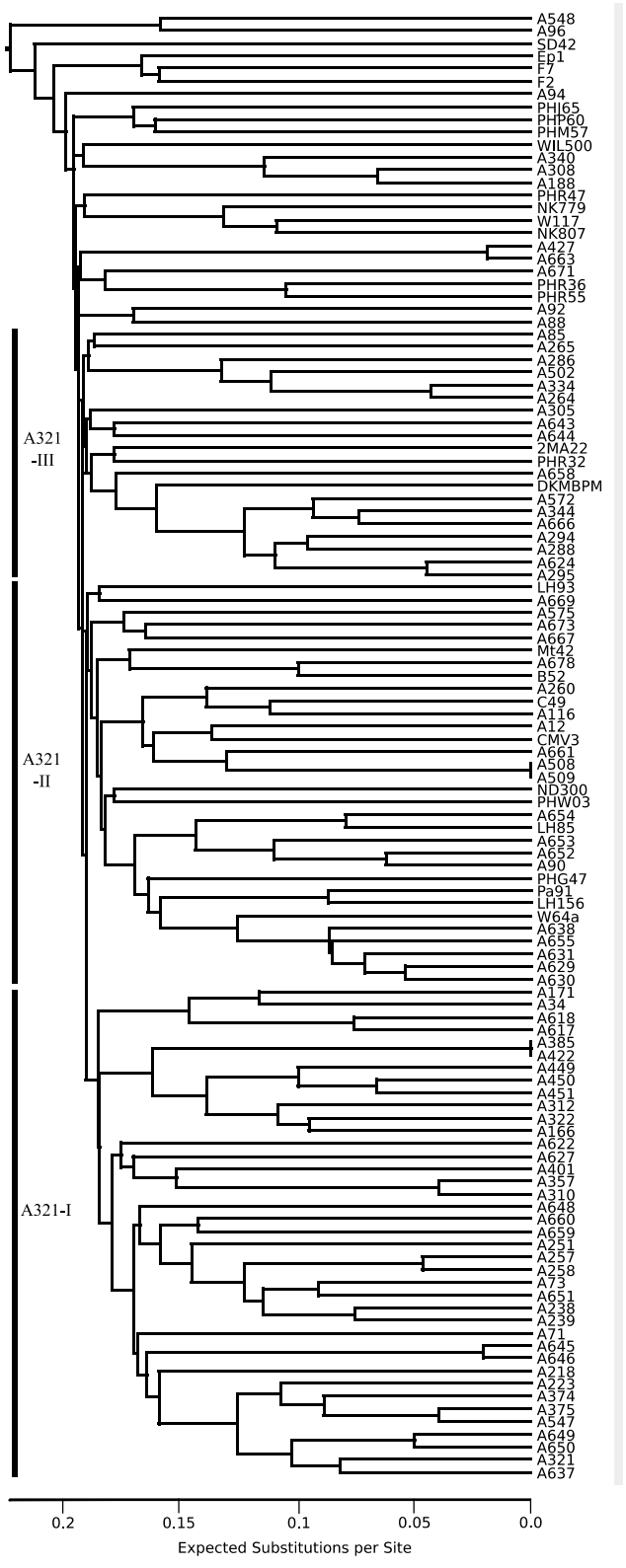
A548
A96
SD42
Ep1
F7
F2
A94
PHI65
PHP60
PHM57
WIL500
A340
A308
A188
PHR47
NK779
W117
NK807
A427
A663
A671
PHR36
PHR55
A92
A88
A85
A265
A286
A502
A334
A264
A305
A643
A644
2MA22
PHR32
A658
DKMBPM
A572
A344
A666
A294
A288
A624
A295
LH93
A669
A575
A673
A667
Mt42
A678
B52
A260
C49
A116
A12
CMV3
A661
A508
A509
ND300
PHW03
A654
LH85
A653
A652
A90
PHG47
Pa91
LH156
W64a
A638
A655
A631
A629
A630
A171
A34
A618
A617
A385
A422
A449
A450
A451
A312
A322
A166
A622
A627
A401
A357
A310
A648
A660
A659
A251
A257
A258
A73
A651
A238
A239
A71
A645
A646
A218
A223
A374
A375
A547
A649
A650
A321
A637
A321
-III
A321
-II
A321-I
0.2
0.15
0.1
0.05
0.0
Expected Substitutions per Site

Figure 3: Dendrogram of UPGMA cluster analysis of the A321 subpopulation using a dissimilarity matrix generated with TASSEL software. Three distinct clusters identified in the analysis by common branching in the dendrogram were marked with vertical bars.

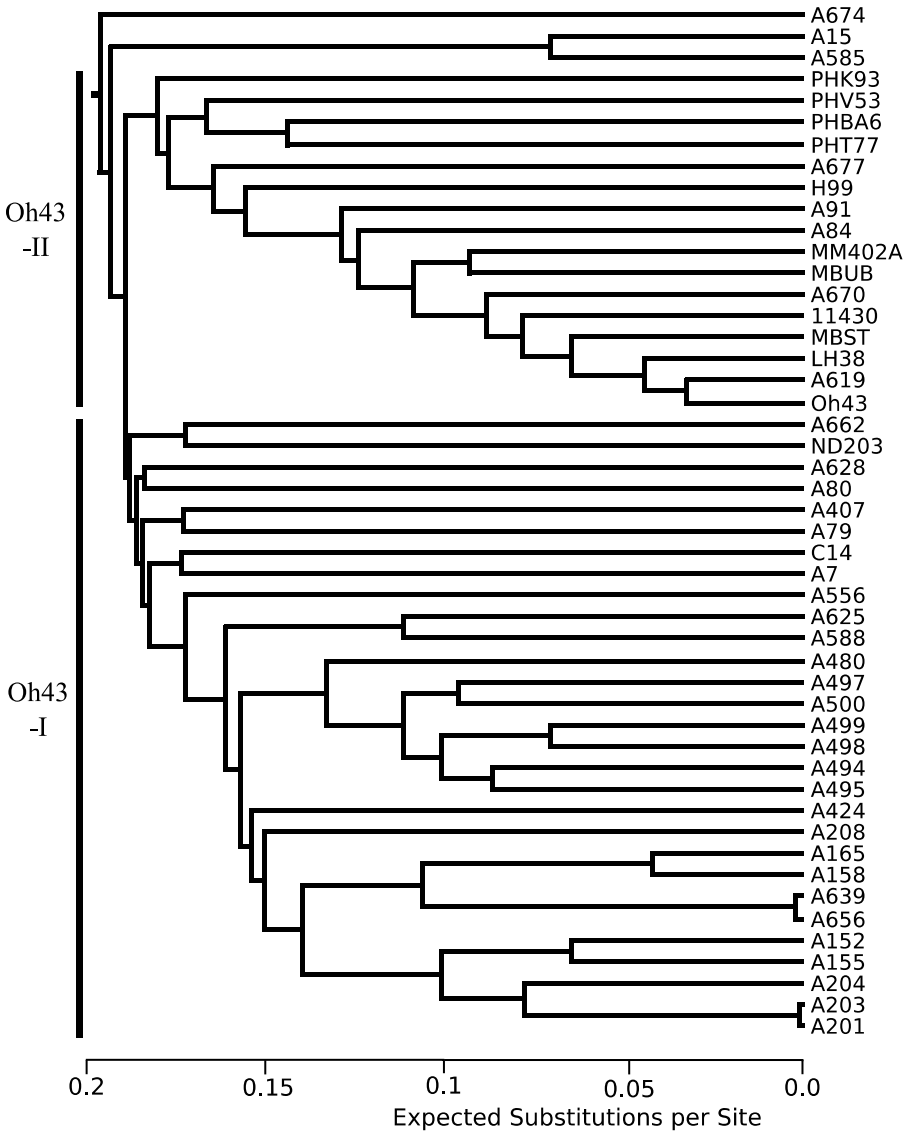

Figure 4: Dendrogram of UPGMA cluster analysis of the Oh43 subpopulation using dissimilarities generated with TASSEL software. Two distinct clusters identified in the analysis by common branching in the dendrogram were marked with vertical bars.

Chapter 2: Pollen control and spatial and temporal adjustment in evaluation of kernel composition of maize inbreds

Introduction

When a maize (*Zea mays* L.) plant is open pollinated, it produces seed fertilized by pollen from itself and from neighboring maize plants flowering concurrently. The xenia effect, which is the immediate effect of pollen on the developing kernel, has been implicated in kernel oil, protein, and starch concentration (East and Jones, 1920; Curtis et al., 1956; Letchworth and Lambert, 1998), kernel size (Leng, 1949), and kernel development (Pixley and Bjarnason, 1994; Seka and Cross, 1995; Bulant and Gallais, 1998). Double fertilization results in the embryo developing from equal contributions of the maternal and paternal genome, while the endosperm develops from the union of one sperm and two polar nuclei, increasing the influence of the maternal parent on endosperm characteristics (Kiesselbach, 1999).

Multiple studies have agreed that, when investigating oil concentration, entries should be self pollinated as both the maternal parent and pollen parent influence oil concentration (Miller and Brimhall, 1951; Curtis et al., 1956; Letchworth and Lambert, 1998). Large numbers of entries need to be evaluated across multiple environments in inbred development programs or in linkage mapping and association mapping studies to map quantitative trait loci (QTL). Experiments to map QTL for oil and protein concentration in maize have been conducted using only self-pollinated kernel samples (Goldman et al., 1993, 1994; Laurie et al., 2004; Clark et al., 2006; Wassom et al., 2008; Cook et al., 2012).

While previous studies have shown the effect of both male and female parents on kernel composition, most studies have included few entries and have not considered the impact of pollen source on the ranking of entries between open- and self-pollinated treatments (East and Jones, 1920; Curtis et al., 1956; Letchworth and Lambert, 1998). Also, previous studies have utilized germplasm previously selected for either protein or oil concentration instead of germplasm that is more representative of the variation in kernel composition traits in the U.S. Corn Belt (East and Jones, 1920; Miller and Brimhall, 1951; Curtis et al., 1956; Letchworth and Lambert, 1998). Furthermore, procedures for adjusting for spatial or temporal variation have been used for grain yield in maize (Brownie et al., 1993; Moreau et al., 1999) and in wheat (*Triticum aestivum* L.; Stroup et al., 1994), but their usefulness for kernel composition traits has not been studied. Therefore, our objectives were to (i) characterize the effect of pollen control on protein, oil, and starch concentrations in maize inbreds, (ii) determine the impact of open and self pollination on relative ranking of inbreds, and (iii) determine if spatial or temporal adjustments are useful for kernel composition when plants are open pollinated.

Materials and Methods

A collection of 30 maize inbreds were evaluated for kernel protein, oil, and starch concentrations in open- and self-pollinated treatments. The 30 inbreds included 18 publicly developed inbreds and 12 privately developed inbreds with expired U.S. Plant Variety Protection Act certificates. The inbreds used in this study were not chosen based on known kernel composition or known previous selection for kernel composition traits, nor did they contain known major genes modifying kernel traits. The 30 inbreds used

were as follows: 4N506, A7, A116, A239, A310, A385, A495, A632, A634, A639, A648, A654, A664, A674, B73, B84, DJ7, DKFAPW, DKMDF-13D, LH82, LH149, NK807, Oh43, Pa91, PHG47, PHG84, PHJ75, PHW17, W64a, and WIL900. Seed for most inbreds was provided by the USDA North Central Regional Plant Introduction Station at Ames, Iowa, USA.

The inbreds were evaluated at two planting dates in St. Paul, Minnesota, USA in summer 2011. The 14d difference between the two planting dates (16 May and 31 May 2011) permitted replication in time, which may influence the availability of pollen from the same plant and the extent of natural self- versus cross-pollination. The experiment for each planting date was conducted in a split-plot design with three replications. The two main-plot treatments were open pollination and self pollination and the subplot treatments were the 30 maize inbreds.

Each inbred was planted in a single row at a plant population density of 86,500 plants ha^{-1}. The plots were 4.72m long and spaced 0.76m apart. Border plots were planted around each replication with a balanced bulk of seed from 56 maize inbreds. In the open-pollinated treatment, all plots were allowed to open pollinate. In the self-pollinated treatment, ear shoots were covered prior to silk emergence and 10-12 plants were self pollinated. Ears from 6-8 plants within a row were hand harvested, bulked, and mechanically shelled. Whole kernel samples were scanned using a Perten DA 7200 near infrared reflectance analyzer (Springfield, Illinois, USA) and commercially available equations were used to predict oil, protein and starch concentrations. Concentrations were converted to a dry matter basis (g kg^{-1}). Analysis of variance (ANOVA) was conducted with pollination treatment and inbred as fixed effects and planting date and replication as

random effects using PROC GLM in SAS/STAT software (SAS Institute, 2009). To increase the power of the tests, the error sums of squares for the main plots and subplots were pooled when the corresponding mean squares were not significantly different at P = 0.25 (Carmer et al., 1969). Standard F-tests for combined split-plot experiments were conducted as outlined by McIntosh (1983). Least squares estimates of treatment means were calculated and Fisher's LSD (P = 0.05) was used for mean separation, where applicable.

In a separate field experiment, days to anthesis expressed as growing degree days (GDD) was recorded on the same 30 inbreds as part of a larger experiment grown in an adjacent section of the same field in St. Paul in summer 2011. This experiment was conducted in an augmented randomized complete block design with two replications and was planted on the same date (16 May 2011) as the first planting of the kernel composition experiment previously described. Identical crop management practices were applied to both experiments. An ANOVA was conducted and least squares means for inbreds were calculated using PROC GLM in SAS/STAT (SAS Institute, 2009). Least squares means for days to anthesis were used for developing covariates for kernel composition data.

Two methods were used to adjust kernel composition data in the open-pollinated treatment, one based on spatial distribution and the other on temporal distribution. The first method was a nearest neighbor adjustment based on the Papadakis method using two covariates (Wilkinson et al., 1983; Gezan et al., 2010). One covariate was the mean residual from two adjacent rows and the second covariate was the mean residual from two neighboring plots from the adjacent ranges. Border plots were assumed to have the

experiment mean for kernel composition traits and were included in the spatial adjustment calculation.

For the temporal adjustment, all plots within each replication that reached anthesis within 100 GDD of a given plot were averaged and used as a single covariate. An analysis of covariance was conducted for each method using the spatial or temporal covariates and least squares means were calculated using PROC GLM in SAS/STAT software (SAS Institute, 2009).

Simple (Pearson) correlations and Spearman rank correlations were calculated between least squares means of inbreds from the open- and self-pollinated treatments and the spatially and temporally adjusted data using PROC CORR in SAS software (SAS Institute, 2009). Fisher *z*-transformation was used to test the significance of differences among correlations. All comparisons were made in relation to the means of the self-pollinated treatment as these were assumed to be the more accurate estimates of kernel composition for a given inbred.

Results

The inbreds differed significantly in their oil concentration (Table 4), with inbred means ranging from 38 to 59 g kg^{-1} in both the open and self-pollinated treatments (Figure 5). However, effects of pollination treatment and the interaction between pollination treatment and inbred were not significant (Table 4). Rank changes among inbreds between open and self-pollinated treatments for oil concentration were minimal, with simple and rank correlations of 0.93 ($P < 0.001$; Table 5). Simple and rank correlations between adjusted and self-pollinated least squares means were 0.93 for the

spatial adjustment and 0.91–0.92 for the temporal adjustment ($P < 0.001$; Table 5). No significant difference was found among simple and rank correlations. Temporal adjustments were based on flowering date, and the mean difference between the earliest-flowering inbred (A495) and the latest-flowering inbred (PHG84) was 484 GDD (approximately 18 calendar days). The number of plots used in the each temporal adjustment ranged from 2 to 15.

Inbred, planting date by pollination treatment interaction, planting date by inbred interaction, and pollination treatment by inbred interaction significantly affected protein concentration (Table 4). Protein concentration among inbreds ranged from 93 to 158 g kg^{-1} in the open-pollinated treatment and from 101 to 173 g kg^{-1} in the self-pollinated treatment (Figure 5). The difference between means of the open and self-pollinated treatments for protein concentration was 6 g kg^{-1} for the first planting date and 12 g kg^{-1} for the second planting date. Three inbreds (A7, A310, and LH149) had significantly higher protein concentration in the self-pollinated treatment than in the open-pollinated treatment (Figure 5). The rank correlation for protein concentration between pollination treatments was 0.83 ($P < 0.001$; Table 5). Rank changes among inbreds between open and self-pollinated treatments were minimal with the exception of inbred A310, which moved 20 positions between pollination treatments. Rank correlations between adjusted and self-pollinated least squares means for protein concentration were 0.83 for the spatial adjustment and 0.84 for the temporal adjustment ($P < 0.001$; Table 5). The corresponding simple correlations were 0.85. No significant difference was found among simple and rank correlations.

Inbred, planting date by inbred interaction, and planting date by pollination treatment by inbred interaction significantly affected starch concentration (Table 4), with inbred means ranging from 639 to 736 g kg^{-1} in the open-pollinated treatment and from 637 to 721 g kg^{-1} in the self-pollinated treatment (Figure 5). The rank correlation between pollination treatments for starch concentration was 0.73 ($P < 0.001$; Table 5). Rank changes among inbreds were more erratic for starch concentration than for oil or protein concentration. Rank correlations between adjusted and self-pollinated least squares means for protein concentration were 0.75 for the spatial adjustment and 0.73 for the temporal adjustment ($P < 0.001$; Table 5). The corresponding simple correlations were 0.80–0.82. No difference was found among simple and rank correlations.

Discussion

Three primary conclusions were made from this study. First, method of pollination did not influence protein, oil, or starch concentrations. Second, high correlations between open and self-pollination treatments indicated that open-pollinated evaluations would be sufficient when screening a large number of inbreds for oil, protein, and starch concentrations for the purpose of selection. Third, neither spatial nor temporal adjustments improved estimates of open- pollinated kernel composition over unadjusted, open-pollinated means.

When the purpose of the experiment is to determine the actual kernel composition of inbreds (instead of the relative performance of inbreds), open versus self pollination must not have an effect on the mean concentration. Pollination treatment did not significantly affect oil, protein, or starch concentrations among the 30 maize inbreds in

this study, and this finding conflicted with previous research. In a study using commercial hybrids and hybrids selected for protein content, mean oil and starch concentrations were significantly greater in the open pollinated treatment, and protein concentration was significantly greater in the self-pollinated treatment (Letchworth and Lambert, 1998). In studies utilizing inbreds and populations derived from the Illinois long-term selection experiment, the pollen parent was found to influence oil and protein concentrations (Miller and Brimhall, 1951; Curtis et al., 1956). For example, oil concentration increased from 42 g kg^{-1} with a low oil pollen parent to 72 g kg^{-1} with a high oil pollen parent (Curtis et al., 1956). The direct comparison of the findings of the present study and those of Miller and Brimhall (1951) and Curtis et al. (1956) was confounded by the genetic background of the germplasm studied.

When the purpose of the experiment is to rank and select the best inbreds for kernel composition, pollination treatment by inbred interaction as well as rank changes between pollination treatments must be minimal. Pollination treatment by inbred interaction was significant only for protein concentration. Three inbreds (A7, A310, and LH149) had significant differences between open- and self-pollinated treatments, with all three inbreds having higher protein concentrations in the self-pollinated treatment (Figure 5). However, the simple and rank correlations between open and self-pollinated treatments were high for protein concentration (0.83–0.85; Table 5), indicating that selection for protein concentration can be done in open-pollinated experiments. This result supports previous research that found the female parent to have a much greater effect on protein concentration compared to the pollen parent (Letchworth and Lambert, 1998). Similarly, high simple and rank correlations for oil (0.93) and starch (0.73–0.82)

concentrations between open- and self-pollinated treatments indicated that selection for these traits can be done in open-pollinated experiments (Table 5).

Spatial adjustment by nearest neighbor analysis has been shown to effectively account for plot-to-plot variation for grain yield in maize (Brownie et al., 1993; Moreau et al., 1999) and in wheat (Stroup et al., 1994). In open-pollinated evaluations of kernel composition, pollen from adjacent plots is very likely to land on receptive silks of the plot of interest. Temporal adjustment of kernel composition based on relative days to anthesis was also of interest as only inbreds flowering concurrently can influence kernel composition of a given plot. However, neither spatial adjustment nor temporal adjustment increased the simple or rank correlations between pollination treatments (Table 5). The range of 100 GGD, equivalent to about 4 calendar days during the time of flowering (data not shown), was used in estimating the temporal covariate as it is a reasonable timeframe in which airborne pollen may land on receptive silks in the plot of interest.

In this study, planting date was found to affect protein and starch concentrations but not oil concentration (Table 4). While our experiments were limited to two planting dates at the same location and a previous study (Bulant and Gallais, 1998) indicated that xenia effects were subject to genotype by environment interaction, this previous study also showed that xenia effects were repeatable across environments. The interaction of planting date with inbred was also significant for protein and starch concentrations in the present study (Table 4). These results support previous research showing a significant genotype by environment interaction for protein and starch concentration but not for oil concentration (Berke and Rocheford, 1995). Our results as well as previous studies

indicate the importance of conducting kernel composition experiments in more than one environment.

Overall, our results showed that maize inbreds can be evaluated for oil, protein, and starch concentrations without the pollen source confounding differences among entries when relative performance of inbreds is more critical than absolute concentrations. Spatial and temporal adjustments were not useful for kernel composition. We note that all inbreds in our experiment were of temperate background, and our conclusions may not necessarily apply to other germplasm (e.g., tropical inbreds, landraces, sweet corn, etc.) with different kernel characteristics. Further experiments with larger numbers of temperate inbreds, with other types of germplasm, and with diverse environments would be helpful. Nevertheless, modern genetic methodologies such as genomewide association analysis (Zhu et al., 2008; Yan et al., 2011) and large scale selection experiments in temperate maize require the evaluation of large numbers of entries where absolute kernel composition estimations are not necessary and reducing labor requirements is of interest. Our results suggest that open pollination of the entries would be adequate in such situations.

Table 4: Mean squares (MS) and significance of effects from analyses of variance for oil, protein, and starch concentration for open- and self-pollinated treatments of 30 maize inbreds evaluated at two planting dates in St. Paul, Minnesota, USA in summer 2011.

	df	Oil MS	Protein MS	Starch MS
Planting date	1	116	4315*	8591*
Replication/planting date	4	51*	211*	919*
Pollination treatment	1	71	8029	20971
Planting date × pollination treatment	1	27	551*	414
Inbred	29	358*	2761*	3890*
Planting date × inbred	29	9	184*	238*
Pollination treatment × inbred	29	15	232*	395
Planting date × pollination treatment × inbred	29	13	111*	257*
Pooled error	230	9	43	107

* Significant at P = 0.05

Table 5: Simple and rank correlations of open-pollinated inbred means (unadjusted or after spatial and temporal adjustment) with self-pollinated inbred means for oil, protein, and starch concentrations. All correlations were significantly different from zero ($P < 0.001$).

Adjustment method	Oil		Protein		Starch	
	Simple	Rank	Simple	Rank	Simple	Rank
Unadjusted	0.93	0.93	0.85	0.83	0.82	0.73
Spatial	0.93	0.93	0.85	0.83	0.82	0.75
Temporal	0.91	0.92	0.85	0.84	0.80	0.73

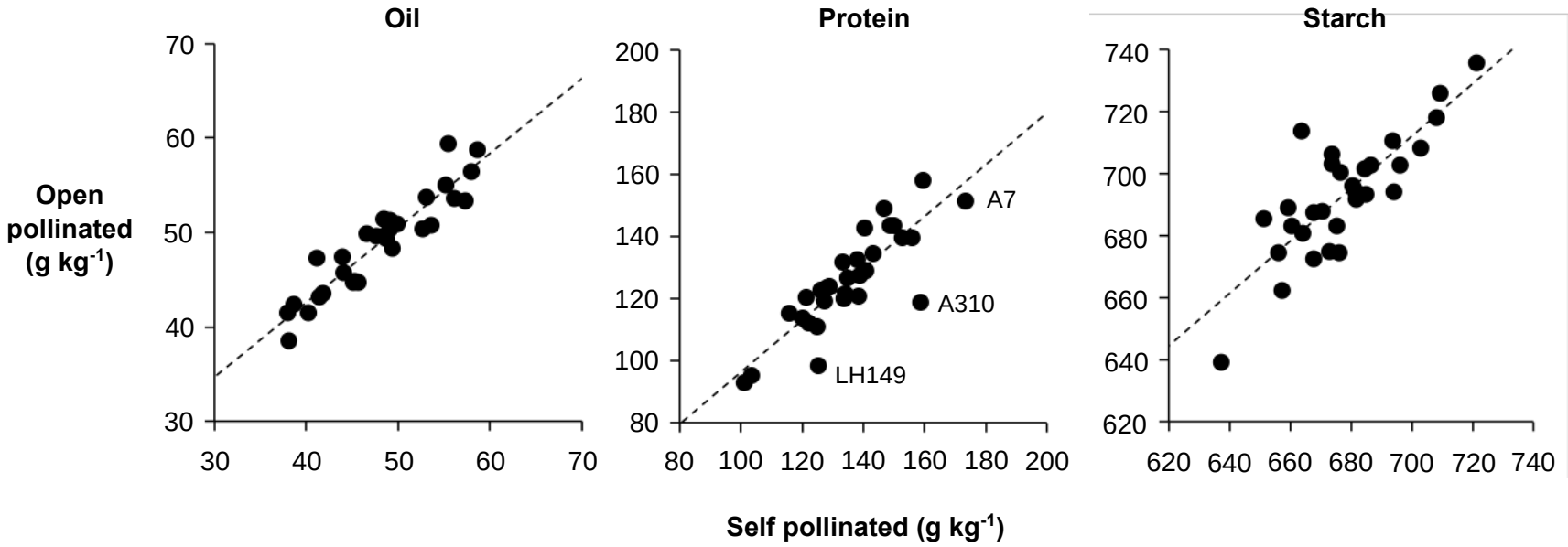

Figure 5: Means of 30 maize inbreds for kernel composition in open-pollinated and self-pollinated treatments. Inbreds that significantly differed between pollination treatments (P = 0.05) are labeled and the dashed lines represent the simple regression lines.

Chapter 3: Genomewide association mapping of flowering time, kernel composition, and disease resistance in historical Minnesota maize inbreds

Introduction

The appropriate strategies for marker-assisted selection depend on the genetic architecture of the trait of interest (Bernardo, 2008). For highly complex traits (e.g., grain yield) that are controlled by many loci of small effect, a prediction-based approach such as genomewide selection is appropriate (Bernardo and Yu, 2007; Lorenz et al., 2011). For less complex traits for which major genes or major quantitative trait loci (QTL) are likely present, an introgression approach has been found useful (Anderson et al., 2007; Neeraja et al., 2007). Major genes or QTL can be exploited by (i) identifying a unique germplasm source with the trait of interest, (ii) mapping major QTL, (iii) validating the effects of major QTL effects in diverse genetic backgrounds, and (iv) introgressing one or a few QTL into elite breeding germplasm (Bernardo, 2008). In maize (*Zea mays* L.), major loci have been found for days to flowering (e.g., *Vgt1* and *Dwarf8*; Thornsberry et al., 2001; Salvi et al., 2007), kernel composition (e.g., *DGAT1-2*; Zheng et al., 2008), and disease resistance (e.g., *Ht1*, *Ht2*, and *Htn1*; Bentolila et al., 1991; Simcox and Bennetzen, 1993; Chung et al., 2010).

Association mapping has been useful in identifying major QTL in maize (Thornsberry et al., 2001; Beló et al., 2008; Van Inghelandt et al., 2012). Highly diverse inbred panels, including both exotic and adapted germplasm, have been utilized in many of the association mapping studies in maize (Thornsberry et al., 2001; Flint-Garcia et al., 2005; Yan et al., 2009; Cook et al., 2012). However, introgressing QTL from highly

diverse germplasm (e.g., tropical inbreds) or specialized germplasm (e.g., Illinois high oil strains) can be difficult and time consuming due to unfavorable linkages and large deficiencies in agronomic performance (Crossa et al., 1987; Goodman, 2005; Zheng et al., 2008). Other association mapping panels have been developed to encompass the genetic diversity within a restricted phenology (Hansey et al., 2011) or to explore variation in elite breeding material (Beló et al., 2008; Van Inghelandt et al., 2012).

Historical inbreds that represent unique germplasm groups are a potential source of major QTL, and from which introgression would be easier due to the closer genetic relationship and agronomic similarity with elite germplasm. To our knowledge, however, association mapping has not been used to explore allelic variation in historical inbred collections from within a breeding program. In a previous study, we examined the population structure of historical inbreds developed at the University of Minnesota along with inbreds developed in other breeding programs (Chapter 1). We found that 60% of the Minnesota inbreds belonged to the A321 genetic group and were different from the B73, Mo17, Oh43, A321, and PH207 genetic backgrounds represented by the other inbreds studied.

The Minnesota inbreds therefore might have major QTL alleles that would be useful in breeding. Our objectives in this study were to (i) characterize genomewide linkage disequilibrium in a collection of historical Minnesota and non-Minnesota inbreds; (ii) assess the variation in this inbred collection for flowering time, kernel composition, northern corn leaf blight, and Goss's wilt and blight; and (iii) identify major QTL for these traits by genomewide association mapping.

Materials and Methods

Plant material

The collection of 284 historical inbreds used in this study included 143 A inbreds (developed at the University of Minnesota), 26 publicly developed inbreds from different programs, and 115 privately developed inbreds with expired U.S. Plant Variety Protection Act status (ex-PVPA; Chapter 1). Seed for many of the public and all of the private inbreds was provided by the USDA North Central Regional Plant Introduction Station at Ames, IA, with the remaining inbreds being available from the University of Minnesota germplasm collection.

Genotyping and linkage disequilibrium

Leaf tissue samples were collected from a single plant of each inbred in summer 2011 and were sent to DNA LandMarks (Saint-Jean-sur-Richelieu, Quebec) for DNA extraction and marker analysis. Markers were assayed using the Maize SNP50 Beadchip (Illumina, San Diego, CA), containing 56,110 single nucleotide polymorphism (SNP) markers (Ganal et al., 2011). Physical positions of marker loci were obtained from the B73 Ref Gen_v1 reference sequence (Schnable et al., 2009). Replicated assays indicated the genotyping error rate to be less than 0.01%. Inbred BCC03 was removed prior to any further analysis due to missing allele calls at more than 15% of the loci. Markers with a minor allele frequency less than 7% or with more than 10% of missing genotype information were removed prior to further analysis to reduce the potential of including allele-calling errors. Additionally, all markers with unknown physical position were removed, leaving a total of 39,166 SNP markers.

Linkage disequilibrium (LD) was estimated, with HAPLOVIEW v4.0 (Barrett et al., 2005), as the squared allele-frequency correlation (r^2) for all marker pairs on a per chromosome basis. The decay of LD with physical distance was characterized by non-linear regression in R software (R Core Development Team, 2012) given the predicted r^2 values (Hill and Weir, 1988). Mean r^2 between adjacent markers was calculated using TASSEL v3 (Bradbury et al., 2007).

Flowering, height, and kernel composition

The inbreds were evaluated for flowering time, plant and ear height, and kernel composition at six locations across Minnesota in 2011 and 2012. Experiments were planted on 16 May at St. Paul, 18 May at Rosemount, 27 May at Waseca, 1 June at Lamberton, and 18 May at Morris, MN in 2011 and 14 May at St. Paul, MN in 2012. Inbreds were evaluated in single-row plots arranged in an augmented randomized complete block design, with two replications per location. Within a replication, inbreds were divided into four sets, each containing 69-70 experimental inbreds and five check inbreds (A619, A81, B73, Mo17, and PHG80). Plots were 4.72m long and spaced 0.76m apart, and were planted at a target density of 86,500 plants ha^{-1}.

Days to anthesis and days to silking were measured as the number of growing degree days (GDD) from planting to when 50% of the plants within the row were shedding pollen (anthesis) or extruding silks (silking). The accumulation of GDD was calculated as GDD = (T_{max} + T_{min} / 2) - 10° C, where T_{max} was the maximum daily temperature (≤ 30° C), and T_{min} was the minimum daily temperature (≥ 10° C). Days to anthesis and days to silking were measured only in St. Paul, Rosemount, and Waseca in 2011 and in St. Paul in 2012. Plant and ear height (cm) were measured on a whole plot

basis as the distance from the soil surface to the collar of the flag leaf (plant height) and of the ear leaf (ear height).

A separate study with a subset of the same inbreds indicated that kernel composition can be assessed reliably even with open-pollination (Chapter 2), and all plots were open pollinated. Plots were harvested mechanically (Rosemount, Waseca, Lamberton, and Morris locations) or by hand (St. Paul, MN in 2011 and 2012). In plots that were mechanically harvested, the entire row was harvested and a subsample was taken during harvesting. In plots that were hand harvested, 8-10 ears were harvested, bulked, mechanically shelled, and subsampled. Whole kernel samples were dried and were scanned using a Perten DA 7200 (Springfield, IL) near infrared reflectance analyzer. Oil, protein and starch concentrations were predicted using commercially available equations. Raw data were converted to a dry matter basis (g kg^{-1}).

The five replicated inbred checks were used to adjust for set effects within each replication by adjusting raw data by the difference between the mean of the inbred checks and the mean of the replication. Analysis of variance (ANOVA) was conducted and least squares means were calculated to account for replication and location effects using PROC GLM in SAS/STAT software (SAS Institute, 2009). Least squares means of inbreds across environments were used in the subsequent association mapping.

Northern corn leaf blight

The inbreds were evaluated for resistance to northern corn leaf blight (NCLB) in two locations in 2011 and 2012. In 2011, this experiment was conducted using a completely randomized design with one replication and was planted on 19 May at Kenyon, MN, in cooperation with AgReliant Genetics. In 2012, this experiment was

conducted at St. Paul, MN using a randomized complete block design with two replications and was planted on 14 May 2012. Both experiments had single-row plots, each 1.5m long and 0.76m apart, that were planted at a target density of 10 plants plot^{-1} or 87,700 plants ha^{-1}. Five inbreds were used as checks (Oh43 and Mo17 [intermediate]; A619, A632, and B73 [susceptible]; Carson, 1995a and 1995b; Poland et al., 2011).

Inoculations were performed using a balanced blend of *Setosphaeria turcica* conidial spores from race 1 and race 2 isolates provided in 2011 by Professional Seed Research (Sugar Grove, IL) and in 2012 by the laboratory of Dr. Carl Bradley (Univ. of IL; race 1) and Professional Seed Research (race 2). A conidial suspension of *S. turcica* was prepared as directed by Professional Seed Research, blending one 100mm petri dish of prepared culture of each race per 11.4 L of tap water. All plants within a row were inoculated by applying approximately 10ml of the prepared spore suspension into the whorl at the V4-V5 leaf stage (30 June) in 2011 and V6-V8 leaf stage (26 June) in 2012.

Resistance to NCLB was characterized by latent period (LP) and diseased leaf area. Latent period was measured on a whole-plot basis as the number of days from inoculation to when lesions, characteristic of NCLB, were present on at least 50% of the plants within a row. Diseased leaf area was estimated on a whole plot basis as the percentage of the total leaf area covered by NCLB lesions. Diseased leaf area was estimated four times in 2011 and three times in 2012 at ~10 d intervals beginning when inbred B73 reached anthesis. Diseased leaf area measurements were used to calculate the standardized area under the disease progress curve (sAUDPC), standardized by the time interval in which measurements were taken, as $sAUDPC = \sum_{i=1}^{j-1}((x_{i+1} + x_i)/2 \times (t_{i+1} - t_i))]/(t_j - t_1)$, where x_i was the diseased leaf area estimated at the *i*th

observation and t_i was the day at which the ith observation was taken, with i = 1 to j observations (Wisser et al., 2008). Data for both latent period and sAUDPC were skewed right and were therefore log transformed to normalize the trait distribution and equalize the distribution of residuals prior to further analysis. ANOVA was conducted with data combined across experiments and least squares means were estimated using PROC GLM in SAS/STAT software (SAS Institute, 2009).

Goss's wilt and blight

The inbreds were evaluated for resistance to Goss's wilt and blight (GWB) in summer 2012. This experiment was conducted in a randomized complete block design with two replications at UMore Park in Rosemount, MN and was planted on 15 May 2012. Plots consisted of single rows 1.5m long and 0.76m apart; plots were planted at a target density of 10 plants $plot^{-1}$ or 87,700 plants ha^{-1}. Ten inbreds (A662, H99, and Mo17 [resistant]; A619 and B73 [intermediate]; A632, A634, A654, A665, and B14 [susceptible]) were duplicated within replications as checks (Treat et al., 1990 and Ngong-Nassah et al., 1992).

Inoculations were made using ED1-11A, a *Clavibacter michiganensis* susp. *nebraskensis* strain isolated from infected maize tissue collected from a nearby field in 2011 (provided by the laboratory of Dr. Dean Malvick, University of Minnesota). When most plots had reached the V8 leaf stage (2 July 2011), the three uppermost fully-expanded leaves of each plant within a row were inoculated using a suspension of approximately 1×10^8 colony forming units ml^{-1} in a 0.85% NaCl buffer. The pin-prick inoculation method was employed using a wooden clapper with a block of small nails on

one side of the clapper and a sponge attached to the opposite side of the clapper (Calub et al., 1974).

Phenotypic data were recorded for diseased leaf area of the uppermost-inoculated leaf, as the percentage (0-100) of the leaf exhibiting GWB lesions. Diseased leaf area was estimated on a whole plot basis four weeks (30 July) and six weeks (13 August) after inoculation; the mean of the two ratings was used for subsequent analyses. Diseased leaf area data were skewed to the right and residual values were not evenly distributed, therefore a square root transformation was used to scale the raw data. ANOVA was conducted and least squares means of inbreds were calculated across replications using PROC GLM in SAS/STAT software (SAS Institute, 2009).

Variation due to inbreds and subpopulations

Heritability was undefined because the inbreds were not members of the same random-mating population. We instead estimated the proportion of the phenotypic variance (V_P) that was due to the effects of inbreds, i.e., R^2_{Inb}. The value of R^2_{Inb} for each trait was estimated as $[\Sigma\tau_i^2/(N-1)]/V_P$, where τ_i was the effect of the *i*th inbred, N was the number of inbreds, and the V_P for the trait was on an inbred-mean basis. The values of $\Sigma\tau_i^2/(N-1)$ and of V_P were estimated using PROC MIXED in SAS/STAT software (SAS Institute, 2009).

The effect of substructure on the inbred means was determined with a general linear model with the inbred means as the dependent variable and four out of five subpopulation membership coefficients as fixed independent variables. The R^2 due to subpopulation effects (referred to as R^2_{Pop}) was calculated using PROC GLM in SAS/STAT (SAS Institute, 2009).

Genomewide association mapping

The QK model (Yu et al., 2006) is widely used in association mapping studies in plants. A recent study (Bernardo, 2013) showed that the G model, which accounts for QTL effects on background chromosomes through genomewide markers instead of kinship, is superior to the QK model. In particular, adherence to the nominal significance level and the power to detect QTL is better with the G model than with the QK model (Bernardo, 2013). Preliminary analysis of our data in the current study (results not shown) indicated that the number of markers found significant for each trait was indeed much lower with the QK model than with the G model. We therefore used the G model as described by Bernardo (2013).

To reduce multicolinearity among markers, markers were removed prior to association analysis based on pairwise $r^2 > 0.9$ within a sliding window of 50 markers using PLINK software (Purcell et al., 2007), leaving a total of 28,626 SNP markers used in the G model analysis. The G model as implemented in this study had three steps. In the first step, marker effects were estimated for all markers by ridge regression-best linear unbiased prediction in the rrBLUP package in R (Endelman, 2011; R Core Development Team, 2012).

In the second step, association analysis was conducted on a chromosome-by-chromosome basis after adjusting for genomewide marker effects across the chromosome not being tested for marker-QTL associations (Bernardo, 2013). To test for QTL on chromosome 1, single-marker regression on this chromosome was initially conducted and was followed by multiple regression by backward elimination. Single-marker regression was needed to prevent overfitting in multiple regression, i.e., ensure that the number of

markers on a chromosome did not exceed the total number of inbreds. Markers were ranked based on the *p*-values from single-marker analysis, and the 200 markers with the lowest *p*-value were included in the subsequent multiple regression analysis. This process was repeated for chromosomes 2 to 10. In multiple regression, we used a Bonferroni-adjusted significance level that corresponded to an experiment-wise significance level of $P = 0.01$.

In the third step, multiple regression was conducted to estimate coefficients for markers identified in the second step, using the unadjusted phenotypic data as the dependent variable. The third step was implemented only for estimating marker effects and not for determining significance. The proportion of the phenotypic variation explained by the simultaneous fit of all significant markers (R^2_{SNP}) was calculated. All steps in the G model analysis were implemented in R software (R Core Development Team, 2012).

Results

Phenotypic analysis

Days to anthesis among the 276 inbreds (some inbreds had missing data) had a mean of 1421 GDD and range of 1094 to 1788 GDD (Table 7). Days to silking had a mean of 1464 GDD and range of 1105 to 1807 GDD across the inbred collection (Table 7). The A321 and Oh43 subpopulations had fewer days to anthesis and days to silking than the B73, Mo17 and PH207 subpopulations. In addition, the B73 and Mo17 subpopulations had more days to silking than the PH207 subpopulation. The A321

subpopulation had the lowest minimum days to anthesis (1094 for inbred F2) and the highest maximum days to anthesis (1788 for inbred PHJ65).

Plant height had a mean of 148 cm and range of 91 to 208 cm, whereas ear height had a mean of 62 cm and range of 30 to 99 cm (Table 7). The A321 subpopulation had a lower mean plant height than the B73, Mo17 and PH207 subpopulations, and the A321 subpopulation had the greatest range in plant heights (91 for inbred F7 to 207 cm for inbred PHJ65). The PH207 subpopulation had the lowest mean ear height and the B73 and Mo17 subpopulations had higher mean ear heights than the A321, Oh43, and PH207 subpopulations.

Kernel composition traits ranged from inbred means of 38 to 64 g kg^{-1} for oil, 97 to 175 g kg^{-1} for protein, and 640 to 775 g kg^{-1} for starch concentrations. Mean oil concentration was 47 g kg^{-1}, protein concentration was 129 g kg^{-1}, and starch concentration was 726 g kg^{-1} (Table 7). The PH207 subpopulation had lower mean oil concentration than all other subpopulations and the Oh43 and A321 subpopulations had higher oil concentration than all other subpopulations. The A321 subpopulation had the greatest range in oil concentration, ranging from 38 (inbred A655) to 64 g kg^{-1} (inbred WIL500). The B73, Mo17 and PH207 subpopulations had lower mean protein concentrations than the A321 and Oh43 subpopulations. Mean starch concentration was lower in the Oh43 and A321 subpopulations than the B73 and PH207 subpopulations. The B73 subpopulation had higher starch concentration than all other subpopulations.

Resistance to NCLB as measured by the sAUDPC (lower values indicate greater resistance) ranged from 1.0 to 66.1 across inbreds, with a mean of 7.4 (Table 7). Resistance to NCLB as measured by latent period ranged from 7.0 to 33.9 d across

inbreds, with a mean of 14.1 d. The Mo17 subpopulation had lower sAUDPC and higher latent period than all other subpopulations. The Oh43 and A321 subpopulations had higher mean sAUDPC than all other subpopulations and the B73 subpopulation had a shorter latent period than the PH207 and Mo17 subpopulations.

Resistance to GWB, measured as diseased leaf area, ranged from 0.4 to 97.5% across all inbreds, with a mean of 28.8 %. The Mo17 subpopulation had the lowest GWB diseased leaf area whereas the A321 and Oh43 subpopulations showed the highest diseased leaf area.

The proportion of the phenotypic variation due to inbreds, R^2_{Inb}, was high for all traits except latent period of NCLB (R^2_{Inb} = 0.13), while the range for all other traits was from 0.87 for diseased leaf area of GWB to 0.99 for days to anthesis (Table 7). Population substructure had a significant effect on each trait, with R^2_{Pop} from 0.13 for diseased leaf area of GWB to 0.23 for protein concentration (Table 7).

LD decay

The physical distance at which LD decayed (r^2=0.1) among chromosomes ranged from 529 kb for chromosome 2 to 1419 kb for chromosome 10, with a mean distance to LD decay across chromosomes of 802 kb (Table 6). Mean r^2 between adjacent markers among chromosomes ranged from 0.35 for chromosome 9 to 0.39 for chromosome 4, with a mean of 0.38 across chromosomes (Table 6).

Association mapping

Genomewide association analysis via the G model revealed significant marker-trait associations (P = 0.01, pre-Bonferroni correction) for days to anthesis (8 SNPs), days to silking (11 SNPs), oil concentration (11 SNPs), starch concentration (2 SNPs),

sAUDPC of NCLB (13 SNPs), and diseased leaf area of GWB (9 SNPs; Table 8). The proportion of phenotypic variation explained by significant markers (R^2_{SNP}) was moderate for starch concentration (0.24), and high for days to anthesis (0.44), days to silking (0.61), oil concentration (0.47), sAUDPC for NCLB (0.55), and diseased leaf area for GWB (0.47; Table 8). None of the SNP markers had a significant effect on plant height, ear height, protein concentration, or latent period of NCLB.

The frequency of the favorable QTL alleles had a mean of 0.47 and ranged from 0 to 1 among subpopulations and from 0.04 to 0.99 among developer groups (Table 9). The A321 subpopulation had higher favorable allele frequencies (P = 0.05) than the other subpopulations at two QTL, one for days to silking (PZE-103078773) and one for oil concentration (PZE-104123457). The favorable QTL allele frequency differed between A inbreds and non-A inbreds for 38 of the 54 QTL (Table 9).

Discussion

Association mapping in historical inbreds

We detected major QTL for flowering time, kernel composition, and disease resistance among the historical inbreds—mostly developed at the University of Minnesota from the 1910s to the 1980s—that we studied. Some of the marker-trait associations were in regions with previously identified major genes and QTL "hot-spots" whereas other associations were novel. More broadly, our results support the utilization genomewide association mapping in historical inbred collections as a method to identify and mine allelic variation for use in modern maize breeding programs.

Differences among inbred means accounted for a large part of the phenotypic variation for all traits (R^2_{Inb} = 0.87–0.99) except NCLB latent period (R^2_{Inb} = 0.13), thereby facilitating the detection of marker-trait associations for most of the traits studied. However, QTL for plant height, ear height, or protein concentration were not detected.

QTL for days to flowering

Out of the 8 significant QTL for days to anthesis, two associations were found in bin 8.05, with one of the markers near 134 Mbp (PZE-108079256) being in close proximity to *Vgt1*, a major gene shown to regulate flowering time in maize (Salvi et al., 2007). Overall, the total number of marker-trait associations found in this study fit well within the range of the number of QTL for flowering time commonly identified in mapping studies (Salvi et al., 2009). In addition, four out of the eight associations from this study were within previously identified QTL hot spots for flowering time in bins 8.03, 8.05, 9.04, and 10.04 (Chardon et al., 2004).

None of the marker-trait associations found in this study corresponded with the region containing *Dwarf8* (bin 1.10), which has been associated with flowering time in a previous association mapping study (Thornsberry et al., 2001). The lack of association in this region was consistent with other studies using elite European germplasm, for which the lack of association with *Dwarf8* was likely due to a lack of variation at the *Dwarf8* locus in the germplasm studied (Andersen et al., 2005; Van Inghelandt et al., 2012). In addition, no associations were identified near either the *ZFL1* and *ZFL2* genes, which have previously been associated with flowering time (Chardon et al., 2004; Buckler et al., 2009).

QTL for kernel oil and starch concentration

The QTL for oil concentration found in bin 6.04 (PZE-106054182; ~105Mbp) was within the *DGAT1-2* gene, a known locus regulating oil concentration (Zheng et al., 2008). This marker was found to have a large effect in our study, with the effect of the major allele being –1.23 (g kg^{-1}; Table 7). This genomic region was also found to affect oil concentration in the maize nested association mapping population (Cook et al, 2012). One marker (PZE-104123457) in bin 4.09 was associated with decreased oil concentration and increased starch concentration (Table 8). This marker-trait association represents a potentially novel QTL, as this region has not been previously associated with either oil or starch concentration. On the other hand, the lack of significant markers associated with protein concentration may be partially explained by differences in the complexity of the genetic architecture of the kernel composition traits, as oil concentration is thought to be controlled by fewer loci (14-69) compared to protein concentration (102-178; Moose et al., 2004).

To eliminate the influence of the xenia effect, previous QTL mapping studies of kernel composition traits have used self-pollinated ears. In contrast, open-pollinated ears were analyzed in the present study. The xenia effect, or the immediate effect of pollen on a developing kernel, has been shown to influence the actual (as opposed to relative) concentrations of oil, protein, and starch in maize kernels (Curtis et al., 1956; Letchworth and Lambert, 1998). However, a recent study has shown that rank correlations were high (0.73-0.93) between open- and control-pollinated treatments among inbreds for oil, protein, and starch concentrations, suggesting that open-pollinated evaluation of kernel composition was sufficient for mapping major QTL (Chapter 2). The open-pollinated

evaluation of kernel composition in the present study allowed for increased replication of the mapping experiment across locations.

QTL for disease resistance

Resistance to NCLB in the U.S. Corn Belt has historically been conferred through major qualitative loci: *Ht1*, mapped to bin 2.08 (Bentolila et al., 1991); *Ht2*, mapped to bin 8.06 (Chung et al., 2010); *Ht3* (Hooker, 1981); and *Htn1*, mapped to bin 8.06 (Simcox and Bennetzen, 1993). However, resistance conferred by these loci is incomplete and has often been unstable in different environments and genetic backgrounds (Welz and Geiger, 2000).

Out of the 13 QTL identified for sAUDPC of NCLB, four markers corresponded to regions with previously identified resistance loci or QTL hot-spots (Table 8). One significant marker-trait association was identified in bin 8.05 (PZE-108088403; 144Mb), corresponding to a genomic region in which qualitative resistance (*Ht2* and *Htn1*; Simcox and Bennetzen, 1993; Yin, 2003) and quantitative resistance have been identified (Balint-Kurti et al., 2010; Chung et al., 2010). Chung et al. (2010) fine mapped the QTL they identified to a 0.47Mb region on chromosome 8 and showed that it was likely allelic or tightly linked to the *Ht2* locus; the marker identified in bin 8.05 in the present study was immediately adjacent to the fine-mapped marker interval. Significant markers in bins 3.09, 5.03, and 10.05 identified in the present study correspond to regions containing putative QTL identified in other recent studies (Balint-Kurti et al., 2010; Poland et al., 2011; Van Inghelandt et al., 2012). The marker in bin 10.05 (SYN18729) was about 1Mb from a candidate gene identified by Poland et al. (2011), which putatively encoded a

multi-antimicrobial extrusion protein, and was within a genomic hot-spot of disease resistance identified by Wisser et al. (2008).

Goss's wilt and blight was first discovered in the 1960s but has not been a major disease across the U.S. Corn Belt until recent years and was identified in Minnesota only since 2009 (Malvick et al., 2010). As a result, resistance to GWB has not been an important trait in maize breeding programs and genes for GWB resistance have not been mapped. However, QTL mapping has been conducted for Stewart's wilt, a bacterial disease caused by *Erwinia stewartii*. Disease resistance scores for GWB and Stewart's wilt were highly correlated (≥0.64; Pataky, 1985), suggesting shared resistance genes between the two diseases. Eight QTL for resistance to Stewart's wilt were mapped in a sweet corn population (Brown et al., 2001). Of the markers associated with GWB in the present study, one marker (PZE-101231891 in bin 1.10) corresponded with the Stewart's wilt QTL. In addition, markers in bins 5.04 and 5.05 associated with GWB in this study correspond with a previously identified hot-spot region associated with resistance to multiple diseases of maize (Wisser et al., 2006).

Our QTL results for GWB should be interpreted with caution because the experiment was conducted in only one environment. Previous multi-year studies have shown that a genotype × year interaction exists for GWB, however this interaction was not testable in this experiment and could potentially confound differences among the inbreds tested (Treat et al., 1990; Ngong-Nassah et al., 1992).

A inbreds and A321 subpopulation

Most QTL allele frequencies were higher among A inbreds for days to anthesis (5 of 8 QTL), days to silking (8 of 11 QTL), and oil concentration (8 of 11 QTL) and lower

among A inbreds for starch concentration (2 of 2 QTL), NCLB – sAUDPC (9 of 13 QTL), and GWB – disease leaf area (6 of 9 QTL; P = 0.05; Table 9). In other words, the A inbreds were enriched for favorable QTL alleles for days to flowering and oil concentration but the non-A inbreds were enriched for favorable QTL alleles for starch concentration and disease resistance. Association mapping studies are most useful for identifying common variants, and are less useful for capturing the effects of rare variants (Visscher et al., 2008; Yan et al., 2011). Therefore, it is not surprising that most of the QTL identified in this study were common across subpopulations, with 53 of 54 QTL having a favorable allele frequency between 0.1 and 0.9, and within subpopulations, with the lowest maximum within subpopulation frequency being 0.21 (Table 9). To identify rare variants, a QTL mapping approach utilizing parents representing the extreme trait means would be most useful.

The A321 subpopulation contains 116 inbreds (114 of which have phenotypic data in the present study), many of which were derived from the Minnesota 13 open-pollinated cultivar and were found to form subclusters of inbreds unique to germplasm developed at Minnesota (Chapter 1). The inbreds in the A321 subpopulation, which included 29 inbreds not developed in Minnesota, had either or both the minimum and maximum inbred mean values for all traits except protein concentration (Table 7). This result reflected the higher genetic diversity found in the A321 subpopulation than in the B73, Mo17, Oh43, or PH207 subpopulations (Chapter 1). A comparison of the range of inbred means between the A321 subpopulation and any other individual subpopulation is confounded by differences in the size of each subpopulation, e.g., N = 108 to 114 (depending on the trait) inbreds in the A321 subpopulation versus N = 28 inbreds in the

PH207 subpopulation. On the other hand, if the four non-A321 subpopulations are pooled so that comparisons of the range of inbred means are no longer confounded by differences in the number of inbreds (i.e., N = 108 to 114 in the A321 subpopulation versus N = 162 to 167 in the pool of non-A321 subpopulations), the A321 subpopulation still had either or both the minimum and maximum inbred mean values for all traits except protein concentration. The range in phenotypic diversity indicates that inbreds in the A321 subpopulation represent potential candidates for biparental QTL mapping studies for identifying rare variants. In addition, the genetic diversity and phenotypic diversity observed in the A321 subpopulation reinforce the historical and future importance of the Minnesota 13 background to hybrid breeding (Troyer and Hendrickson, 2007).

LD decay

The extent of LD was much greater in the historical inbreds in this study than in highly diverse germplasm (Remington et al., 2001; Yan et al., 2009), but was consistent with the LD in mapping panels of breeding germplasm (Jung et al., 2004; Van Inghelandt et al., 2011). As in previous studies (Yan et al., 2009; Van Inghelandt et al., 2011), the rate of LD decay in the present study varied by chromosome, ranging from 529 kb on chromosome 2 to 1419 on chromosome 10 (Table 6). However, the rank of chromosomes by rate of LD decay differed between this study and previous studies, with such differences being likely due to population composition and marker number, type, and ascertainment. In a study using a diverse set of 632 inbreds and 943 SNPs, chromosome 1 had the most rapid decay (1.5-2 kb), chromosomes 6 and 10 had moderate decay (2-5 kb), and the remainder of the chromosomes had the slowest rate of decay (5-10 kb; Yan et al.,

2009). In a collection of 1,537 elite inbreds, the rate of LD decay was most rapid in chromosomes 8 (0.06 cM) and 9 (0.04 cM), whereas LD extended furthest in chromosome 10 (1.29 cM; Van Inghelandt et al., 2011).

Mean r^2 of adjacent markers varied only slightly across chromosomes and was higher than in previous studies (Table 6; Van Inghelandt et al., 2011; Massman et al., 2013). A high r^2 between QTL and flanking (adjacent) markers increases the power to detect QTL. In a previous study in maize (Van Inghelandt et al., 2011), mean r^2 between adjacent markers in a collection of 1,537 elite inbreds ranged from 0.24 to 0.28 among heterotic groups, with the mean of 0.27 in the population. In another study in maize (Massman et al., 2013), mean r^2 between adjacent markers was 0.26 in one heterotic group and 0.35 in a second heterotic group. Differences in mean r^2 between adjacent markers in this study compared to Van Inghelandt et al. (2011) and Massman et al. (2013) was likely due to the combined effects of differences in marker density, number of inbreds, and genetic diversity.

Future directions and implications for breeders

Collections of historical inbreds exist across the U.S. Corn Belt as inbred development programs were established at many land grant universities, public institutions, and private companies upon the advent of hybrid maize breeding (Gerdes et al., 1993; Troyer, 1999). In this study, we utilized a mapping panel composed of inbreds developed by the University of Minnesota breeding program and by 26 public and private breeding programs (Chapter 1). Even though the mapping panel used in the present study was not a collection of historical inbreds from a single breeding program (i.e., Minnesota), the composition of the present collection would be similar to that of a single

breeding program that routinely utilizes germplasm developed elsewhere. Based on the phenotypic variation present and the significant marker-trait associations identified in this study, we believe that association mapping in historical inbred collections could identify major QTL useful in modern breeding programs.

Focusing on major QTL, and on traits likely to have major QTL (Buckler et al., 2009; Poland et al., 2011), leads to a straightforward breeding approach for introgressing such major QTL into elite germplasm (Bernardo, 2008). On the other hand, highly complex traits such as grain yield are potentially controlled by hundreds of loci of small effect (Mackay, 2001). Genomewide selection has shown promise as an approach for capturing variation due small-effect loci in plant species (Bernardo and Yu, 2007; Heffner et al., 2009). To efficiently utilize variation present for quantitative traits in historical germplasm, a combination of genomewide association mapping, as was applied in this study, and genomewide selection may be necessary.

Table 6: Decay of LD ($r^2 = 0.1$) and mean r^2 between adjacent markers among 283 maize inbreds genotyped with 39,166 SNP markers. LD decay was characterized by non-linear regression (Hill and Weir, 1988).

Chromosome	LD decay (kb)	Mean r^2 between adjacent markers
1	569	0.377
2	529	0.362
3	700	0.380
4	962	0.391
5	628	0.383
6	655	0.372
7	1040	0.382
8	755	0.378
9	759	0.350
10	1419	0.382
Mean	802	0.376

Table 7: Trait means and ranges, proportion of the phenotypic variance due to the effects of inbreds (R^2_{Inb}), and proportion of phenotypic variance explained by population structure (R^2_{Pop}) for N = 270-276 inbreds belonging to different subpopulations.

Trait	Subpopulation	N	Low†	High	Mean	R^2_{Inb}	R^2_{Pop}
Days to anthesis (GDD)	Whole panel	276	1094	1788	1421	0.99	0.16
	B73	61	1216	1678	1477		
	Mo17	29	1193	1682	1496		
	Oh43	47	1176	1707	1364		
	A321	114	1094	1788	1389		
	PH207	28	1168	1700	1447		
	LSD (0.05)				52		
Days to silking (GDD)	Whole panel	276	1105	1807	1464	0.98	0.17
	B73	61	1241	1690	1513		
	Mo17	29	1272	1727	1555		
	Oh43	47	1210	1777	1407		
	A321	114	1105	1807	1432		
	PH207	28	1184	1771	1497		
	LSD (0.05)				56		
Plant height (cm)	Whole panel	276	91	207	148	0.98	0.19
	B73	61	122	196	161		
	Mo17	29	115	200	160		
	Oh43	47	106	201	142		
	A321	114	91	207	140		
	PH207	28	109	175	148		
	LSD (0.05)				8		
Ear height (cm)	Whole panel	276	30	99	62	0.96	0.16
	B73	61	43	99	69		
	Mo17	29	37	92	67		
	Oh43	47	38	89	56		
	A321	114	30	90	58		
	PH207	28	37	47	43		
	LSD (0.05)				5		
Oil concentration (g kg^{-1})	Whole panel	276	38	64	47	0.94	0.16
	B73	61	40	54	46		
	Mo17	29	40	55	46		
	Oh43	47	39	58	48		
	A321	114	38	64	49		
	PH207	28	38	47	43		

	LSD (0.05)				2		
Protein concentration ($g\ kg^{-1}$)	Whole panel	276	97	175	129	0.95	0.23
	B73	61	97	152	121		
	Mo17	29	106	151	124		
	Oh43	47	112	175	132		
	A321	114	111	163	135		
	PH207	28	109	144	122		
	LSD (0.05)				5		
Starch concentration ($g\ kg^{-1}$)	Whole panel	276	640	775	726	0.95	0.18
	B73	61	684	775	741		
	Mo17	29	659	748	727		
	Oh43	47	651	754	722		
	A321	114	640	754	719		
	PH207	28	698	751	730		
	LSD (0.05)				8		
NCLB - sAUDPC	Whole panel	275	1.0	66.0	7.4	0.92	0.16
	B73	61	1.3	56.2	6.0		
	Mo17	29	1.0	31.7	3.6		
	Oh43	48	1.0	63.0	9.1		
	A321	109	1.1	66.0	9.6		
	PH207	28	1.6	24.5	6.4		
	LSD (0.05)				1.5		
NCLB - Latent period (d)	Whole panel	270	7.0	33.9	14.1	0.13	0.19
	B73	61	8.3	32.0	13.1		
	Mo17	26	12.3	33.9	20.6		
	Oh43	47	9.0	28.5	13.5		
	A321	108	7.0	33.4	13.5		
	PH207	28	9.3	31.5	14.5		
	LSD (0.05)				1.1		
GWB - Diseased leaf area (%)	Whole panel	272	0.4	97.5	28.8	0.87	0.13
	B73	61	0.6	80.0	23.6		
	Mo17	29	1.0	57.4	14.8		
	Oh43	45	0.4	93.7	34.3		
	A321	109	1.7	97.5	34.2		
	PH207	28	3.6	66.2	27.8		
	LSD (0.05)				0.7		

† All transformed data were presented in original units.

Table 8: Single nucleotide polymorphism (SNP) marker loci significantly associated with days to anthesis (GDD), days to silking (GDD), oil concentration (g kg^{-1}), starch concentration (g kg^{-1}), sAUDPC of NCLB, and diseased leaf area of GWB (%). Significant markers were identified by genomewide association mapping with the G model. Physical positions are in reference to the B73 Ref Gen_v1 sequence.

Trait	Marker locus	Chr. bin	Position (bp)	Allele	Effect of major allele†	Minor allele freq.	R^2_{SNP}	Candidate gene or QTL hot-spot	Reference
Days to anthesis (GDD)	PZE-105100862	5.04	150743784	G/A	-64.94	0.11			
	PZE-103075282	3.04	120913906	C/A	-43.65	0.11			
	PZE-108079256	8.05	134036635	G/A	38.23	0.12		*Vgt1*	Salvi et al., 2007
	PZE-108047666	8.03	79028620	G/A	-38.06	0.21		QTL hot-spot	Chardon et al., 2004
	PZE-109067329	9.04	107509569	A/G	32.49	0.15		QTL hot-spot	Chardon et al., 2004
	PZE-110052085	10.04	98234797	A/C	28.28	0.35		QTL hot-spot	Chardon et al., 2004
	PZE-103162577	3.08	211275824	C/A	27.18	0.42			
	PZE-108075125	8.05	129402501	G/A	23.61	0.41		QTL hot-spot	Chardon et al., 2004
	Simultaneous fit						0.44		

Days to silking (GDD)	PZE-105100862	5.04	150743784	G/A	-42.65	0.11			
	PZE-108070237	8.04	121767961	C/A	38.00	0.34		QTL hot-spot	Chardon et al., 2004
	PZE-108032226	8.03	37477116	C/A	37.33	0.19		QTL hot-spot	Chardon et al., 2004
	PZA02272.2	2.02	9917126	G/T	-35.69	0.19			
	PUT-163a-71445640-3380	10.03	22176206	C/T	33.82	0.47			
	PZE-102102479	2.05	122457135	C/A	31.65	0.23			
	SYN2755	9.02	12731775	G/T	27.38	0.13			
	PZE-103078773	3.05	126382719	G/A	24.72	0.32			
	PZE-105082431	5.04	96878522	C/G	-22.84	0.49			
	PZE-105127896	5.05	184583154	G/A	-18.52	0.30			
	PZE-105077151	5.04	85486093	C/T	10.08	0.50			
	Simultaneous fit						0.61		
Oil concentration (g kg^{-1})	PZE-104123457	4.09	206188393	A/G	-1.46	0.23			
	PZE-108058478	8.03	103237484	G/A	1.46	0.07			
	SYNGENTA14068	10.03	27531758	G/C	-1.39	0.16			
	PZE-106054182	6.04	105013351	A/G	-1.23	0.16		*DGAT1-2*	Zheng et al., 2008
	PZE-101140751	1.06	181733125	T/C	1.06	0.48			
	PZE-108078317	8.05	132748808	A/G	1.05	0.40			
	PZE-104045293	4.05	74481105	A/G	0.95	0.12			
	SYN2434	1.01	10061660	C/T	0.72	0.49			

	PZE-106080513	6.05	137607023	A/G	0.55	0.23			
	PZE-103071251	3.04	113222833	C/A	-0.51	0.39			
	SYN35006	1.04	55173734	C/T	-0.45	0.45			
	Simultaneous fit						0.47		
Starch concentration (g kg^{-1})	PZE-109061922	9.04	100692646	G/A	-8.62	0.26			
	PZE-104123457	4.09	206188393	A/G	7.64	0.23			
	Simultaneous fit						0.24		
NCLB - sAUDPC	SYN3974	6.01	23654414	A/C	1.39	0.20			
	PZE-106030288	6.01	70059550	A/G	1.34	0.44			
	PZE-103171220	3.09	216700526	G/T	-1.22	0.18		QTL hot-spot	Wisser et al., 2006
	PZE-105103729	5.04	156467966	G/A	1.22	0.33		QTL hot-spot	Wisser et al., 2006
	SYN18729	10.05	135551614	T/C	1.21	0.32		QTL hot-spot	Poland et al., 2011
	PZE-104020409	4.04	21537032	C/T	-1.21	0.16			
	PZE-109099702	9.06	140099217	A/C	-1.20	0.34			
	PZE-105050111	5.03	41871943	T/C	1.19	0.22			
	PZE-103019961	3.03	12050933	A/C	-1.19	0.34			
	PZE-108037289	8.03	55644755	G/A	1.17	0.25			
	PZE-103165058	3.08	213221621	G/A	-1.14	0.47			
	PZE-108088403	8.05	144401020	G/A	1.14	0.28		*Ht2* and *Htn1*	Chung et al., 2010
	SYN34247	9.03	73940812	C/T	-1.08	0.29			
	Simultaneous fit						0.55		
GWB - DLA (%)	PZE-101231891	1.10	279722046	A/C	-1.12	0.33		QTL for Stewart's wilt	Brown et al., 2001

PZE-101151522	1.06	195018417	G/A	0.68	0.14	
PZE-104051430	4.05	88562761	C/G	0.55	0.23	
PZE-109020070	9.02	20379523	C/T	0.32	0.14	
PZE-105134487	5.05	189945330	T/C	0.25	0.33	
PZE-105080933	5.04	92983626	G/A	-0.22	0.25	
PZE-109092156	9.06	134852084	A/G	0.20	0.28	
PZE-107025795	7.02	30579200	C/A	0.17	0.44	
PZE-104132140	4.09	220507264	T/C	0.14	0.32	
Simultaneous fit						0.47

† All marker effects are presented in original units.

Table 9: Frequency of favorable alleles of QTL for days to anthesis (GDD), days to silking (GDD), oil concentration (g kg^{-1}), starch concentration (g kg^{-1}), NCLB - sAUDPC, and GWB – diseased leaf area (%) by subpopulation and developer group.

		Subpopulation					Developer group	
Trait	Marker locus	B73	Mo17	Oh43	A321	PH207	A inbreds	non-A inbreds
Days to anthesis (GDD)†	PZE-105100862	0.93	0.64	0.91	0.93	0.84	0.95*	0.82
	PZE-103075282	0.97	0.69	0.87	0.90	0.93	0.93*	0.85
	PZE-108079256	0.07	0.10	0.21	0.14	0.07	0.15	0.10
	PZE-108047666	0.89	0.29	0.96	0.75	0.91	0.90*	0.67
	PZE-109067329	0.03	0.38	0.11	0.19	0.04	0.18	0.11
	PZE-110052085	0.15	0.21	0.67	0.43	0.07	0.49*	0.21
	PZE-103162577	0.07	0.75	0.62	0.54	0.04	0.55*	0.28
	PZE-108075125	0.26	0.75	0.49	0.43	0.18	0.46	0.36
Days to silking (GDD)	PZE-105100862	0.93	0.64	0.91	0.93	0.84	0.95*	0.82
	PZE-108070237	0.21	0.26	0.51	0.41	0.07	0.44*	0.23
	PZE-108032226	0.20	0.17	0.26	0.20	0.00	0.25*	0.11
	PZA02272.2	0.89	0.28	0.89	0.85	0.82	0.93*	0.67
	PUT-163a-71445640-3380	0.18	0.10	0.60	0.61	0.68	0.63*	0.30
	PZE-102102479	0.07	0.10	0.41	0.23	0.34	0.27	0.18
	SYN2755	0.31	0.04	0.04	0.15	0.45	0.16	0.21
	PZE-103078773	0.03	0.28	0.28	0.52	0.18	0.47*	0.15
	PZE-105082431	0.16	0.31	0.81	0.62	0.46	0.64*	0.36

	PZE-105127896	0.69	0.59	0.89	0.75	0.29	0.81*	0.58
	PZE-105077151	0.22	0.79	0.72	0.53	0.27	0.55	0.44
Oil concentration (g kg^{-1})	PZE-104123457	0.00	0.21	0.21	0.41	0.00	0.34*	0.10
	PZE-108058478	1.00	1.00	0.98	0.99	0.36	0.99*	0.87
	SYNGENTA14068	0.02	0.14	0.11	0.27	0.07	0.20*	0.10
	PZE-106054182	0.03	0.22	0.38	0.16	0.00	0.24*	0.08
	PZE-101140751	0.90	0.69	0.38	0.44	0.04	0.53	0.51
	PZE-108078317	0.39	0.31	0.79	0.67	0.71	0.69*	0.49
	PZE-104045293	0.90	0.97	0.96	0.82	0.89	0.84	0.93*
	SYN2434	0.15	0.52	0.32	0.68	0.86	0.55	0.45
	PZE-106080513	0.25	0.93	0.89	0.92	0.88	0.84*	0.69
	PZE-103071251	0.11	0.41	0.47	0.46	0.54	0.45*	0.32
	SYN35006	0.48	0.28	0.66	0.47	0.11	0.51*	0.38
Starch concentration (g kg^{-1})	PZE-109061922	0.62	0.10	0.05	0.19	0.29	0.15	0.39*
	PZE-104123457	1.00	0.79	0.79	0.59	1.00	0.66	0.90*
NCLB - sAUDPC	SYN3974	0.72	0.07	0.13	0.03	0.04	0.10	0.31*
	PZE-106030288	0.28	0.59	0.53	0.52	0.18	0.45	0.43
	PZE-103171220	1.00	1.00	0.62	0.73	0.96	0.70	0.96*
	PZE-105103729	0.08	0.72	0.23	0.40	0.32	0.32	0.33
	SYN18729	0.10	0.86	0.21	0.23	0.74	0.19	0.45*
	PZE-104020409	1.00	0.86	0.83	0.78	0.89	0.79	0.93*
	PZE-109099702	0.66	0.86	0.47	0.61	0.93	0.47	0.84*
	PZE-105050111	0.13	0.32	0.17	0.18	0.36	0.14	0.27*
	PZE-103019961	0.70	0.83	0.77	0.56	0.57	0.57	0.74*
	PZE-108037289	0.06	0.41	0.20	0.27	0.52	0.18	0.32*

	PZE-103165058	0.70	0.24	0.61	0.39	0.93	0.38	0.70*
	PZE-108088403	0.38	0.34	0.28	0.23	0.14	0.31	0.24
	SYN34247	0.61	0.97	0.79	0.63	0.86	0.68	0.74
GWB - Diseased leaf area (%)	PZE-101231891	0.70	0.53	0.68	0.72	0.50	0.68	0.65
	PZE-101151522	0.10	0.59	0.04	0.09	0.14	0.04	0.24*
	PZE-104051430	0.02	0.41	0.28	0.25	0.38	0.25	0.22
	PZE-109020070	0.23	0.21	0.22	0.10	0.00	0.06	0.24*
	PZE-105134487	0.28	0.79	0.16	0.30	0.36	0.23	0.43*
	PZE-105080933	0.90	0.83	0.84	0.58	0.86	0.64	0.86*
	PZE-109092156	0.56	0.03	0.29	0.09	0.61	0.17	0.39*
	PZE-107025795	0.85	0.66	0.11	0.39	0.18	0.39	0.53*
	PZE-104132140	0.21	0.50	0.36	0.33	0.11	0.30	0.30
Approximate SE ‡		0.06	0.09	0.07	0.05	0.09		

† The favorable allele was for lower days to anthesis, days to silking, NCLB – sAUDPC, and GWB – diseased leaf area, and higher oil concentration and starch concentration.

‡ Approximate standard errors were calculated conservatively by assuming allele frequencies of 0.50.

* Significantly different (P=0.05) between the A inbreds and the non-A inbreds.

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Appendix

Supplemental Table 1

No.	Inbred name	GRIN ID	Developer	PVPA ID	PVPA expira-tion date	Seed source	Derivation
1	11430	PI 601558	Cargill, Inc.	8800177	3/31/07	GRIN	Oh43, H99, and Mo17 Composite
2	2FACC	PI 601808	DeKalb Plant Genetics	9000016	8/31/08	GRIN	4676A x PB80
3	2MA22	PI 601560	DeKalb-Pfizer Genetics	8800193	1/31/07	GRIN	4780 x 5P9-1
4	3IBZ2	PI 554616	DeKalb Plant Genetics	9100223	4/30/10	GRIN	IBC2 x ZZZ38
5	4N506	PI 601745	Funk Seeds International, Inc.	8900263	9/28/08	GRIN	B73 x BSSS 2
6	6M502	PI 601561	DeKalb-Pfizer Genetics	8800191	7/31/08	GRIN	MAWU x 4913
7	87916W	PI 601563	DeKalb-Pfizer Genetics	8800189	1/31/07	GRIN	B73 x W37-2
8	A1	.	Minnesota	.	.	.	Minn #13
9	A2	.	Minnesota	.	.	.	Minn #13
10	A3	.	Minnesota	.	.	.	Minn #13
11	A4	.	Minnesota	.	.	.	Minn #13
12	A5	.	Minnesota	.	.	.	Minn #13
13	A6	.	Minnesota	.	.	.	Minn #13
14	A7	NSL 42872	Minnesota	.	.	GRIN	Minn #13
15	A8	.	Minnesota	.	.	.	Minn #13
16	A9	.	Minnesota	.	.	.	Minn #13
17	A10	.	Minnesota	.	.	.	Minn #13
18	A12	NSL 42873	Minnesota	.	.	GRIN	Minn #13
19	A13	.	Minnesota	.	.	.	Kalmoes #13
20	A14	.	Minnesota	.	.	.	Kalmoes #13
21	A15	Ames 23389	Minnesota	.	.	GRIN	Kalmoes #13
22	A16	.	Minnesota	.	.	.	Kalmoes #13
23	A17	.	Minnesota	.	.	.	Kalmoes #13
24	A18	.	Minnesota	.	.	.	Kalmoes #13
25	A19	.	Minnesota	.	.	.	Golden Gate
26	A20	.	Minnesota	.	.	.	Golden Gate

No.	Inbred name	GRIN ID	Developer	PVPA ID	PVPA expira-tion date	Seed source	Derivation
27	A21	.	Minnesota	.	.	.	Golden Gate
28	A22	.	Minnesota	.	.	.	Golden Gate
29	A23	.	Minnesota	.	.	.	Golden Gate
30	A24	.	Minnesota	.	.	.	Golden Gate
31	A25	Ames 23390	Minnesota	.	.	GRIN**	Purdue Yellow Dent
32	A26	.	Minnesota	.	.	.	Osterland Yellow Dent
33	A27	.	Minnesota	.	.	.	Osterland Yellow Dent
34	A28	.	Minnesota	.	.	.	Golden Glow
35	A28	.	Minnesota	.	.	.	Minn #13
36	A29	.	Minnesota	.	.	.	Minn #13
37	A30	.	Minnesota	.	.	.	Minn #13
38	A31	.	Minnesota	.	.	.	Holbert
39	A32	.	Minnesota	.	.	.	Holbert
40	A33	.	Minnesota	.	.	.	Rustler White Dent
41	A33	.	Minnesota	.	.	.	Rustler White Dent
42	A34	Ames 23391	Minnesota	.	.	GRIN	Rustler White Dent
43	A35	.	Minnesota	.	.	.	Rustler White Dent
44	A35	.	Minnesota	.	.	.	Rustler White Dent
45	A36	.	Minnesota	.	.	.	Rustler White Dent
46	A36	.	Minnesota	.	.	.	Rustler White Dent
47	A37	.	Minnesota	.	.	.	Rustler White Dent
48	A38	.	Minnesota	.	.	.	Rustler White Dent
49	A38	.	Minnesota	.	.	.	Rustler White Dent
50	A39	.	Minnesota	.	.	.	Rustler White Dent
51	A40	.	Minnesota	.	.	.	Rustler White Dent
52	A41	.	Minnesota	.	.	.	Rustler White Dent
53	A42	.	Minnesota	.	.	.	Rustler White Dent
54	A43	.	Minnesota	.	.	.	Rustler White Dent
55	A44	.	Minnesota	.	.	.	Rustler White Dent
56	A45	.	Minnesota	.	.	.	Rustler White Dent
57	A46	.	Minnesota	.	.	.	Rustler White Dent

No.	Inbred name	GRIN ID	Developer	PVPA ID	PVPA expira-tion date	Seed source	Derivation
58	A47	.	Minnesota	.	.	.	Northwestern Dent
59	A48	.	Minnesota	.	.	.	Northwestern Dent
60	A49	.	Minnesota	.	.	.	Northwestern Dent
61	A50	.	Minnesota	.	.	.	Northwestern Dent
62	A51	.	Minnesota	.	.	.	Northwestern Dent
63	A52	.	Minnesota	.	.	.	Northwestern Dent
64	A53	.	Minnesota	.	.	.	Northwestern Dent
65	A54	.	Minnesota	.	.	.	Northwestern Dent
66	A55	.	Minnesota	.	.	.	Northwestern Dent
67	A56	.	Minnesota	.	.	.	Northwestern Dent
68	A57	.	Minnesota	.	.	.	Northwestern Dent
69	A58	.	Minnesota	.	.	.	Minn #23
70	A59	.	Minnesota	.	.	.	Minn #23
71	A60	.	Minnesota	.	.	.	Minn #23
72	A61	.	Minnesota	.	.	.	Minn #23
73	A62	.	Minnesota	.	.	.	Minn #23
74	A63	.	Minnesota	.	.	.	Minn #23
75	A64	.	Minnesota	.	.	.	Longfellow
76	A65	.	Minnesota	.	.	.	Longfellow
77	A66	.	Minnesota	.	.	.	Longfellow
78	A67	.	Minnesota	.	.	.	Longfellow
79	A68	.	Minnesota	.	.	.	King Phillip
80	A69	.	Minnesota	.	.	.	King Phillip
81	A70	.	Minnesota	.	.	.	Unknown
82	A71	NSL 42875	Minnesota	.	.	GRIN	Funk Yellow Dent
83	A72	.	Minnesota	.	.	.	R3 x AR9
84	A73	Ames 22439	Minnesota	.	.	GRIN	G3 x AR9
85	A74	.	Minnesota	.	.	.	15 x A36
86	A75	.	Minnesota	.	.	.	15 x A36
87	A76	.	Minnesota	.	.	.	58 x 60
88	A77	.	Minnesota	.	.	.	58 x 60

No.	Inbred name	GRIN ID	Developer	PVPA ID	PVPA expira-tion date	Seed source	Derivation
89	A78	.	Minnesota	.	.	.	A48 x A50
90	A79	.	Minnesota	.	.	.	A48 x A50
91	A80	.	Minnesota	.	.	.	A48 x A12
92	A81	.	Minnesota	.	.	.	A48 x A9
93	A82	.	Minnesota	.	.	.	A48 x A9
94	A83	.	Minnesota	.	.	.	A48 x A9
95	A84	.	Minnesota	.	.	.	A48 x A9
96	A85	.	Minnesota	.	.	.	A48 x A9
97	A86	.	Minnesota	.	.	.	A48 x A12
98	A87	.	Minnesota	.	.	.	A48 x A12
99	A88	.	Minnesota	.	.	.	A48 x A39
100	A89	.	Minnesota	.	.	.	A48 x A39
101	A90	Ames23392	Minnesota	.	.	GRIN	A48 x A39
102	A91	.	Minnesota	.	.	.	A48 x 4-29
103	A92	.	Minnesota	.	.	.	A48 x 4-29
104	A93	.	Minnesota	.	.	.	A48 x H
105	A94	.	Minnesota	.	.	.	A48 x H
106	A95	.	Minnesota	.	.	.	A48 x H
107	A96	Ames 23393	Minnesota	.	.	GRIN	A48 x H
108	A97	.	Minnesota	.	.	.	A48 x H
109	A98	.	Minnesota	.	.	.	A9 x A39
110	A99	.	Minnesota	.	.	.	A9 x A39
111	A100	.	Minnesota	.	.	.	A9 x A26
112	A101	.	Minnesota	.	.	.	A9 x A26
113	A102	.	Minnesota	.	.	.	A9 x A26
114	A103	.	Minnesota	.	.	.	A9 x A26
115	A104	.	Minnesota	.	.	.	A9 x A26
116	A106	.	Minnesota	.	.	.	A9 x A26
117	A107	.	Minnesota	.	.	.	A9 x A26
118	A108	.	Minnesota	.	.	.	A9 x A26
119	A109	.	Minnesota	.	.	.	A9 x A26

No.	Inbred name	GRIN ID	Developer	PVPA ID	PVPA expira-tion date	Seed source	Derivation
120	A110	.	Minnesota	.	.	.	A9 x A26
121	A111	.	Minnesota	.	.	.	A9 x A26
122	A112	.	Minnesota	.	.	.	A9 x A26
123	A113	.	Minnesota	.	.	.	A9 x A26
124	A114	.	Minnesota	.	.	.	A9 x A26
125	A115	.	Minnesota	.	.	.	A9 x A26
126	A116	Ames 23394	Minnesota	.	.	GRIN	A9 x A26
127	A117	.	Minnesota	.	.	.	A9 x A26
128	A118	.	Minnesota	.	.	.	A9 x A26
129	A119	.	Minnesota	.	.	.	A9 x A26
130	A120	.	Minnesota	.	.	.	A9 x A26
131	A121	.	Minnesota	.	.	.	A9 x A26
132	A122	.	Minnesota	.	.	.	A9 x A26
133	A123	.	Minnesota	.	.	.	A9 x A26
134	A124	.	Minnesota	.	.	.	A9 x A26
135	A125	.	Minnesota	.	.	.	A12 x A39
136	A126	.	Minnesota	.	.	.	A12 x A39
137	A127	.	Minnesota	.	.	.	A12 x A39
138	A128	.	Minnesota	.	.	.	A12 x A39
139	A129	.	Minnesota	.	.	.	A12 x A39
140	A130	.	Minnesota	.	.	.	A12 x A39
141	A131	.	Minnesota	.	.	.	A12 x A39
142	A132	.	Minnesota	.	.	.	A39 x A25
143	A133	.	Minnesota	.	.	.	A39 x 9
144	A134	.	Minnesota	.	.	.	A39 x A26
145	A135	.	Minnesota	.	.	.	A39 x A26
146	A136	.	Minnesota	.	.	.	A39 x A26
147	A137	.	Minnesota	.	.	.	A39 x A26
148	A138	.	Minnesota	.	.	.	A39 x A26
149	A139	.	Minnesota	.	.	.	A39 x A26
150	A140	.	Minnesota	.	.	.	A39 x A26

No.	Inbred name	GRIN ID	Developer	PVPA ID	PVPA expira-tion date	Seed source	Derivation
151	A141	.	Minnesota	.	.	.	A39 x A26
152	A142	.	Minnesota	.	.	.	A39 x A26
153	A143	.	Minnesota	.	.	.	A39 x 9
154	A144	.	Minnesota	.	.	.	A39 x A26
155	A145	.	Minnesota	.	.	.	A39 x A26
156	A146	.	Minnesota	.	.	.	A39 x A26
157	A147	.	Minnesota	.	.	.	A39 x H
158	A148	.	Minnesota	.	.	.	A2 x A7
159	A149	.	Minnesota	.	.	.	A2 x A7
160	A150	.	Minnesota	.	.	.	A2 x A7
161	A151	.	Minnesota	.	.	.	A2 x A7
162	A152	Ames 23395	Minnesota	.	.	GRIN	A2 x A7
163	A153	.	Minnesota	.	.	.	A2 x A7
164	A154	.	Minnesota	.	.	.	A2 x A7
165	A155	Ames 23396	Minnesota	.	.	GRIN	A2 x A7
166	A156	.	Minnesota	.	.	.	A2 x A7
167	A157	.	Minnesota	.	.	.	A2 x 47
168	A158	Ames 23397	Minnesota	.	.	GRIN	A2 x 47
169	A159	.	Minnesota	.	.	.	A2 x 47
170	A160	.	Minnesota	.	.	.	A2 x 47
171	A161	.	Minnesota	.	.	.	A2 x 47
172	A162	.	Minnesota	.	.	.	A2 x 47
173	A163	.	Minnesota	.	.	.	A2 x 47
174	A164	.	Minnesota	.	.	.	A2 x 47
175	A165	NSL 42877	Minnesota	.	.	GRIN	A2 x 47
176	A166	Ames 23398	Minnesota	.	.	UMN	A9 x A39
177	A167	.	Minnesota	.	.	.	Rustler White Dent
178	A171	NSL 42878	Minnesota	.	.	UMN	Complex cross
179	A172	.	Minnesota	.	.	.	Complex cross
180	A173	.	Minnesota	.	.	.	Complex cross
181	A177	.	Minnesota	.	.	.	Complex cross (composite)

No.	Inbred name	GRIN ID	Developer	PVPA ID	PVPA expira-tion date	Seed source	Derivation
182	A181	.	Minnesota	.	.	.	(8 x 10) x 8(2)
183	A182	.	Minnesota	.	.	.	(8 x 10) x 10(2)
184	A183	.	Minnesota	.	.	.	(88 x 91) x 88(2)
185	A184	.	Minnesota	.	.	.	(88 x 91) x 91(2)
186	A185	.	Minnesota	.	.	.	(4-29 x A48) x 4-29(4)
187	A186	.	Minnesota	.	.	.	(4-29 x A48) x 4-29(4)
188	A187	.	Minnesota	.	.	.	(4-29 x A48) x 4-29(4)
189	A188	Ames 22443	Minnesota	.	.	GRIN	(4-29 x A48) x 4-29(4)
190	A189	.	Minnesota	.	.	.	Sweepstakes
191	A190	.	Minnesota	.	.	.	Sweepstakes
192	A191	.	Minnesota	.	.	.	Sweepstakes
193	A192	.	Minnesota	.	.	.	Sweepstakes
194	A193	.	Minnesota	.	.	.	Sweepstakes
195	A200	.	Minnesota	.	.	.	(A2 x C23) x A2(2)
196	A201	Ames 23399	Minnesota	.	.	GRIN	(A2 x C23) x A2(2)
197	A202	.	Minnesota	.	.	.	(A2 x C23) x A2(3)
198	A203	Ames 23400	Minnesota	.	.	GRIN	(A2 x C23) x A2(3)
199	A204	Ames 23401	Minnesota	.	.	GRIN	(A2 x C23) x A2(3)
200	A205	.	Minnesota	.	.	.	(A2 x C23) x A2(2)
201	A206	.	Minnesota	.	.	.	(A2 x C23) x A2(2)
202	A208	Ames 23402	Minnesota	.	.	GRIN	(A2 x C23) x A2(2)
203	A209	.	Minnesota	.	.	.	(A2 x C23) x A2(3)
204	A210	.	Minnesota	.	.	.	(A1 x A374) x A1(1)
205	A211	.	Minnesota	.	.	.	(A1 x A374) x A1(2)
206	A212	.	Minnesota	.	.	.	(A9 x A10) x A10(2)
207	A213	.	Minnesota	.	.	.	(A9 x A10) x A10(2)
208	A214	.	Minnesota	.	.	.	[(A9 x A10) x A2] x A10(2)
209	A215	.	Minnesota	.	.	.	(A1 x A374) x A1(3)
210	A216	.	Minnesota	.	.	.	(A1 x A374) x A1(2)
211	A217	.	Minnesota	.	.	.	(A1 x A374) x A1(2)
212	A218	Ames 23403	Minnesota	.	.	UMN	(A1 x A374) x A1(2)

No.	Inbred name	GRIN ID	Developer	PVPA ID	PVPA expira-tion date	Seed source	Derivation
213	A219	.	Minnesota	.	.	.	(A9 x A10) x A10(2)
214	A220	.	Minnesota	.	.	.	(A1 x A374) x A374(2)
215	A221	.	Minnesota	.	.	.	(A1 x A374) x A374(3)
216	A222	.	Minnesota	.	.	.	(A1 x A374) x A374(3)
217	A223	Ames 23404	Minnesota	.	.	UMN	(A1 x A374) x A374(3)
218	A230	.	Minnesota	.	.	.	(A2 x C23) x C23(2)
219	A231	.	Minnesota	.	.	.	(A2 x C23) x C23(3)
220	A232	.	Minnesota	.	.	.	(A2 x C23) x C23(3)
221	A233	.	Minnesota	.	.	.	(A2 x C23) x C23(2)
222	A234	.	Minnesota	.	.	.	(A2 x C23) x C23(2)
223	A237	.	Minnesota	.	.	.	(A2 x C23) x A2(2)
224	A238	NSL 81595	Minnesota	.	.	GRIN	A347 x A73
225	A239	Ames 23405	Minnesota	.	.	GRIN	A347 x A73
226	A240	.	Minnesota	.	.	.	A347 x A73
227	A241	.	Minnesota	.	.	.	A347 x A73
228	A242	.	Minnesota	.	.	.	A347 x A73
229	A243	.	Minnesota	.	.	.	A347 x A73
230	A244	.	Minnesota	.	.	.	A347 x A73
231	A245	.	Minnesota	.	.	.	A347 x Os420
232	A247	.	Minnesota	.	.	.	A347 x Os420
233	A248	.	Minnesota	.	.	.	A375 x Ia234
234	A249	.	Minnesota	.	.	.	A375 x Ia234
235	A250	.	Minnesota	.	.	.	A73 x Oh51A
236	A251	Ames 23406	Minnesota	.	.	GRIN	A73 x Oh51A
237	A252	.	Minnesota	.	.	.	A73 x Oh51A
238	A254	.	Minnesota	.	.	.	A344 x CC36
239	A255	.	Minnesota	.	.	.	A344 x CC36
240	A256	.	Minnesota	.	.	.	A344 x CC36
241	A257	Ames 23407	Minnesota	.	.	GRIN	A73 x Os420
242	A258	NSL 81596	Minnesota	.	.	GRIN	A73 x Os420
243	A259	.	Minnesota	.	.	.	A73 x Os420

No.	Inbred name	GRIN ID	Developer	PVPA ID	PVPA expira-tion date	Seed source	Derivation
244	A260	Ames 23408	Minnesota	.	.	GRIN	A367 x IndFe
245	A261	.	Minnesota	.	.	.	A367 x IndFe
246	A262	.	Minnesota	.	.	.	A334 x Oh40B
247	A263	.	Minnesota	.	.	.	(A334 x Oh40B) x A334(2)
248	A264	Ames 23409	Minnesota	.	.	GRIN	(A334 x Oh40B) x A334
249	A265	Ames 23410	Minnesota	.	.	UMN	(B164 x H76) x B164(2)
250	A266	Ames 23411	Minnesota	.	.	GRIN**	(B164 x H76) x B164(2)
251	A267	Ames 23412	Minnesota	.	.	GRIN**	Horowty Flint
252	A268	.	Minnesota	.	.	.	A163 x Ky55
253	A269	.	Minnesota	.	.	.	(A334 x 389) x A334(3)
254	A270	.	Minnesota	.	.	.	(A334 x 389) x A334(3)
255	A271	.	Minnesota	.	.	.	(A375 x 401) x A375(3)
256	A272	.	Minnesota	.	.	.	(A375 x 401) x A375(3)
257	A273	.	Minnesota	.	.	.	(A375 x 401) x A375(3)
258	A274	.	Minnesota	.	.	.	(A73 x 399) x A73(3)
259	A275	.	Minnesota	.	.	.	(A73 x 399) x A73(3)
260	A276	.	Minnesota	.	.	.	(A73 x 399) x A73(3)
261	A277	.	Minnesota	.	.	.	A322 x R4
262	A278	.	Minnesota	.	.	.	A322 x R4
263	A279	.	Minnesota	.	.	.	A322 x R4
264	A280	.	Minnesota	.	.	.	A322 x R4
265	A281	.	Minnesota	.	.	.	A334 x Oh7
266	A282	.	Minnesota	.	.	.	A334 x Oh7
267	A284	.	Minnesota	.	.	.	A334 x Oh7
268	A285	.	Minnesota	.	.	.	A334 x Oh7
269	A286	Ames 23413	Minnesota	.	.	UMN	A334 x Oh7
270	A287	.	Minnesota	.	.	.	A334 x Oh7
271	A288	Ames 23414	Minnesota	.	.	GRIN	A344 x L317
272	A289	.	Minnesota	.	.	.	A344 x L317
273	A290	.	Minnesota	.	.	.	A344 x L317
274	A291	.	Minnesota	.	.	.	A344 x L317

No.	Inbred name	GRIN ID	Developer	PVPA ID	PVPA expira-tion date	Seed source	Derivation
275	A292	.	Minnesota	.	.	.	A344 x L317
276	A293	.	Minnesota	.	.	.	A344 x L317
277	A294	.	Minnesota	.	.	UMN	A344 x L317
278	A295	Ames 23415	Minnesota	.	.	GRIN	A344 x L317
279	A296	.	Minnesota	.	.	.	A340 x Mo940
280	A297	Ames 23416	Minnesota	.	.	GRIN**	A340 x Mo940
281	A298	.	Minnesota	.	.	.	A347 x Mich77
282	A299	.	Minnesota	.	.	.	A347 x Mich77
283	A300	.	Minnesota	.	.	.	4-29 x A48
284	A301	.	Minnesota	.	.	.	6-29 x H
285	A302	.	Minnesota	.	.	.	A26 x H
286	A303	.	Minnesota	.	.	.	Golden King
287	A304	.	Minnesota	.	.	.	G25 Composite (Wisc. Lines)
288	A305	Ames 23417	Minnesota	.	.	UMN	C1 x H
289	A306	.	Minnesota	.	.	.	C1 x H
290	A307	.	Minnesota	.	.	.	Unknown
291	A308	Ames 23418	Minnesota	.	.	UMN	A34 x A25
292	A309	.	Minnesota	.	.	.	Silver King
293	A310	Ames 23419	Minnesota	.	.	GRIN	6-29 x H
294	A311	.	Minnesota	.	.	.	A39 x A25
295	A312	Ames 23420	Minnesota	.	.	UMN	A34 x A25
296	A313	.	Minnesota	.	.	.	A34 x A25
297	A314	.	Minnesota	.	.	.	A34 x A25
298	A315	.	Minnesota	.	.	.	6-29 x H
299	A316	.	Minnesota	.	.	.	6-29 x H
300	A317	.	Minnesota	.	.	.	Silver King
301	A321	Ames 23421	Minnesota	.	.	GRIN	Holbert
302	A322	Ames 23422	Minnesota	.	.	UMN	A39 x A25
303	A332	.	Minnesota	.	.	.	Golden King
304	A333	.	Minnesota	.	.	.	Rustler
305	A334	Ames 23423	Minnesota	.	.	UMN	Golden King

No.	Inbred name	GRIN ID	Developer	PVPA ID	PVPA expira-tion date	Seed source	Derivation
306	A335	.	Minnesota	.	.	.	4-29 x A48
307	A337	.	Minnesota	.	.	.	G6-9276-4 (Wisc. Lines)
308	A339	.	Minnesota	.	.	.	4-29 x A48
309	A340	Ames 23424	Minnesota	.	.	GRIN	4-29 x A48
310	A342	.	Minnesota	.	.	.	4-29 x A48
311	A344	Ames 23425	Minnesota	.	.	GRIN	U.S. 153 (Iowa)
312	A345	.	Minnesota	.	.	.	6-29 x H
313	A347	.	Minnesota	.	.	.	6-29 x H
314	A348	.	Minnesota	.	.	.	6-29 x H
315	A349	.	Minnesota	.	.	.	6-29 x H
316	A351	.	Minnesota	.	.	.	6-29 x H
317	A356	.	Minnesota	.	.	.	6-29 x H
318	A357	Ames 23426	Minnesota	.	.	GRIN	6-29 x H
319	A359	.	Minnesota	.	.	.	6-29 x H
320	A367	.	Minnesota	.	.	.	A26 x A9
321	A374	Ames 23427	Minnesota	.	.	UMN	Reids Yellow Dent (Holberts)
322	A375	Ames 23428	Minnesota	.	.	GRIN	Reids Yellow Dent (Holberts)
323	A385	Ames 23429	Minnesota	.	.	GRIN	A39 x H
324	A387	.	Minnesota	.	.	.	A34 x H
325	A389	.	Minnesota	.	.	.	A34 x H
326	A392	.	Minnesota	.	.	.	A39 x H
327	A394	.	Minnesota	.	.	.	Unknown
328	A395	.	Minnesota	.	.	.	(B164 x C37) x B164(2)
329	A396	.	Minnesota	.	.	.	(B164 x C37) x B164(2)
330	A400	.	Minnesota	.	.	.	A347 x K230
331	A401	Ames 23430	Minnesota	.	.	GRIN	A347 x K230
332	A402	.	Minnesota	.	.	.	A347 x K230
333	A404	.	Minnesota	.	.	.	A392 x K230
334	A405	.	Minnesota	.	.	.	Taos VI
335	A406	.	Minnesota	.	.	.	A392 x Mich106
336	A407	Ames 23431	Minnesota	.	.	GRIN	A96 x H

No.	Inbred name	GRIN ID	Developer	PVPA ID	PVPA expira-tion date	Seed source	Derivation
337	A408	.	Minnesota	.	.	.	A96 x H
338	A409	.	Minnesota	.	.	.	A131 x Oh7
339	A410	.	Minnesota	.	.	.	A131 x Oh7
340	A411	.	Minnesota	.	.	.	A131 x Oh7
341	A412	.	Minnesota	.	.	.	A131 x Oh7
342	A413	.	Minnesota	.	.	.	A131 x Oh7
343	A414	.	Minnesota	.	.	.	A131 x Oh7
344	A415	.	Minnesota	.	.	.	A148 x CC5
345	A416	.	Minnesota	.	.	.	A148 x CC5
346	A417	.	Minnesota	.	.	.	A148 x CC5
347	A418	.	Minnesota	.	.	.	A116 x L317
348	A419	Ames 23432	Minnesota	.	.	GRIN**	A21 x A163
349	A420	.	Minnesota	.	.	.	A21 x A163
350	A421	.	Minnesota	.	.	.	A21 x W283
351	A422	Ames 23433	Minnesota	.	.	GRIN	A21 x W283
352	A423	.	Minnesota	.	.	.	A2 x LSR
353	A424	Ames 23434	Minnesota	.	.	UMN	A2 x LSR
354	A425	.	Minnesota	.	.	.	A2 x LSR
355	A426	.	Minnesota	.	.	.	A95 x A344
356	A427	Ames 23435	Minnesota	.	.	UMN	CC36 x A405
357	A428	.	Minnesota	.	.	.	CC36 x A405
358	A429	.	Minnesota	.	.	.	A131 x A230
359	A430	.	Minnesota	.	.	.	A131 x A230
360	A431	.	Minnesota	.	.	.	A131 x A230
361	A432	.	Minnesota	.	.	.	(A131 x A230) x A131
362	A433	.	Minnesota	.	.	.	(A131 x A230) x A131
363	A434	.	Minnesota	.	.	.	(A34 x Oh93) x A34(2)
364	A435	.	Minnesota	.	.	.	(A34 x Oh93) x A34(2)
365	A436	.	Minnesota	.	.	.	(A340 x HS187-2) x A340(2)
366	A437	.	Minnesota	.	.	.	(A357 x HS187-2) x A357(2)
367	A438	.	Minnesota	.	.	.	(A97 x 398) x A97(3)

No.	Inbred name	GRIN ID	Developer	PVPA ID	PVPA expira-tion date	Seed source	Derivation
368	A439	.	Minnesota	.	.	.	(A97 x 398) x A97(3)
369	A440	.	Minnesota	.	.	.	(A97 x 398) x A97(3)
370	A441	.	Minnesota	.	.	.	(A97 x 398) x A97(3)
371	A442	.	Minnesota	.	.	.	(A97 x 398) x A97(3)
372	A443	.	Minnesota	.	.	.	A334 x Oh40B
373	A446	.	Minnesota	.	.	.	(A322 x POP) x A322(3)
374	A447	.	Minnesota	.	.	.	(A322 x POP) x A322(3)
375	A448	.	Minnesota	.	.	.	(A322 x POP) x A322(3)
376	A449	Ames 23436	Minnesota	.	.	GRIN	(A322 x POP) x A322(3)
377	A450	Ames 23437	Minnesota	.	.	GRIN	(A322 x POP) x A322(3)
378	A451	Ames 23438	Minnesota	.	.	GRIN	(A322 x POP) x A322(3)
379	A453	.	Minnesota	.	.	.	(A334 x Picuris) x A334(3)
380	A454	.	Minnesota	.	.	.	(A334 x Picuris) x A334(3)
381	A455	.	Minnesota	.	.	.	(A334 x Picuris) x A334(3)
382	A456	.	Minnesota	.	.	.	(A334 x POP) x A334(3)
383	A457	.	Minnesota	.	.	.	(A334 x POP) x A334(3)
384	A458	.	Minnesota	.	.	.	(A334 x POP) x A334(3)
385	A459	.	Minnesota	.	.	.	(A334 x POP) x A334(3)
386	A460	.	Minnesota	.	.	.	(A334 x POP) x A334(3)
387	A461	.	Minnesota	.	.	.	(A334 x POP) x A334(3)
388	A462	.	Minnesota	.	.	.	(A334 x POP) x A334(3)
389	A463	.	Minnesota	.	.	.	(A334 x POP) x A334(3)
390	A464	.	Minnesota	.	.	.	(A334 x POP) x A334(3)
391	A465	.	Minnesota	.	.	.	(A334 x POP) x A334(3)
392	A466	.	Minnesota	.	.	.	(A334 x POP) x A334(3)
393	A467	.	Minnesota	.	.	.	(A334 x POP) x A334(3)
394	A468	.	Minnesota	.	.	.	(A334 x POP) x A334(3)
395	A469	.	Minnesota	.	.	.	(A334 x POP) x A334(3)
396	A470	.	Minnesota	.	.	.	(A334 x POP) x A334(3)
397	A471	.	Minnesota	.	.	.	(A334 x POP) x A334(3)
398	A472	.	Minnesota	.	.	.	(A334 x POP) x A334(3)

No.	Inbred name	GRIN ID	Developer	PVPA ID	PVPA expira-tion date	Seed source	Derivation
399	A473	.	Minnesota	.	.	.	(A334 x POP) x A334(3)
400	A474	.	Minnesota	.	.	.	(A334 x POP) x A334(3)
401	A475	.	Minnesota	.	.	.	(A334 x POP) x A334(3)
402	A476	.	Minnesota	.	.	.	(A357 x Zuni Blue) x A357(3)
403	A477	.	Minnesota	.	.	.	(A357 x Zuni Blue) x A357(3)
404	A478	.	Minnesota	.	.	.	A116 x L317
405	A479	.	Minnesota	.	.	.	A334 x Oh7
406	A480	Ames 23439	Minnesota	.	.	GRIN	A21 x A163
407	A481	.	Minnesota	.	.	.	A21 x A163
408	A482	.	Minnesota	.	.	.	A21 x A163
409	A483	.	Minnesota	.	.	.	A21 x A163
410	A484	.	Minnesota	.	.	.	A21 x A163
411	A485	.	Minnesota	.	.	.	A21 x W283
412	A486	.	Minnesota	.	.	.	A21 x W283
413	A487	.	Minnesota	.	.	.	A21 x W283
414	A488	.	Minnesota	.	.	.	A21 x W283
415	A489	.	Minnesota	.	.	.	A21 x W283
416	A490	.	Minnesota	.	.	.	A21 x W283
417	A491	.	Minnesota	.	.	.	A163 x W283
418	A492	.	Minnesota	.	.	.	A163 x W283
419	A493	.	Minnesota	.	.	.	A163 x W283
420	A494	.	Minnesota	.	.	UMN	A163 x W283
421	A495	Ames 23440	Minnesota	.	.	UMN	A163 x W283
422	A496	.	Minnesota	.	.	.	A163 x W283
423	A497	Ames 23441	Minnesota	.	.	UMN	A163 x W283
424	A498	Ames 23442	Minnesota	.	.	UMN	A163 x W283
425	A499	Ames 23443	Minnesota	.	.	GRIN	A163 x W283
426	A500	Ames 23444	Minnesota	.	.	UMN	A163 x W283
427	A501	.	Minnesota	.	.	.	A334 x Haney's #13
428	A502	Ames 23445	Minnesota	.	.	UMN	A334 x Haney's #13
429	A503	.	Minnesota	.	.	.	A334 x Haney's #13

No.	Inbred name	GRIN ID	Developer	PVPA ID	PVPA expira-tion date	Seed source	Derivation
430	A504	.	Minnesota	.	.	.	A344 x Haney's #13
431	A505	.	Minnesota	.	.	.	A344 x Haney's #13
432	A506	.	Minnesota	.	.	.	A357 x Haney's #13
433	A507	.	Minnesota	.	.	.	A357 x Haney's #13
434	A508	Ames 23446	Minnesota	.	.	UMN	A357 x Haney's #13
435	A509	Ames 23447	Minnesota	.	.	UMN	A78 x A109
436	A510	.	Minnesota	.	.	.	A95 x A148
437	A511	.	Minnesota	.	.	.	A95 x A148
438	A512	.	Minnesota	.	.	.	A95 x A148
439	A513	.	Minnesota	.	.	.	A109 x A148
440	A514	.	Minnesota	.	.	.	A109 x A148
441	A515	.	Minnesota	.	.	.	A109 x A148
442	A516	.	Minnesota	.	.	.	A95 x A109
443	A517	.	Minnesota	.	.	.	A95 x A109
444	A518	.	Minnesota	.	.	.	A95 x A109
445	A519	.	Minnesota	.	.	.	A95 x A109
446	A520	.	Minnesota	.	.	.	A116 x L317
447	A521	.	Minnesota	.	.	.	A116 x L317
448	A522	.	Minnesota	.	.	.	A116 x L317
449	A523	.	Minnesota	.	.	.	A116 x L317
450	A524	.	Minnesota	.	.	.	A116 x L317
451	A525	.	Minnesota	.	.	.	A116 x L317
452	A526	.	Minnesota	.	.	.	A116 x L317
453	A527	.	Minnesota	.	.	.	A116 x L317
454	A528	.	Minnesota	.	.	.	A116 x L317
455	A529	.	Minnesota	.	.	.	A116 x L317
456	A530	.	Minnesota	.	.	.	A116 x L317
457	A531	.	Minnesota	.	.	.	A116 x L317
458	A532	.	Minnesota	.	.	.	A116 x L317
459	A533	.	Minnesota	.	.	.	A116 x L317
460	A534	.	Minnesota	.	.	.	A116 x L317

No.	Inbred name	GRIN ID	Developer	PVPA ID	PVPA expira-tion date	Seed source	Derivation
461	A535	.	Minnesota	.	.	.	A116 x L317
462	A536	.	Minnesota	.	.	.	A116 x L317
463	A537	.	Minnesota	.	.	.	A116 x L317
464	A538	.	Minnesota	.	.	.	A116 x L317
465	A539	.	Minnesota	.	.	.	A116 x L317
466	A540	.	Minnesota	.	.	.	A116 x L317
467	A541	.	Minnesota	.	.	.	A116 x L317
468	A542	.	Minnesota	.	.	.	A116 x L317
469	A543	.	Minnesota	.	.	.	A116 x L317
470	A544	.	Minnesota	.	.	.	A116 x L317
471	A545	.	Minnesota	.	.	.	A334 x Oh7
472	A546	.	Minnesota	.	.	.	A334 x Oh7
473	A547	Ames 23448	Minnesota	.	.	UMN	(A375 x Pioneer Long Ear) x A375
474	A548	Ames 23449	Minnesota	.	.	GRIN	(A375 x Pioneer Long Ear) x A375
475	A549	.	Minnesota	.	.	.	A189 x Golden King
476	A550	.	Minnesota	.	.	.	A189 x Golden King
477	A551	.	Minnesota	.	.	.	A192 x Golden King
478	A552	.	Minnesota	.	.	.	A192 x Golden King
479	A553	.	Minnesota	.	.	.	(AM14 x ND230) x ND230(2)
480	A554	PI 587138	Minnesota	.	.	GRIN	(Wf9 x WD) x WD(2)
481	A555	.	Minnesota	.	.	.	B164-886 x A237
482	A556	Ames 23450	Minnesota	.	.	UMN	B164-886 x A237
483	A557	.	Minnesota	.	.	.	A392 x Haney's #13
484	A558	.	Minnesota	.	.	.	A392 x Haney's #13
485	A559	.	Minnesota	.	.	.	A392 x Haney's #13
486	A560	.	Minnesota	.	.	.	A392 x Haney's #13
487	A561	.	Minnesota	.	.	.	A392 x Haney's #13
488	A562	.	Minnesota	.	.	.	(A340 x HS187-2) x A340(2)
489	A563	.	Minnesota	.	.	.	(A334 x Pioneer Long Ear) x A334
490	A564	.	Minnesota	.	.	.	(A334 x Pioneer Long Ear) x A334
491	A565	.	Minnesota	.	.	.	(A375 x Pioneer Long Ear) x A375

No.	Inbred name	GRIN ID	Developer	PVPA ID	PVPA expira-tion date	Seed source	Derivation
492	A566	.	Minnesota	.	.	.	(A375 x Pioneer Long Ear) x A375
493	A567	.	Minnesota	.	.	.	(A375 x Pioneer Long Ear) x A375
494	A568	.	Minnesota	.	.	.	Golden Jewel
495	A569	.	Minnesota	.	.	.	A73 x Murdock
496	A570	.	Minnesota	.	.	.	Minnesota Synthetic #2
497	A571	.	Minnesota	.	.	.	(A344 x Morris 13) x A344
498	A572	Ames 23451	Minnesota	.	.	GRIN	A344 x Morris 13
499	A573	.	Minnesota	.	.	.	A344 x Ia234
500	A574	.	Minnesota	.	.	.	A344 x A396
501	A575	Ames 23452	Minnesota	.	.	GRIN	A344 x A396
502	A576	.	Minnesota	.	.	.	Hershell's Hardy Cow Gold
503	A577	.	Minnesota	.	.	.	Golden Standard
504	A578	.	Minnesota	.	.	.	W9 x Fort Kent Golden
505	A579	.	Minnesota	.	.	.	(A73 x A21) x A73
506	A580	.	Minnesota	.	.	.	(A73 x A21) x A73
507	A581	.	Minnesota	.	.	.	(A73 x A21) x A73
508	A582	.	Minnesota	.	.	.	(A73 x A21) x A73
509	A583	.	Minnesota	.	.	.	(A15 x Pioneer Long Ear) x A15
510	A584	.	Minnesota	.	.	.	(A15 x Pioneer Long Ear) x A15
511	A585	Ames 23453	Minnesota	.	.	GRIN**	(A15 x Amargo 41-2504B) x A15
512	A586	Ames 23454	Minnesota	.	.	GRIN**	(A21 x Pioneer Long Ear) x A15
513	A587	.	Minnesota	.	.	.	(A21 x HK59) x A21
514	A588	Ames 23455	Minnesota	.	.	UMN	(A165 x Pioneer Long Ear) x A165
515	A589	.	Minnesota	.	.	.	(A116 x Pioneer Long Ear) x A116
516	A590	.	Minnesota	.	.	.	A158 x B2
517	A591	.	Minnesota	.	.	.	(M14 x Wf9) x Mt42
518	A592	.	Minnesota	.	.	.	A344 x ND211
519	A593	.	Minnesota	.	.	.	Iowa Synthetic #1
520	A594	.	Minnesota	.	.	.	Iowa Synthetic #1
521	A595	.	Minnesota	.	.	.	Iowa Synthetic #1
522	A596	.	Minnesota	.	.	.	Iowa Synthetic #1

No.	Inbred name	GRIN ID	Developer	PVPA ID	PVPA expira-tion date	Seed source	Derivation
523	A597	.	Minnesota	.	.	.	Iowa Synthetic #1
524	A598	.	Minnesota	.	.	.	Minnesota Synthetic #1
525	A599	.	Minnesota	.	.	.	Minnesota Synthetic #1
526	A600	.	Minnesota	.	.	.	Minnesota Synthetic #1
527	A601	.	Minnesota	.	.	.	Minnesota Synthetic #2
528	A602	.	Minnesota	.	.	.	Minnesota Synthetic #2
529	A603	.	Minnesota	.	.	.	Minnesota Synthetic #2
530	A604	.	Minnesota	.	.	.	Minnesota Synthetic #2
531	A605	.	Minnesota	.	.	.	Brown County Yellow Dent
532	A606	.	Minnesota	.	.	.	Brown County Yellow Dent
533	A607	.	Minnesota	.	.	.	A25 x B9A
534	A608	.	Minnesota	.	.	.	A25 x B9A
535	A609	.	Minnesota	.	.	.	A25 x Golden King
536	A610	.	Minnesota	.	.	.	A25 x Golden King
537	A611	.	Minnesota	.	.	.	A73 x Murdock L-6
538	A612	.	Minnesota	.	.	.	A73 x Murdock L-35
539	A613	.	Minnesota	.	.	.	(A73 x Oh51A) x A73(2)
540	A614	.	Minnesota	.	.	.	(A73 x Oh51A) x A73(2)
541	A615	.	Minnesota	.	.	.	(A73 x Oh51A) x A73(2)
542	A617	Ames 23456	Minnesota	.	.	GRIN	A434 x W22
543	A618	Ames 23457	Minnesota	.	.	GRIN	A434 x W22
544	A619	PI 587139	Minnesota	.	.	UMN	(A171 x Oh43) x Oh43
545	A620	.	Minnesota	.	.	.	A166 x A277
546	A621	.	Minnesota	.	.	.	(A166 x A277) x A277
547	A622	Ames 23459	Minnesota	.	.	GRIN	(A298 x Amargo 41-2504B) x A298(2)
548	A623	.	Minnesota	.	.	.	Unknown
549	A624	Ames 23460	Minnesota	.	.	GRIN	(ND230 x A295) x A295
550	A625	Ames 23461	Minnesota	.	.	GRIN	(A165 x Pioneer Long Ear) x A165
551	A626	Ames 23462	Minnesota	.	.	GRIN**	A322 x B2
552	A627	Ames 23463	Minnesota	.	.	GRIN	A392 x R61
553	A628	Ames 23464	Minnesota	.	.	GRIN	(M14 x A206) x Oh4c

No.	Inbred name	GRIN ID	Developer	PVPA ID	PVPA expira-tion date	Seed source	Derivation
554	A629	Ames 23465	Minnesota	.	.	GRIN	(V3 x Wf9) x Wf9
555	A630	Ames 23466	Minnesota	.	.	UMN	(A116 x Wf9) x Wf9(3)
556	A631	Ames 23467	Minnesota	.	.	GRIN	(A509 x Wf9) x Wf9(3)
557	A632	PI 587140	Minnesota	.	.	UMN	(Mt42 x B14) x B14(3)
558	A633	Ames 23471	Minnesota	.	.	GRIN	(Mt42 x B14) x B14(3)
559	A634	Ames 19308	Minnesota	.	.	GRIN	(Mt42 x B14) x B14(3)
560	A635	Ames 19309	Minnesota	.	.	GRIN	(ND203 x B14) x B14(2)
561	A636	Ames 23474	Minnesota	.	.	GRIN	(ND203 x B14) x B14(3)
562	A637	Ames 23475	Minnesota	.	.	GRIN	CO106 x A321
563	A638	Ames 23476	Minnesota	.	.	GRIN	(V3 x Wf9) x Wf9
564	A639	Ames 19310	Minnesota	.	.	GRIN**	A158 x B14
565	A640	Ames 23477	Minnesota	.	.	UMN	ND203 x B14
566	A641	Ames 19311	Minnesota	.	.	GRIN	ND203 x B14
567	A642	.	Minnesota	.	.	.	Koric Early Dent x Reid Yellow Dent
568	A643	Ames 23478	Minnesota	.	.	GRIN	Iowa Synthetic A
569	A644	Ames 23479	Minnesota	.	.	UMN	Iowa Synthetic A
570	A645	Ames 23480	Minnesota	.	.	GRIN	Minnesota Synthetic 3
571	A646	Ames 23481	Minnesota	.	.	UMN	Minnesota Synthetic 3
572	A647	.	Minnesota	.	.	.	Minnesota Synthetic 3
573	A648	NSL 81597	Minnesota	.	.	GRIN	Minnesota Synthetic 3
574	A649	Ames 23482	Minnesota	.	.	GRIN	(V3 x A321) x A321
575	A650	Ames 23483	Minnesota	.	.	GRIN	(V3 x A321) x A321
576	A651	Ames 23484	Minnesota	.	.	GRIN	(A73 x Q573) x A73
577	A652	Ames 23485	Minnesota	.	.	GRIN	A90 x Wf9
578	A653	Ames 23486	Minnesota	.	.	GRIN	A90 x Wf9
579	A654	PI 587141	Minnesota	.	.	UMN	A116 x Wf9
580	A655	Ames 23487	Minnesota	.	.	GRIN	(A488 x Wf9) x Wf9
581	A656	Ames 23488	Minnesota	.	.	GRIN	(Mt42 x B14) x B14
582	A657	NSL 81598	Minnesota	.	.	GRIN	Iowa Stiff Stalk Synthetic (Early)
583	A658	Ames 23489	Minnesota	.	.	GRIN**	Penn State Sythetic 2
584	A659	NSL 81599	Minnesota	.	.	GRIN	Minnesota Synthetic 3

No.	Inbred name	GRIN ID	Developer	PVPA ID	PVPA expira-tion date	Seed source	Derivation
585	A660	NSL81600	Minnesota	.	.	GRIN	Minnesota Synthetic 3
586	A661	PI 607521	Minnesota	.	.	GRIN	Minnesota Synthetic AS-A
587	A662	PI 607522	Minnesota	.	.	GRIN	Minnesota Synthetic AS-A
588	A663	PI 607523	Minnesota	.	.	GRIN	(A427 x Cuzco) x A427(2)
589	A664	PI 607524	Minnesota	.	.	GRIN	(ND203 x A636) x A636(2)
590	A665	PI 607525	Minnesota	.	.	GRIN	(ND203 x A635) x A635(3)
591	A666	Ames 23490	Minnesota	.	.	GRIN	Minnesota Synthetic C
592	A667	Ames 23491	Minnesota	.	.	GRIN	(W33 x 38-11) x 38-11
593	A668	Ames 23492	Minnesota	.	.	GRIN	(A509 x C103) x C103(2)
594	A669	Ames 23493	Minnesota	.	.	GRIN	(W33 x Hy2) x Hy2(3)
595	A670	Ames 23494	Minnesota	.	.	GRIN	(A632 x A619) x A619(4)
596	A671	Ames 23495	Minnesota	.	.	GRIN	(W103 x N13A) x N13A(2)
597	A672	Ames 23496	Minnesota	.	.	GRIN	(Golden Mine-Dent x A632) x A632
598	A673	Ames 23497	Minnesota	.	.	GRIN	UC D73
599	A674	Ames 23498	Minnesota	.	.	GRIN	ULR
600	A675	Ames 23499	Minnesota	.	.	GRIN	B73 x A662
601	A676	Ames 23500	Minnesota	.	.	GRIN	B70 x A662
602	A677	Ames 23501	Minnesota	.	.	GRIN	Oh545 x A90
603	A678	Ames 23502	Minnesota	.	.	GRIN	(B52 x A662) x B52
604	A679	PI 587142	Minnesota	.	.	GRIN	(B73 x A662) x B73(3)
605	A680	Ames 23503	Minnesota	.	.	GRIN	(B73 x A662) x B73(3)
606	A681	Ames 23504	Minnesota	.	.	GRIN	(B73 x A662) x B73(3)
607	A682	PI 587143	Minnesota	.	.	GRIN	(Mo17 x AS-D) x Mo17(2)
608	A683	Ames 23505	Minnesota	.	.	GRIN	(Mo17 x AS-D) x Mo17(2)
609	AS5707	PI 601269	Asgrow Seed Company	8600036	8/31/04	GRIN	C123Ht x Va59
610	B14	NSL 65866	Iowa State	.	.	GRIN	BSSS
611	B37	PI 550467	Iowa State	.	.	GRIN	BSSS
612	B52	PI 550454	Iowa State	.	.	GRIN	Unknown
613	B73	PI 550473	Iowa State	.	.	GRIN	BSSS C5
614	B84	PI 608767	Iowa State	.	.	GRIN	BS13(S2)C0
615	BCC03	PI 544065	Novartis Seeds, Inc.	9100002	5/29/10	GRIN	3224 x LH51

No.	Inbred name	GRIN ID	Developer	PVPA ID	PVPA expira-tion date	Seed source	Derivation
616	C103	Ames 19284	Connecticut	.	.	GRIN	Lancaster Sure Crop
617	C14	NSL 42874	Minnesota	.	.	GRIN	Minn #13
618	C49	Ames 28290	Minnesota	.	.	GRIN	Minn #13
619	CM105	PI 587124	Agriculture Canada	.	.	GRIN	V3 x B14(2)
620	CMV3	Ames 27104	Agriculture Canada	.	.	GRIN	A21 x W185
621	CR14	PI 601683	The J.C. Robinson Seed Company	8900095	12/31/08	GRIN	B73Ht, CM105, and CQ187 Synthetic
622	CR1Ht	PI 601080	The J.C. Robinson Seed Company	8400042	3/29/03	GRIN	W117Ht x Mo17Ht
623	DJ7	PI 601191	Edward J. Funk & Sons, Inc.	8500086	2/28/04	GRIN	B73 x BS16 Synthetic
624	DK4676A	PI 601300	DeKalb-Pfizer Genetics	8600092	12/31/04	GRIN	1067-1 x B-Line Composite
625	DK78004	PI 601210	DeKalb-Pfizer Genetics	8600091	12/31/04	GRIN	B73 x A634
626	DKFAPW	PI 600958	DeKalb-Pfizer Genetics	8200152	2/27/02	GRIN	B14AHt x B37Ht
627	DKFBHJ	PI 601439	DeKalb-Pfizer Genetics	8700173	7/29/06	GRIN	(FBAB x B84) x FBAB
628	DKHBA1	PI 601172	DeKalb-Pfizer Genetics	8500069	9/30/04	GRIN	Pioneer Hyb 3195 x Pioneer Hyb 3199
629	DKIBO14	PI 601208	DeKalb-Pfizer Genetics	8500123	4/30/04	GRIN	(Pioneer Hyb 3901 x H99) x Pioneer Hyb 3901
630	DKMBPM	PI 601440	DeKalb-Pfizer Genetics	8700175	9/30/06	GRIN	Composite 400M
631	DKMDF-13D	PI 600956	DeKalb-Pfizer Genetics	8200151	2/27/02	GRIN	H4101 x Composite 800M
632	E8501	PI 601724	Novartis Seeds, Inc.	8900233	10/31/08	GRIN	387 x FRMo17
633	Ep1	Ames 27111	Spain	.	.	GRIN	Spanish population 'Lizargarate'
634	F2	PI 257506	France	.	.	GRIN	OP Lacaune
635	F7	PI 257507	France	.	.	GRIN	OP Lacaune
636	F42	PI 601026	FFR Cooperative	8300157	11/30/02	GRIN	B73 Mutation selection
637	H99	PI 587129	Indiana	.	.	GRIN	Illinois Synthetic 60C
638	IBB14	PI 601565	DeKalb Plant Genetics	8800192	7/31/08	GRIN	Pioneer Hyb 3710 x Pioneer Hyb 3732
639	L 127	PI 601726	Lifaco Seed Corporation	8900201	12/31/08	GRIN	P 3901 x W117
640	L 135	PI 601727	Lifaco Seed Corporation	8900202	12/31/08	GRIN	P 3901 x W117
641	L 139	PI 601728	Lifaco Seed Corporation	8900203	12/31/08	GRIN	P 3901 x P 3780
642	LH38	PI 600791	Iowa State University Research Foundation	8000066	2/26/99	GRIN	Unknown
643	LH57	PI 601317	Holden's Foundation Seeds, Inc.	8600129	1/30/05	GRIN	(Mo17 x H99) x LH53

No.	Inbred name	GRIN ID	Developer	PVPA ID	PVPA expira-tion date	Seed source	Derivation
644	LH59	PI 601466	Holden's Foundation Seeds, Inc.	8700213	4/29/06	GRIN	(Mo17 x H99) x LH53
645	LH60	PI 601404	Holden's Foundation Seeds, Inc.	8700087	7/31/05	GRIN	LH55 x LH47
646	LH61	PI 601416	Holden's Foundation Seeds, Inc.	8700137	3/11/06	GRIN	(ASA x Mo17) x Mo17(2)
647	LH82	PI 601170	Holden's Foundation Seeds, Inc.	8500037	7/26/03	GRIN	Holden Line 610 x LH7
648	LH85	PI 601405	Holden's Foundation Seeds, Inc.	8700088	3/31/06	GRIN	Pioneer Hyb 3987
649	LH93	PI 601171	Holden's Foundation Seeds, Inc.	8500038	3/31/04	GRIN	BS11(FR)C3
650	LH119	PI 600954	Holden's Foundation Seeds, Inc.	8200064	5/26/01	GRIN	(H93 x B73) x B73
651	LH123HT	PI 601079	Holden's Foundation Seeds, Inc.	8400030	2/22/03	GRIN	Pioneer Hyb 3535
652	LH127	PI 538007	Holden's Foundation Seeds, Inc.	9000064	5/31/09	GRIN	LH122 x LH58
653	LH128	PI 547086	Holden's Foundation Seeds, Inc.	9100067	10/31/09	GRIN	LH51 x BS11LHC3
654	LH145	PI 600959	Holden's Foundation Seeds, Inc.	8300102	6/29/02	GRIN	A632Ht x CM105
655	LH149	PI 601493	Holden's Foundation Seeds, Inc.	8800053	11/30/06	GRIN	(A662 x B73) x B73(2)
656	LH156	PI 601403	Holden's Foundation Seeds, Inc.	8700090	1/15/06	GRIN	Va85 x Pa91
657	LH160	PI 539920	Holden's Foundation Seeds, Inc.	9000122	1/31/09	GRIN	ND246 x Early Mo17 Composite
658	LH190	PI 539922	Holden's Foundation Seeds, Inc.	9000124	1/31/09	GRIN	B73Ht x B68Ht
659	LH193	PI 539927	Holden's Foundation Seeds, Inc.	9000141	6/28/09	GRIN	LHE137 x LHE136
660	LH194	PI 539923	Holden's Foundation Seeds, Inc.	9000125	5/31/09	GRIN	LH117 x LHE137
661	LH196	PI 538009	Holden's Foundation Seeds, Inc.	9000066	6/28/09	GRIN	LH74 x LH119
662	LH202	PI 539924	Holden's Foundation Seeds, Inc.	9000126	6/28/09	GRIN	(A662 x B73) x B73(2)
663	LH205	PI 537099	Holden's Foundation Seeds, Inc.	9000049	5/31/09	GRIN	LH74 x LH119
664	LH208	PI 547088	Holden's Foundation Seeds, Inc.	9100069	10/31/09	GRIN	LH74 x CB59G
665	LH215	PI 552815	Holden's Foundation Seeds, Inc.	9100201	4/30/10	GRIN	R177 Synthetic x Mo17 Synthetic
666	MBST	PI 601566	DeKalb-Pfizer Genetics	8800194	2/28/07	GRIN	LH38 x 4726-1
667	MBUB	PI 548839	DeKalb Plant Genetics	9100135	4/30/10	GRIN	LH38 x MANS
668	MM402A	PI 554615	DeKalb Plant Genetics	9100222	4/30/10	GRIN	LH38 x MANS
669	Mo17	PI 558532	Missouri	.	.	GRIN	C.I. 187-2 x C103
670	Mt42	Ames 20140	Montana	.	.	GRIN	Minn #13
671	NC268	PI 587145	North Carolina	.	.	GRIN	(B73 x NC250) x B73
672	ND203	NSL 32732	North Dakota	.	.	GRIN	Haney's Minn #13
673	ND300	PI 607527	North Dakota	.	.	GRIN	W739 x W845
674	NK740	PI 601489	Novartis Seeds, Inc.	8800028	6/30/06	GRIN	(Mo17 x Mexican Deep Kernel) x Mo17(2)

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675	NK764	PI 601374	Novartis Seeds, Inc.	8700036	6/30/05	GRIN	NK235 x B73
676	NK779	PI 601376	Novartis Seeds, Inc.	8700041	8/31/05	GRIN	CM7 x W117
677	NK793	PI 601492	Novartis Seeds, Inc.	8800031	8/31/06	GRIN	NK235 x B73
678	NK807	PI 601430	Novartis Seeds, Inc.	8700151	4/29/06	GRIN	W117 x B37
679	NKS8326	PI 601612	Novartis Seeds, Inc.	8800154	11/30/06	GRIN	(W117 x Mo17) x Mo17
680	Oh43	Ames 19288	Ohio	.	.	GRIN	W8 x Oh40B
681	OQ603	PI 601584	DowElanco	8800150	4/27/07	GRIN	Pioneer Hyb 3713
682	Pa91	PI 587147	Pennsylvania	.	.	GRIN	(Wf9 x Oh40B) x [(38-11 x L317) x 38-11]
683	PH207	PI 601005	Pioneer Hi-Bred International, Inc.	8300144	12/21/02	GRIN	PHG3BD2 x PHG3RZ1
684	PHB09	PI 601007	Pioneer Hi-Bred International, Inc.	8300142	12/21/02	GRIN	PH555 x PH031
685	PHBA6	PI 559935	Pioneer Hi-Bred International, Inc.	9200078	6/30/10	GRIN	PHZ51 x PHG47
686	PHG29	PI 601270	Pioneer Hi-Bred International, Inc.	8600047	9/30/04	GRIN	PH207 x (PH207 x PH806)
687	PHG47	PI 601318	Pioneer Hi-Bred International, Inc.	8600131	1/30/05	GRIN	PH041 x MKSDTE C10
688	PHG50	PI 601006	Pioneer Hi-Bred International, Inc.	8300143	12/21/02	GRIN	PH848 x PH207
689	PHG80	PI 601037	Pioneer Hi-Bred International, Inc.	8400128	7/26/03	GRIN	PH495 x PH331
690	PHG84	PI 601320	Pioneer Hi-Bred International, Inc.	8600130	1/30/05	GRIN	PH848 x PH595
691	PHG86	PI 601442	Pioneer Hi-Bred International, Inc.	8700170	3/31/06	GRIN	B64 x B73
692	PHH93	PI 601567	Pioneer Hi-Bred International, Inc.	8800216	2/28/07	GRIN	PH806 x PH207
693	PHJ33	PI 601774	Pioneer Hi-Bred International, Inc.	8900308	9/28/08	GRIN	PHG83 x CE18
694	PHJ65	PI 543840	Pioneer Hi-Bred International, Inc.	9000245	8/30/09	GRIN	PHG63 x PHG65
695	PHJ75	PI 601776	Pioneer Hi-Bred International, Inc.	8900310	10/31/08	GRIN	207 x G96
696	PHK29	PI 601468	Pioneer Hi-Bred International, Inc.	8700214	5/31/06	GRIN	PHB47 x PHAC54
697	PHK35	PI 601777	Pioneer Hi-Bred International, Inc.	8900311	10/31/08	GRIN	AC34 x G93H
698	PHK42	PI 601495	Pioneer Hi-Bred International, Inc.	8800035	7/29/06	GRIN	PH207 x (PH207 x PH806)
699	PHK76	PI 601496	Pioneer Hi-Bred International, Inc.	8800036	7/29/06	GRIN	PHAD18 x PHB02
700	PHK93	PI 548800	Pioneer Hi-Bred International, Inc.	9100094	4/30/10	GRIN	PHB72 x PHT60
701	PHM57	PI 601779	Pioneer Hi-Bred International, Inc.	8900313	10/31/08	GRIN	B97 x 595
702	PHM81	PI 548801	Pioneer Hi-Bred International, Inc.	9100095	4/30/10	GRIN	PHG72 x PHG68
703	PHN11	PI 601497	Pioneer Hi-Bred International, Inc.	8800037	7/29/06	GRIN	PH207 x (PH207 x PH806)
704	PHN29	PI 601780	Pioneer Hi-Bred International, Inc.	8900314	10/31/08	GRIN	G69 x C40
705	PHN47	PI 601569	Pioneer Hi-Bred International, Inc.	8800217	3/31/07	GRIN	207 x PHB60

No.	Inbred name	GRIN ID	Developer	PVPA ID	PVPA expira-tion date	Seed source	Derivation
706	PHN66	PI 548802	Pioneer Hi-Bred International, Inc.	9100096	4/30/10	GRIN	PHG53 x PHG21
707	PHN82	PI 601783	Pioneer Hi-Bred International, Inc.	8900317	11/30/08	GRIN	PHG29 x HD38
708	PHP55	PI 601784	Pioneer Hi-Bred International, Inc.	8900318	11/30/08	GRIN	PHG44 x PHG29
709	PHP60	PI 601785	Pioneer Hi-Bred International, Inc.	8900319	11/30/08	GRIN	AT2 x 805
710	PHP76	PI 543846	Pioneer Hi-Bred International, Inc.	9000251	8/30/09	GRIN	G50 x PHEJ8
711	PHP85	PI 559944	Pioneer Hi-Bred International, Inc.	9200087	6/30/10	GRIN	PHK29 x PHW52
712	PHPR5	PI 559945	Pioneer Hi-Bred International, Inc.	9200088	6/30/10	GRIN	PHK76 x PHW52
713	PHR32	PI 601571	Pioneer Hi-Bred International, Inc.	8800218	3/31/07	GRIN	PHB82 x PHG61
714	PHR36	PI 601361	Pioneer Hi-Bred International, Inc.	8700017	5/29/05	GRIN	[(PH203 x PH549) x PH549] x PH848
715	PHR47	PI 601572	Pioneer Hi-Bred International, Inc.	8800213	1/31/07	GRIN	G39 x PHB49
716	PHR55	PI 548804	Pioneer Hi-Bred International, Inc.	9100098	4/30/10	GRIN	PH005 x PHG84
717	PHR58	PI 548805	Pioneer Hi-Bred International, Inc.	9100099	4/30/10	GRIN	PH383 x PHG16
718	PHR62	PI 601786	Pioneer Hi-Bred International, Inc.	8900320	11/30/08	GRIN	G50 x G35
719	PHT10	PI 601573	Pioneer Hi-Bred International, Inc.	8800214	2/28/07	GRIN	B73 x G39
720	PHT22	PI 601788	Pioneer Hi-Bred International, Inc.	8900322	11/30/08	GRIN	207 x HD12
721	PHT55	PI 601498	Pioneer Hi-Bred International, Inc.	8800046	8/31/06	GRIN	A33GB4 x A34CB4
722	PHT77	PI 601499	Pioneer Hi-Bred International, Inc.	8800038	7/29/06	GRIN	PH814 x PH995
723	PHV53	PI 559952	Pioneer Hi-Bred International, Inc.	9200095	6/30/10	GRIN	PHB89 x PHDT2
724	PHV78	PI 601470	Pioneer Hi-Bred International, Inc.	8800003	5/31/06	GRIN	PHG42 x PH595
725	PHVA9	PI 559953	Pioneer Hi-Bred International, Inc.	9200096	6/30/10	GRIN	PHK29 x PHGP8
726	PHW03	PI 601790	Pioneer Hi-Bred International, Inc.	8900324	11/30/08	GRIN	801 x G48
727	PHW17	PI 601362	Pioneer Hi-Bred International, Inc.	8700018	5/29/05	GRIN	(PHID11 x B73) x [B73 x (B73 x PH051)]
728	PHW30	PI 548808	Pioneer Hi-Bred International, Inc.	9100102	4/30/10	GRIN	PHG42 x PHV15
729	PHW43	PI 601792	Pioneer Hi-Bred International, Inc.	8900326	11/30/08	GRIN	995 x G35
730	PHW51	PI 543849	Pioneer Hi-Bred International, Inc.	9000254	8/30/09	GRIN	PHDF2 x PHW51
731	PHW52	PI 601575	Pioneer Hi-Bred International, Inc.	8800215	2/28/07	GRIN	B73 x G39
732	PHW65	PI 601501	Pioneer Hi-Bred International, Inc.	8800040	8/31/06	GRIN	PH861 x PH595
733	PHZ51	PI 601322	Pioneer Hi-Bred International, Inc.	8600132	3/31/05	GRIN	PH814 x PH848
734	SD42	PI 508277	South Dakota State	.	.	GRIN	SDp332 x H96
735	Va35	PI 587150	Virginia	.	.	GRIN	(C103 x T8) x T8
736	W117	PI 587153	Wisconsin	.	.	GRIN	643 x Minn #13

No.	Inbred name	GRIN ID	Developer	PVPA ID	PVPA expira-tion date	Seed source	Derivation
737	W64a	PI 587152	Wisconsin	.	.	GRIN	Wf9 x C.I. 187-2
738	W8304	PI 601502	Novartis Seeds, Inc.	8800032	3/31/07	GRIN	(B14A x B73) x B14A
739	W8555	PI 601729	Novartis Seeds, Inc.	8900227	9/28/08	GRIN	B73Ht x B84
740	WIL500	PI 601689	Wilson Hybrids, Inc.	8900156	7/31/08	GRIN	82C25 Composite
741	WIL900	PI 601684	Wilson Hybrids, Inc.	8900092	5/31/09	GRIN	82C43 Composite
742	WIL901	PI 601685	Wilson Hybrids, Inc.	8900093	5/31/09	GRIN	82C232 Composite

No.	Year developed	Year released	Pedigree source	Status in study	Model-based cluster	B73	Mo17	Oh43	A321	PH207
1	.	.	Nelson et al., 2008	Included	Oh43	0.0092	0.0016	0.5884	0.396	0.0048
2	.	.	PVPA Certificate	Included	B73	0.7754	0.0048	0.0416	0.176	0.0022
3	.	.	Nelson et al., 2008	Included	A321	0.0318	0.0852	0.34	0.3871	0.156
4	.	.	PVPA Certificate	Included	PH207	0.001	0.1234	0.114	0.1316	0.6299
5	.	.	PVPA Certificate	Included	B73	0.857	0.0024	0.0022	0.075	0.0634
6	.	.	PVPA Certificate	Included	Mo17	0.0038	0.4031	0.3537	0.2275	0.0118
7	.	.	PVPA Certificate	Included	B73	0.7813	0.001	0.0332	0.1797	0.0048
8	.	1950	UM Records	No seed available	.	.	.	.	.	.
9	.	1950	UM Records	No seed available	.	.	.	.	.	.
10	.	.	UM Records	No seed available	.	.	.	.	.	.
11	.	.	UM Records	No seed available	.	.	.	.	.	.
12	.	.	UM Records	No seed available	.	.	.	.	.	.
13	.	.	UM Records	No seed available	.	.	.	.	.	.
14	.	.	UM Records	Included	Oh43	0.0322	0.027	0.4809	0.3838	0.0762
15	.	.	UM Records	No seed available	.	.	.	.	.	.
16	.	.	UM Records	No seed available	.	.	.	.	.	.
17	.	.	UM Records	No seed available	.	.	.	.	.	.
18	.	1950	UM Records	Included	A321	0.1132	0.0248	0.4004	0.4158	0.0458
19	.	.	UM Records	No seed available	.	.	.	.	.	.
20	.	.	UM Records	No seed available	.	.	.	.	.	.
21	.	.	UM Records	Included	Oh43	0.0268	0.1016	0.4305	0.4246	0.0166
22	.	.	UM Records	No seed available	.	.	.	.	.	.
23	.	.	UM Records	No seed available	.	.	.	.	.	.
24	.	.	UM Records	No seed available	.	.	.	.	.	.
25	.	.	UM Records	No seed available	.	.	.	.	.	.
26	.	.	UM Records	No seed available	.	.	.	.	.	.
27	.	1950	UM Records	No seed available	.	.	.	.	.	.
28	.	.	UM Records	No seed available	.	.	.	.	.	.
29	.	.	UM Records	No seed available	.	.	.	.	.	.
30	.	.	UM Records	No seed available	.	.	.	.	.	.

No.	Year developed	Year released	Pedigree source	Status in study	Model-based cluster	B73	Mo17	Oh43	A321	PH207
31	1935	1950	UM Records	No seed available	.	.	.	.	.	.
32	.	.	UM Records	No seed available	.	.	.	.	.	.
33	.	.	UM Records	No seed available	.	.	.	.	.	.
34	1935	.	UM Records	No seed available	.	.	.	.	.	.
35	1935	.	UM Records	No seed available	.	.	.	.	.	.
36	.	.	UM Records	No seed available	.	.	.	.	.	.
37	.	.	UM Records	No seed available	.	.	.	.	.	.
38	.	.	UM Records	No seed available	.	.	.	.	.	.
39	.	.	UM Records	No seed available	.	.	.	.	.	.
40	.	.	UM Records	No seed available	.	.	.	.	.	.
41	.	.	UM Records	No seed available	.	.	.	.	.	.
42	.	1950	UM Records	Included	A321	0.0372	0.0232	0.3483	0.5135	0.0778
43	.	.	UM Records	No seed available	.	.	.	.	.	.
44	.	.	UM Records	No seed available	.	.	.	.	.	.
45	.	.	UM Records	No seed available	.	.	.	.	.	.
46	.	.	UM Records	No seed available	.	.	.	.	.	.
47	.	.	UM Records	No seed available	.	.	.	.	.	.
48	.	.	UM Records	No seed available	.	.	.	.	.	.
49	.	.	UM Records	No seed available	.	.	.	.	.	.
50	.	.	UM Records	No seed available	.	.	.	.	.	.
51	.	.	UM Records	No seed available	.	.	.	.	.	.
52	.	.	UM Records	No seed available	.	.	.	.	.	.
53	.	.	UM Records	No seed available	.	.	.	.	.	.
54	.	.	UM Records	No seed available	.	.	.	.	.	.
55	.	.	UM Records	No seed available	.	.	.	.	.	.
56	.	.	UM Records	No seed available	.	.	.	.	.	.
57	.	.	UM Records	No seed available	.	.	.	.	.	.
58	.	.	UM Records	No seed available	.	.	.	.	.	.
59	.	.	UM Records	No seed available	.	.	.	.	.	.
60	.	.	UM Records	No seed available	.	.	.	.	.	.
61	.	.	UM Records	No seed available	.	.	.	.	.	.

No.	Year developed	Year released	Pedigree source	Status in study	Model-based cluster	B73	Mo17	Oh43	A321	PH207
62	.	.	UM Records	No seed available	.	.	.	.	.	.
63	.	.	UM Records	No seed available	.	.	.	.	.	.
64	.	.	UM Records	No seed available	.	.	.	.	.	.
65	.	.	UM Records	No seed available	.	.	.	.	.	.
66	.	.	UM Records	No seed available	.	.	.	.	.	.
67	.	.	UM Records	No seed available	.	.	.	.	.	.
68	.	.	UM Records	No seed available	.	.	.	.	.	.
69	.	.	UM Records	No seed available	.	.	.	.	.	.
70	.	.	UM Records	No seed available	.	.	.	.	.	.
71	.	.	UM Records	No seed available	.	.	.	.	.	.
72	.	.	UM Records	No seed available	.	.	.	.	.	.
73	.	.	UM Records	No seed available	.	.	.	.	.	.
74	.	.	UM Records	No seed available	.	.	.	.	.	.
75	.	.	UM Records	No seed available	.	.	.	.	.	.
76	.	.	UM Records	No seed available	.	.	.	.	.	.
77	.	.	UM Records	No seed available	.	.	.	.	.	.
78	.	.	UM Records	No seed available	.	.	.	.	.	.
79	.	.	UM Records	No seed available	.	.	.	.	.	.
80	.	.	UM Records	No seed available	.	.	.	.	.	.
81	.	.	UM Records	No seed available	.	.	.	.	.	.
82	1935	1950	UM Records	Included	A321	0.0886	0.0094	0.1545	0.6444	0.1032
83	1935	.	UM Records	No seed available	.	.	.	.	.	.
84	1935	1950	UM Records	Included	A321	0.0312	0.0004	0.001	0.9664	0.001
85	.	.	UM Records	No seed available	.	.	.	.	.	.
86	.	.	UM Records	No seed available	.	.	.	.	.	.
87	1933	.	UM Records	No seed available	.	.	.	.	.	.
88	1933	.	UM Records	No seed available	.	.	.	.	.	.
89	.	.	UM Records	No seed available	.	.	.	.	.	.
90	.	.	UM Records	Included	Oh43	0.0512	0.0462	0.4061	0.3806	0.116
91	.	.	UM Records	Included	Oh43	0.001	0.103	0.4744	0.3478	0.0738
92	.	.	UM Records	Included	B73	0.7968	0.0006	0.0546	0.1464	0.0016

No.	Year developed	Year released	Pedigree source	Status in study	Model-based cluster	B73	Mo17	Oh43	A321	PH207
93	.	.	UM Records	No seed available	.	.	.	.	.	.
94	.	.	UM Records	No seed available	.	.	.	.	.	.
95	.	.	UM Records	Included	Oh43	0.0654	0.0562	0.4898	0.3876	0.001
96	.	.	UM Records	Included	A321	0.2744	0.0052	0.2246	0.4685	0.0274
97	.	.	UM Records	No seed available	.	.	.	.	.	.
98	.	.	UM Records	No seed available	.	.	.	.	.	.
99	.	.	UM Records	Included	A321	0.0214	0.0852	0.3567	0.5121	0.0246
100	.	.	UM Records	Included	B73	0.8622	0.0002	0.0486	0.0876	0.0014
101	.	1950	UM Records	Included	A321	0.0008	0.0056	0.359	0.6254	0.0092
102	.	.	UM Records	Included	Oh43	0.0022	0.0338	0.5191	0.4421	0.0028
103	.	.	UM Records	Included	A321	0.1488	0.0568	0.3174	0.3742	0.1028
104	.	.	UM Records	No seed available	.	.	.	.	.	.
105	.	.	UM Records	Included	A321	0.3088	0.0572	0.2937	0.3191	0.0212
106	.	.	UM Records	No seed available	.	.	.	.	.	.
107	.	1950	UM Records	Included	A321	0.0078	0.0012	0.1744	0.8156	0.001
108	.	.	UM Records	No seed available	.	.	.	.	.	.
109	.	.	UM Records	No seed available	.	.	.	.	.	.
110	.	.	UM Records	No seed available	.	.	.	.	.	.
111	.	.	UM Records	No seed available	.	.	.	.	.	.
112	.	.	UM Records	No seed available	.	.	.	.	.	.
113	.	.	UM Records	No seed available	.	.	.	.	.	.
114	.	.	UM Records	No seed available	.	.	.	.	.	.
115	.	.	UM Records	No seed available	.	.	.	.	.	.
116	.	.	UM Records	No seed available	.	.	.	.	.	.
117	.	.	UM Records	No seed available	.	.	.	.	.	.
118	.	.	UM Records	No seed available	.	.	.	.	.	.
119	.	.	UM Records	No seed available	.	.	.	.	.	.
120	.	.	UM Records	No seed available	.	.	.	.	.	.
121	.	1950	UM Records	No seed available	.	.	.	.	.	.
122	.	.	UM Records	No seed available	.	.	.	.	.	.
123	.	.	UM Records	No seed available	.	.	.	.	.	.

No.	Year developed	Year released	Pedigree source	Status in study	Model-based cluster	B73	Mo17	Oh43	A321	PH207
124	.	.	UM Records	No seed available	.	.	.	.	.	.
125	.	.	UM Records	No seed available	.	.	.	.	.	.
126	.	1950	UM Records	Included	A321	0.002	0.0492	0.3393	0.5175	0.092
127	.	.	UM Records	No seed available	.	.	.	.	.	.
128	.	.	UM Records	No seed available	.	.	.	.	.	.
129	.	.	UM Records	No seed available	.	.	.	.	.	.
130	.	.	UM Records	No seed available	.	.	.	.	.	.
131	.	.	UM Records	No seed available	.	.	.	.	.	.
132	.	.	UM Records	No seed available	.	.	.	.	.	.
133	.	.	UM Records	No seed available	.	.	.	.	.	.
134	.	.	UM Records	No seed available	.	.	.	.	.	.
135	.	.	UM Records	No seed available	.	.	.	.	.	.
136	.	.	UM Records	No seed available	.	.	.	.	.	.
137	.	.	UM Records	No seed available	.	.	.	.	.	.
138	.	.	UM Records	No seed available	.	.	.	.	.	.
139	.	.	UM Records	No seed available	.	.	.	.	.	.
140	.	.	UM Records	No seed available	.	.	.	.	.	.
141	.	1950	UM Records	No seed available	.	.	.	.	.	.
142	.	.	UM Records	No seed available	.	.	.	.	.	.
143	.	.	UM Records	No seed available	.	.	.	.	.	.
144	.	.	UM Records	No seed available	.	.	.	.	.	.
145	.	.	UM Records	No seed available	.	.	.	.	.	.
146	.	.	UM Records	No seed available	.	.	.	.	.	.
147	.	.	UM Records	No seed available	.	.	.	.	.	.
148	.	.	UM Records	No seed available	.	.	.	.	.	.
149	.	.	UM Records	No seed available	.	.	.	.	.	.
150	.	.	UM Records	No seed available	.	.	.	.	.	.
151	.	.	UM Records	No seed available	.	.	.	.	.	.
152	.	.	UM Records	No seed available	.	.	.	.	.	.
153	.	.	UM Records	No seed available	.	.	.	.	.	.
154	.	.	UM Records	No seed available	.	.	.	.	.	.

No.	Year developed	Year released	Pedigree source	Status in study	Model-based cluster	B73	Mo17	Oh43	A321	PH207
155	.	.	UM Records	No seed available	.	.	.	.	.	.
156	.	.	UM Records	No seed available	.	.	.	.	.	.
157	.	.	UM Records	No seed available	.	.	.	.	.	.
158	.	1950	UM Records	No seed available	.	.	.	.	.	.
159	.	.	UM Records	No seed available	.	.	.	.	.	.
160	.	.	UM Records	No seed available	.	.	.	.	.	.
161	.	.	UM Records	No seed available	.	.	.	.	.	.
162	.	.	UM Records	Included	Oh43	0	0.0006	0.9956	0.0034	0.0004
163	.	.	UM Records	No seed available	.	.	.	.	.	.
164	.	.	UM Records	No seed available	.	.	.	.	.	.
165	.	.	UM Records	Included	Oh43	0.0002	0.0004	0.9798	0.0192	0.0004
166	.	.	UM Records	No seed available	.	.	.	.	.	.
167	.	.	UM Records	No seed available	.	.	.	.	.	.
168	.	1950	UM Records	Included	Oh43	0	0	0.9998	0.0002	0
169	.	.	UM Records	No seed available	.	.	.	.	.	.
170	.	.	UM Records	No seed available	.	.	.	.	.	.
171	.	.	UM Records	No seed available	.	.	.	.	.	.
172	.	.	UM Records	No seed available	.	.	.	.	.	.
173	.	.	UM Records	No seed available	.	.	.	.	.	.
174	.	.	UM Records	No seed available	.	.	.	.	.	.
175	.	1950	UM Records	Included	Oh43	0	0	0.9996	0.0004	0
176	.	1950	UM Records	Included	A321	0.0182	0.001	0.314	0.5764	0.0904
177	.	.	UM Records	No seed available	.	.	.	.	.	.
178	.	1950	UM Records	Included	A321	0.0286	0.0212	0.3853	0.4417	0.1232
179	.	.	UM Records	No seed available	.	.	.	.	.	.
180	.	.	UM Records	No seed available	.	.	.	.	.	.
181	.	.	Gerdes et al., 1993	No seed available	.	.	.	.	.	.
182	.	.	UM Records	No seed available	.	.	.	.	.	.
183	.	.	UM Records	No seed available	.	.	.	.	.	.
184	.	.	UM Records	No seed available	.	.	.	.	.	.
185	.	.	UM Records	No seed available	.	.	.	.	.	.

No.	Year developed	Year released	Pedigree source	Status in study	Model-based cluster	B73	Mo17	Oh43	A321	PH207
186	.	.	UM Records	No seed available	.	.	.	.	.	.
187	.	.	UM Records	No seed available	.	.	.	.	.	.
188	.	.	UM Records	No seed available	.	.	.	.	.	.
189	.	1950	UM Records	Included	A321	0.0178	0.1581	0.3351	0.481	0.008
190	.	.	UM Records	No seed available	.	.	.	.	.	.
191	.	.	UM Records	No seed available	.	.	.	.	.	.
192	.	.	UM Records	No seed available	.	.	.	.	.	.
193	.	.	UM Records	No seed available	.	.	.	.	.	.
194	.	.	UM Records	No seed available	.	.	.	.	.	.
195	1938	.	UM Records	No seed available	.	.	.	.	.	.
196	1938	.	UM Records	Included	Oh43	0	0.0002	0.9624	0.0366	0.0008
197	1938	.	UM Records	No seed available	.	.	.	.	.	.
198	1938	.	UM Records	Included	Oh43	0	0	0.9606	0.039	0.0004
199	1938	.	UM Records	Included	Oh43	0.001	0.001	0.904	0.0916	0.0024
200	1943	.	UM Records	No seed available	.	.	.	.	.	.
201	1943	.	UM Records	No seed available	.	.	.	.	.	.
202	1943	.	UM Records	Included	Oh43	0.0038	0.0044	0.6778	0.3066	0.0074
203	1943	.	UM Records	No seed available	.	.	.	.	.	.
204	1938	.	UM Records	No seed available	.	.	.	.	.	.
205	1938	.	UM Records	No seed available	.	.	.	.	.	.
206	1938	.	UM Records	No seed available	.	.	.	.	.	.
207	1938	.	UM Records	No seed available	.	.	.	.	.	.
208	1938	.	UM Records	No seed available	.	.	.	.	.	.
209	1938	.	UM Records	No seed available	.	.	.	.	.	.
210	1938	.	UM Records	No seed available	.	.	.	.	.	.
211	1943	.	UM Records	No seed available	.	.	.	.	.	.
212	1943	.	UM Records	Included	A321	0.0028	0.001	0.406	0.518	0.0722
213	1938	.	UM Records	No seed available	.	.	.	.	.	.
214	1938	.	UM Records	No seed available	.	.	.	.	.	.
215	1938	.	UM Records	No seed available	.	.	.	.	.	.
216	1938	.	UM Records	No seed available	.	.	.	.	.	.

No.	Year developed	Year released	Pedigree source	Status in study	Model-based cluster	B73	Mo17	Oh43	A321	PH207
217	1943	.	UM Records	Included	A321	0.0058	0.002	0.0034	0.9564	0.0324
218	1938	.	UM Records	No seed available	.	.	.	.	.	.
219	1938	.	UM Records	No seed available	.	.	.	.	.	.
220	1938	.	UM Records	No seed available	.	.	.	.	.	.
221	1938	.	UM Records	No seed available	.	.	.	.	.	.
222	1943	.	UM Records	No seed available	.	.	.	.	.	.
223	1938	.	UM Records	No seed available	.	.	.	.	.	.
224	1946	1970	UM Records	Included	A321	0.0108	0	0.0214	0.9614	0.0064
225	1946	.	UM Records	Included	A321	0.0032	0	0.0244	0.9724	0
226	1946	.	UM Records	No seed available	.	.	.	.	.	.
227	1946	.	UM Records	No seed available	.	.	.	.	.	.
228	1946	.	UM Records	No seed available	.	.	.	.	.	.
229	1946	.	UM Records	No seed available	.	.	.	.	.	.
230	1946	.	UM Records	No seed available	.	.	.	.	.	.
231	1946	.	UM Records	No seed available	.	.	.	.	.	.
232	1946	.	UM Records	No seed available	.	.	.	.	.	.
233	1946	.	UM Records	No seed available	.	.	.	.	.	.
234	1946	.	UM Records	No seed available	.	.	.	.	.	.
235	1946	.	UM Records	No seed available	.	.	.	.	.	.
236	1946	.	UM Records	Included	A321	0.1142	0.0094	0.1274	0.724	0.025
237	1946	.	UM Records	No seed available	.	.	.	.	.	.
238	1946	.	UM Records	No seed available	.	.	.	.	.	.
239	1946	.	UM Records	No seed available	.	.	.	.	.	.
240	1946	.	UM Records	No seed available	.	.	.	.	.	.
241	1946	.	UM Records	Included	A321	0.044	0.001	0.0734	0.8768	0.0048
242	1946	1970	UM Records	Included	A321	0.041	0.0012	0.0716	0.8355	0.0506
243	1946	.	UM Records	No seed available	.	.	.	.	.	.
244	1946	.	UM Records	Included	A321	0.0782	0.0512	0.2675	0.4597	0.1434
245	1946	.	UM Records	No seed available	.	.	.	.	.	.
246	1946	.	UM Records	No seed available	.	.	.	.	.	.
247	1946	.	UM Records	No seed available	.	.	.	.	.	.

No.	Year developed	Year released	Pedigree source	Status in study	Model-based cluster	B73	Mo17	Oh43	A321	PH207
248	1946	.	UM Records	Included	A321	0.0718	0.028	0.3663	0.4658	0.0682
249	1947	.	UM Records	Included	A321	0.1326	0.0678	0.2776	0.4899	0.032
250	1947	.	UM Records	No seed available	.	.	.	.	.	.
251	1942	.	UM Records	No seed available	.	.	.	.	.	.
252	1947	.	UM Records	No seed available	.	.	.	.	.	.
253	1946	.	UM Records	No seed available	.	.	.	.	.	.
254	1946	.	UM Records	No seed available	.	.	.	.	.	.
255	1946	.	UM Records	No seed available	.	.	.	.	.	.
256	1946	.	UM Records	No seed available	.	.	.	.	.	.
257	1946	.	UM Records	No seed available	.	.	.	.	.	.
258	1946	.	UM Records	No seed available	.	.	.	.	.	.
259	1946	.	UM Records	No seed available	.	.	.	.	.	.
260	1946	.	UM Records	No seed available	.	.	.	.	.	.
261	1947	.	UM Records	No seed available	.	.	.	.	.	.
262	1947	.	UM Records	No seed available	.	.	.	.	.	.
263	1947	.	UM Records	No seed available	.	.	.	.	.	.
264	1947	.	UM Records	No seed available	.	.	.	.	.	.
265	1947	.	UM Records	No seed available	.	.	.	.	.	.
266	1947	.	UM Records	No seed available	.	.	.	.	.	.
267	1947	.	UM Records	No seed available	.	.	.	.	.	.
268	1947	.	UM Records	No seed available	.	.	.	.	.	.
269	1947	.	UM Records	Included	A321	0.1063	0.0302	0.2864	0.5117	0.0654
270	1947	.	UM Records	No seed available	.	.	.	.	.	.
271	1947	.	UM Records	Included	A321	0.001	0.0642	0.3626	0.5032	0.069
272	1947	.	UM Records	No seed available	.	.	.	.	.	.
273	1947	.	UM Records	No seed available	.	.	.	.	.	.
274	1947	.	UM Records	No seed available	.	.	.	.	.	.
275	1947	.	UM Records	No seed available	.	.	.	.	.	.
276	1947	.	UM Records	No seed available	.	.	.	.	.	.
277	1947	.	UM Records	Included	A321	0.0022	0.0778	0.3982	0.447	0.0748
278	1947	.	UM Records	Included	A321	0.001	0.0444	0.4244	0.5274	0.0028

No.	Year developed	Year released	Pedigree source	Status in study	Model-based cluster	B73	Mo17	Oh43	A321	PH207
279	1947	.	UM Records	No seed available	.	.	.	.	.	.
280	1947	1959	UM Records	No seed available	.	.	.	.	.	.
281	1947	.	UM Records	No seed available	.	.	.	.	.	.
282	1947	.	UM Records	No seed available	.	.	.	.	.	.
283	1935	.	UM Records	No seed available	.	.	.	.	.	.
284	1935	.	UM Records	No seed available	.	.	.	.	.	.
285	1937	.	UM Records	No seed available	.	.	.	.	.	.
286	1935	.	UM Records	No seed available	.	.	.	.	.	.
287	1935	.	UM Records	No seed available	.	.	.	.	.	.
288	1937	1950	UM Records	Included	A321	0.1044	0.0938	0.2866	0.4655	0.0496
289	.	.	UM Records	No seed available	.	.	.	.	.	.
290	1937	.	UM Records	No seed available	.	.	.	.	.	.
291	1935	1950	UM Records	Included	A321	0.022	0.1326	0.3474	0.4961	0.002
292	1935	.	UM Records	No seed available	.	.	.	.	.	.
293	.	1950	UM Records	Included	A321	0.0058	0.0809	0.2024	0.7089	0.002
294	1935	1950	UM Records	No seed available	.	.	.	.	.	.
295	1937	1950	UM Records	Included	A321	0.0524	0.0066	0.2542	0.6066	0.0802
296	1937	.	UM Records	No seed available	.	.	.	.	.	.
297	1937	.	UM Records	No seed available	.	.	.	.	.	.
298	1937	.	UM Records	No seed available	.	.	.	.	.	.
299	1937	.	UM Records	No seed available	.	.	.	.	.	.
300	1935	.	UM Records	No seed available	.	.	.	.	.	.
301	1935	.	UM Records	Included	A321	0.0004	0	0.0002	0.9992	0.0002
302	1935	1950	UM Records	Included	A321	0.0018	0.0026	0.2532	0.6472	0.0952
303	1935	.	UM Records	No seed available	.	.	.	.	.	.
304	1935	.	UM Records	No seed available	.	.	.	.	.	.
305	1935	1950	UM Records	Included	A321	0.0672	0.0212	0.325	0.5069	0.0798
306	1935	.	UM Records	No seed available	.	.	.	.	.	.
307	1935	.	UM Records	No seed available	.	.	.	.	.	.
308	1935	.	UM Records	No seed available	.	.	.	.	.	.
309	1935	1950	UM Records	Included	A321	0.048	0.0956	0.3626	0.4927	0.001

No.	Year developed	Year released	Pedigree source	Status in study	Model-based cluster	B73	Mo17	Oh43	A321	PH207
310	1935	.	UM Records	No seed available	.	.	.	.	.	.
311	1938	1950	UM Records	Included	A321	0.0044	0.045	0.4138	0.5224	0.0144
312	1935	.	UM Records	No seed available	.	.	.	.	.	.
313	1935	1950	UM Records	No seed available	.	.	.	.	.	.
314	1935	.	UM Records	No seed available	.	.	.	.	.	.
315	1935	.	UM Records	No seed available	.	.	.	.	.	.
316	1935	.	UM Records	No seed available	.	.	.	.	.	.
317	1935	.	UM Records	No seed available	.	.	.	.	.	.
318	1935	1950	UM Records	Included	A321	0.0018	0.0428	0.1929	0.7613	0.0012
319	1935	.	UM Records	No seed available	.	.	.	.	.	.
320	1935	.	UM Records	No seed available	.	.	.	.	.	.
321	1928	1950	UM Records	Included	A321	0.002	0.0006	0.0018	0.9946	0.001
322	1928	1950	UM Records	Included	A321	0.002	0	0.0006	0.9972	0.0002
323	1935	1950	UM Records	Included	A321	0.001	0.0016	0.4815	0.5135	0.0024
324	1935	.	UM Records	No seed available	.	.	.	.	.	.
325	1935	.	UM Records	No seed available	.	.	.	.	.	.
326	1935	1950	UM Records	No seed available	.	.	.	.	.	.
327	.	.	UM Records	No seed available	.	.	.	.	.	.
328	.	1950	UM Records	No seed available	.	.	.	.	.	.
329	.	.	UM Records	No seed available	.	.	.	.	.	.
330	1947	.	UM Records	No seed available	.	.	.	.	.	.
331	1947	.	UM Records	Included	A321	0.0736	0.062	0.1719	0.6908	0.0018
332	1947	.	UM Records	No seed available	.	.	.	.	.	.
333	1947	.	UM Records	No seed available	.	.	.	.	.	.
334	1941	.	UM Records	No seed available	.	.	.	.	.	.
335	1947	.	UM Records	No seed available	.	.	.	.	.	.
336	1948	.	UM Records	Included	Oh43	0.0412	0.0062	0.544	0.3775	0.031
337	1947	.	UM Records	No seed available	.	.	.	.	.	.
338	1948	.	UM Records	No seed available	.	.	.	.	.	.
339	1948	.	UM Records	No seed available	.	.	.	.	.	.
340	1948	.	UM Records	No seed available	.	.	.	.	.	.

No.	Year developed	Year released	Pedigree source	Status in study	Model-based cluster	B73	Mo17	Oh43	A321	PH207
341	1948	.	UM Records	No seed available	.	.	.	.	.	.
342	1948	.	UM Records	No seed available	.	.	.	.	.	.
343	1948	.	UM Records	No seed available	.	.	.	.	.	.
344	1948	.	UM Records	No seed available	.	.	.	.	.	.
345	1947	.	UM Records	No seed available	.	.	.	.	.	.
346	1948	.	UM Records	No seed available	.	.	.	.	.	.
347	1947	.	UM Records	No seed available	.	.	.	.	.	.
348	1948	.	UM Records	No seed available	.	.	.	.	.	.
349	1948	.	UM Records	No seed available	.	.	.	.	.	.
350	1948	.	UM Records	No seed available	.	.	.	.	.	.
351	1948	.	UM Records	Included	A321	0.001	0.0014	0.4824	0.513	0.0022
352	1948	.	UM Records	No seed available	.	.	.	.	.	.
353	1948	.	UM Records	Included	Oh43	0.001	0.0166	0.7032	0.2718	0.0074
354	1948	.	UM Records	No seed available	.	.	.	.	.	.
355	1948	.	UM Records	No seed available	.	.	.	.	.	.
356	1948	.	UM Records	Included	A321	0.0889	0.0584	0.2049	0.4193	0.2285
357	1948	.	UM Records	No seed available	.	.	.	.	.	.
358	1948	.	UM Records	No seed available	.	.	.	.	.	.
359	1948	.	UM Records	No seed available	.	.	.	.	.	.
360	1948	.	UM Records	No seed available	.	.	.	.	.	.
361	1948	.	UM Records	No seed available	.	.	.	.	.	.
362	1948	.	UM Records	No seed available	.	.	.	.	.	.
363	1948	.	UM Records	No seed available	.	.	.	.	.	.
364	1948	.	UM Records	No seed available	.	.	.	.	.	.
365	1948	.	UM Records	No seed available	.	.	.	.	.	.
366	1948	.	UM Records	No seed available	.	.	.	.	.	.
367	1948	.	UM Records	No seed available	.	.	.	.	.	.
368	1948	.	UM Records	No seed available	.	.	.	.	.	.
369	1948	.	UM Records	No seed available	.	.	.	.	.	.
370	1948	.	UM Records	No seed available	.	.	.	.	.	.
371	1948	.	UM Records	No seed available	.	.	.	.	.	.

No.	Year developed	Year released	Pedigree source	Status in study	Model-based cluster	B73	Mo17	Oh43	A321	PH207
372	1948	.	UM Records	No seed available	.	.	.	.	.	.
373	1948	.	UM Records	No seed available	.	.	.	.	.	.
374	1948	.	UM Records	No seed available	.	.	.	.	.	.
375	1948	.	UM Records	No seed available	.	.	.	.	.	.
376	1948	.	UM Records	Included	A321	0.0008	0.001	0.0972	0.8661	0.035
377	1948	.	UM Records	Included	A321	0.001	0.001	0.1224	0.8662	0.0094
378	1948	.	UM Records	Included	A321	0.0004	0.001	0.1371	0.8605	0.001
379	1948	.	UM Records	No seed available	.	.	.	.	.	.
380	1948	.	UM Records	No seed available	.	.	.	.	.	.
381	1948	.	UM Records	No seed available	.	.	.	.	.	.
382	1948	.	UM Records	No seed available	.	.	.	.	.	.
383	1948	.	UM Records	No seed available	.	.	.	.	.	.
384	1948	.	UM Records	No seed available	.	.	.	.	.	.
385	1948	.	UM Records	No seed available	.	.	.	.	.	.
386	1948	.	UM Records	No seed available	.	.	.	.	.	.
387	1948	.	UM Records	No seed available	.	.	.	.	.	.
388	1948	.	UM Records	No seed available	.	.	.	.	.	.
389	1948	.	UM Records	No seed available	.	.	.	.	.	.
390	1948	.	UM Records	No seed available	.	.	.	.	.	.
391	1948	.	UM Records	No seed available	.	.	.	.	.	.
392	1948	.	UM Records	No seed available	.	.	.	.	.	.
393	1948	.	UM Records	No seed available	.	.	.	.	.	.
394	1948	.	UM Records	No seed available	.	.	.	.	.	.
395	1948	.	UM Records	No seed available	.	.	.	.	.	.
396	1948	.	UM Records	No seed available	.	.	.	.	.	.
397	1948	.	UM Records	No seed available	.	.	.	.	.	.
398	1948	.	UM Records	No seed available	.	.	.	.	.	.
399	1948	.	UM Records	No seed available	.	.	.	.	.	.
400	1948	.	UM Records	No seed available	.	.	.	.	.	.
401	1948	.	UM Records	No seed available	.	.	.	.	.	.
402	1948	.	UM Records	No seed available	.	.	.	.	.	.

No.	Year developed	Year released	Pedigree source	Status in study	Model-based cluster	B73	Mo17	Oh43	A321	PH207
403	1948	.	UM Records	No seed available	.	.	.	.	.	.
404	1948	.	UM Records	No seed available	.	.	.	.	.	.
405	1949	.	UM Records	No seed available	.	.	.	.	.	.
406	1949	.	UM Records	Included	Oh43	0.0006	0.0088	0.7775	0.2121	0.001
407	1949	.	UM Records	No seed available	.	.	.	.	.	.
408	1949	.	UM Records	No seed available	.	.	.	.	.	.
409	1949	.	UM Records	No seed available	.	.	.	.	.	.
410	1949	.	UM Records	No seed available	.	.	.	.	.	.
411	1949	.	UM Records	No seed available	.	.	.	.	.	.
412	1949	.	UM Records	No seed available	.	.	.	.	.	.
413	1949	.	UM Records	No seed available	.	.	.	.	.	.
414	1949	.	UM Records	No seed available	.	.	.	.	.	.
415	1949	.	UM Records	No seed available	.	.	.	.	.	.
416	1949	.	UM Records	No seed available	.	.	.	.	.	.
417	1949	.	UM Records	No seed available	.	.	.	.	.	.
418	1949	.	UM Records	No seed available	.	.	.	.	.	.
419	1949	.	UM Records	No seed available	.	.	.	.	.	.
420	1949	.	UM Records	Included	Oh43	0	0	0.7365	0.2629	0.0006
421	1949	.	UM Records	Included	Oh43	0	0.0006	0.7214	0.277	0.001
422	1949	.	UM Records	No seed available	.	.	.	.	.	.
423	1949	.	UM Records	Included	Oh43	0	0.0002	0.6249	0.3743	0.0006
424	1949	.	UM Records	Included	Oh43	0	0	0.8361	0.1633	0.0006
425	1949	.	UM Records	Included	Oh43	0	0.0006	0.8181	0.1807	0.0006
426	1949	.	UM Records	Included	Oh43	0	0.0006	0.6402	0.3582	0.001
427	1949	.	UM Records	No seed available	.	.	.	.	.	.
428	1949	.	UM Records	Included	A321	0.0374	0.037	0.3866	0.5236	0.0154
429	1949	.	UM Records	No seed available	.	.	.	.	.	.
430	1949	.	UM Records	No seed available	.	.	.	.	.	.
431	1949	.	UM Records	No seed available	.	.	.	.	.	.
432	1949	.	UM Records	No seed available	.	.	.	.	.	.
433	1949	.	UM Records	No seed available	.	.	.	.	.	.

No.	Year developed	Year released	Pedigree source	Status in study	Model-based cluster	B73	Mo17	Oh43	A321	PH207
434	1949	.	UM Records	Included	A321	0.0058	0.0188	0.2781	0.5961	0.1012
435	1949	.	UM Records	Included	A321	0.0072	0.0086	0.2727	0.5925	0.119
436	1949	.	UM Records	No seed available	.	.	.	.	.	.
437	1949	.	UM Records	No seed available	.	.	.	.	.	.
438	1949	.	UM Records	No seed available	.	.	.	.	.	.
439	1949	.	UM Records	No seed available	.	.	.	.	.	.
440	1949	.	UM Records	No seed available	.	.	.	.	.	.
441	1949	.	UM Records	No seed available	.	.	.	.	.	.
442	1949	.	UM Records	No seed available	.	.	.	.	.	.
443	1949	.	UM Records	No seed available	.	.	.	.	.	.
444	1949	.	UM Records	No seed available	.	.	.	.	.	.
445	1949	.	UM Records	No seed available	.	.	.	.	.	.
446	1949	.	UM Records	No seed available	.	.	.	.	.	.
447	1949	.	UM Records	No seed available	.	.	.	.	.	.
448	1949	.	UM Records	No seed available	.	.	.	.	.	.
449	1949	.	UM Records	No seed available	.	.	.	.	.	.
450	1949	.	UM Records	No seed available	.	.	.	.	.	.
451	1949	.	UM Records	No seed available	.	.	.	.	.	.
452	1949	.	UM Records	No seed available	.	.	.	.	.	.
453	1949	.	UM Records	No seed available	.	.	.	.	.	.
454	1949	.	UM Records	No seed available	.	.	.	.	.	.
455	1949	.	UM Records	No seed available	.	.	.	.	.	.
456	1949	.	UM Records	No seed available	.	.	.	.	.	.
457	1949	.	UM Records	No seed available	.	.	.	.	.	.
458	1949	.	UM Records	No seed available	.	.	.	.	.	.
459	1949	.	UM Records	No seed available	.	.	.	.	.	.
460	1949	.	UM Records	No seed available	.	.	.	.	.	.
461	1949	.	UM Records	No seed available	.	.	.	.	.	.
462	1949	.	UM Records	No seed available	.	.	.	.	.	.
463	1949	.	UM Records	No seed available	.	.	.	.	.	.
464	1949	.	UM Records	No seed available	.	.	.	.	.	.

No.	Year developed	Year released	Pedigree source	Status in study	Model-based cluster	B73	Mo17	Oh43	A321	PH207
465	1949	.	UM Records	No seed available	.	.	.	.	.	.
466	1949	.	UM Records	No seed available	.	.	.	.	.	.
467	1949	.	UM Records	No seed available	.	.	.	.	.	.
468	1949	.	UM Records	No seed available	.	.	.	.	.	.
469	1949	.	UM Records	No seed available	.	.	.	.	.	.
470	1949	.	UM Records	No seed available	.	.	.	.	.	.
471	1952	.	UM Records	No seed available	.	.	.	.	.	.
472	1952	.	UM Records	No seed available	.	.	.	.	.	.
473	1953	.	UM Records	Included	A321	0.0006	0.0006	0.0006	0.998	0.0002
474	1953	.	UM Records	Included	A321	0.0036	0.001	0.0462	0.9482	0.001
475	1953	.	UM Records	No seed available	.	.	.	.	.	.
476	1953	.	UM Records	No seed available	.	.	.	.	.	.
477	1953	.	UM Records	No seed available	.	.	.	.	.	.
478	1953	.	UM Records	No seed available	.	.	.	.	.	.
479	1954	.	UM Records	No seed available	.	.	.	.	.	.
480	1954	1960	UM Records	No seed available	.	.	.	.	.	.
481	1949	.	UM Records	No seed available	.	.	.	.	.	.
482	1949	.	UM Records	Included	Oh43	0.0122	0.0018	0.52	0.4148	0.0512
483	1950	.	UM Records	No seed available	.	.	.	.	.	.
484	1950	.	UM Records	No seed available	.	.	.	.	.	.
485	1950	.	UM Records	No seed available	.	.	.	.	.	.
486	1950	.	UM Records	No seed available	.	.	.	.	.	.
487	1950	.	UM Records	No seed available	.	.	.	.	.	.
488	1952	.	UM Records	No seed available	.	.	.	.	.	.
489	1953	.	UM Records	No seed available	.	.	.	.	.	.
490	1953	.	UM Records	No seed available	.	.	.	.	.	.
491	1953	.	UM Records	No seed available	.	.	.	.	.	.
492	1953	.	UM Records	No seed available	.	.	.	.	.	.
493	1953	.	UM Records	No seed available	.	.	.	.	.	.
494	1950	.	UM Records	No seed available	.	.	.	.	.	.
495	1954	.	UM Records	No seed available	.	.	.	.	.	.

No.	Year developed	Year released	Pedigree source	Status in study	Model-based cluster	B73	Mo17	Oh43	A321	PH207
496	1954	.	UM Records	No seed available	.	.	.	.	.	.
497	1952	.	UM Records	No seed available	.	.	.	.	.	.
498	1952	.	UM Records	Included	A321	0.0556	0.0814	0.3388	0.494	0.0302
499	1952	.	UM Records	No seed available	.	.	.	.	.	.
500	1952	.	UM Records	No seed available	.	.	.	.	.	.
501	1952	.	UM Records	Included	A321	0.0286	0.04	0.2528	0.67	0.0086
502	1955	.	UM Records	No seed available	.	.	.	.	.	.
503	1954	.	UM Records	No seed available	.	.	.	.	.	.
504	1954	.	UM Records	No seed available	.	.	.	.	.	.
505	.	.	UM Records	No seed available	.	.	.	.	.	.
506	.	.	UM Records	No seed available	.	.	.	.	.	.
507	.	.	UM Records	No seed available	.	.	.	.	.	.
508	.	.	UM Records	No seed available	.	.	.	.	.	.
509	1957	.	UM Records	No seed available	.	.	.	.	.	.
510	1957	.	UM Records	No seed available	.	.	.	.	.	.
511	1957	.	UM Records	Included	Oh43	0.0588	0.1287	0.4331	0.3473	0.0322
512	1957	.	UM Records	No seed available	.	.	.	.	.	.
513	1957	.	UM Records	No seed available	.	.	.	.	.	.
514	1957	.	UM Records	Included	Oh43	0.016	0.0218	0.7024	0.2558	0.004
515	1957	.	UM Records	No seed available	.	.	.	.	.	.
516	1956	.	UM Records	No seed available	.	.	.	.	.	.
517	1957	.	UM Records	No seed available	.	.	.	.	.	.
518	1957	.	UM Records	No seed available	.	.	.	.	.	.
519	1955	.	UM Records	No seed available	.	.	.	.	.	.
520	1955	.	UM Records	No seed available	.	.	.	.	.	.
521	1955	.	UM Records	No seed available	.	.	.	.	.	.
522	1955	.	UM Records	No seed available	.	.	.	.	.	.
523	1955	.	UM Records	No seed available	.	.	.	.	.	.
524	1954	.	UM Records	No seed available	.	.	.	.	.	.
525	1955	.	UM Records	No seed available	.	.	.	.	.	.
526	1955	.	UM Records	No seed available	.	.	.	.	.	.

No.	Year developed	Year released	Pedigree source	Status in study	Model-based cluster	B73	Mo17	Oh43	A321	PH207
527	1955	.	UM Records	No seed available	.	.	.	.	.	.
528	1955	.	UM Records	No seed available	.	.	.	.	.	.
529	1955	.	UM Records	No seed available	.	.	.	.	.	.
530	1955	.	UM Records	No seed available	.	.	.	.	.	.
531	1955	.	UM Records	No seed available	.	.	.	.	.	.
532	1955	.	UM Records	No seed available	.	.	.	.	.	.
533	1955	.	UM Records	No seed available	.	.	.	.	.	.
534	1954	.	UM Records	No seed available	.	.	.	.	.	.
535	1955	.	UM Records	No seed available	.	.	.	.	.	.
536	1955	.	UM Records	No seed available	.	.	.	.	.	.
537	1955	.	UM Records	No seed available	.	.	.	.	.	.
538	1955	.	UM Records	No seed available	.	.	.	.	.	.
539	1955	.	UM Records	No seed available	.	.	.	.	.	.
540	1955	.	UM Records	No seed available	.	.	.	.	.	.
541	1955	.	UM Records	No seed available	.	.	.	.	.	.
542	1957	.	UM Records	Included	A321	0.0316	0.0032	0.1806	0.7826	0.002
543	1957	.	UM Records	Included	A321	0.0088	0.004	0.2369	0.7443	0.006
544	1957	.	UM Records	Included	Oh43	0	0	0.6	0.4	0
545	1957	.	UM Records	No seed available	.	.	.	.	.	.
546	1957	.	UM Records	No seed available	.	.	.	.	.	.
547	1958	.	UM Records	Included	A321	0.0854	0.0444	0.2354	0.5985	0.0362
548	1958	.	UM Records	No seed available	.	.	.	.	.	.
549	1957	.	UM Records	Included	A321	0.002	0.0392	0.4708	0.487	0.001
550	1957	.	UM Records	Included	Oh43	0.0424	0.057	0.6589	0.2308	0.011
551	1955	.	UM Records	No seed available	.	.	.	.	.	.
552	1956	.	UM Records	Included	A321	0.0022	0.0036	0.2102	0.742	0.042
553	1956	.	UM Records	Included	Oh43	0.0226	0.033	0.4005	0.3433	0.2006
554	1960	1962	UM Records	Included	A321	0.0078	0.0168	0.1595	0.7783	0.0376
555	1960	.	UM Records	Included	A321	0.001	0.003	0.1476	0.8028	0.0456
556	1960	1962	UM Records	Included	A321	0.0032	0.001	0.1651	0.8077	0.023
557	1959	1961	UM Records	Included	B73	0.8118	0.0036	0.0847	0.0988	0.001

No.	Year developed	Year released	Pedigree source	Status in study	Model-based cluster	B73	Mo17	Oh43	A321	PH207
558	1960	.	UM Records	Included	B73	0.8634	0.001	0.0566	0.078	0.001
559	1960	.	UM Records	Included	B73	0.8076	0.0028	0.0884	0.0991	0.002
560	1960	.	UM Records	Included	B73	0.8481	0.0018	0.0646	0.0845	0.001
561	1960	.	UM Records	Included	B73	0.871	0.001	0.058	0.0554	0.0146
562	1959	.	UM Records	Included	A321	0.0014	0.001	0.0094	0.9746	0.0136
563	1959	.	UM Records	Included	A321	0.0226	0.0014	0.1674	0.7268	0.0818
564	1959	.	UM Records	Included	Oh43	0.3641	0	0.6353	0.0006	0
565	1959	.	UM Records	Included	B73	0.5695	0.0162	0.2502	0.1515	0.0126
566	1959	.	UM Records	Included	B73	0.5027	0.0038	0.2421	0.1934	0.058
567	1965	.	UM Records	No seed available	.	.	.	.	.	.
568	1965	.	UM Records	Included	A321	0.054	0.1008	0.2597	0.4637	0.1218
569	1965	.	UM Records	Included	A321	0.0604	0.0902	0.2229	0.5557	0.0708
570	1965	.	UM Records	Included	A321	0.0002	0.001	0.282	0.7108	0.006
571	1965	.	UM Records	Included	A321	0.0002	0.001	0.2806	0.7106	0.0076
572	1965	.	UM Records	No seed available	.	.	.	.	.	.
573	1965	1970	UM Records	Included	A321	0.082	0.0206	0.1976	0.695	0.0048
574	1959	.	UM Records	Included	A321	0.0008	0.0004	0.0394	0.9584	0.001
575	1959	.	UM Records	Included	A321	0.0032	0.001	0.0572	0.9356	0.003
576	1959	.	UM Records	Included	A321	0.001	0.0424	0.1427	0.8129	0.001
577	1959	.	UM Records	Included	A321	0	0.0202	0.2958	0.664	0.02
578	1959	.	UM Records	Included	A321	0.001	0.0038	0.2644	0.7288	0.002
579	1959	.	UM Records	Included	A321	0.001	0.0032	0.3198	0.6142	0.0618
580	1959	.	UM Records	Included	A321	0.0086	0.041	0.2453	0.7001	0.005
581	1959	.	UM Records	Included	Oh43	0.3557	0	0.6437	0.0006	0
582	1969	1971	UM Records	Included	B73	0.3915	0.0042	0.1643	0.3248	0.1152
583	1969	1979	UM Records	Included	A321	0.0296	0.1058	0.2501	0.6086	0.006
584	1969	1971	UM Records	Included	A321	0.0112	0.0034	0.2672	0.7154	0.0028
585	1969	1971	UM Records	Included	A321	0.0128	0.0372	0.2019	0.7464	0.0018
586	1966	1975	UM Records	Included	A321	0.0082	0.0178	0.4422	0.5196	0.0122
587	1966	1975	UM Records	Included	Oh43	0.001	0.0958	0.4461	0.4121	0.045
588	1966	1975	UM Records	Included	A321	0.086	0.0614	0.2092	0.4251	0.2184

No.	Year developed	Year released	Pedigree source	Status in study	Model-based cluster	B73	Mo17	Oh43	A321	PH207
589	.	1975	UM Records	Included	B73	0.6829	0.009	0.1212	0.1276	0.0594
590	1969	1975	UM Records	Included	B73	0.7538	0.003	0.101	0.1338	0.0084
591	1966	1978	UM Records	Included	A321	0.0632	0.0544	0.3771	0.5012	0.004
592	1969	1978	UM Records	Included	A321	0.0128	0.072	0.2628	0.5349	0.1174
593	1969	1978	UM Records	Included	Mo17	0.0634	0.4153	0.21	0.3085	0.0028
594	1969	1978	UM Records	Included	A321	0.1708	0.0126	0.1533	0.4845	0.1788
595	1971	1979	UM Records	Included	Oh43	0.0142	0.0008	0.588	0.3962	0.0008
596	1973	1981	UM Records	Included	A321	0.0108	0.2857	0.2591	0.3952	0.0492
597	1975	1982	UM Records	Included	B73	0.6705	0.0414	0.1202	0.1663	0.0016
598	1978	1984	UM Records	Included	A321	0.0386	0.0174	0.3376	0.5382	0.0682
599	1978	1984	UM Records	Included	Oh43	0.1734	0.101	0.3775	0.3445	0.0036
600	1977	1984	UM Records	Included	B73	0.5927	0.0086	0.1462	0.2161	0.0364
601	1978	1984	UM Records	Included	Mo17	0.0018	0.4095	0.2858	0.2849	0.018
602	1978	1984	UM Records	Included	Oh43	0	0.002	0.5243	0.4523	0.0214
603	1977	1984	UM Records	Included	A321	0.048	0.0066	0.3896	0.5446	0.0112
604	1981	1987	UM Records	Included	B73	1	0	0	0	0
605	1980	1987	UM Records	Included	B73	1	0	0	0	0
606	1980	1987	UM Records	Included	B73	1	0	0	0	0
607	1981	1987	UM Records	Included	Mo17	0.0004	0.9282	0.0668	0.004	0.0006
608	1981	1987	UM Records	Included	Mo17	0	0.8305	0.0034	0.1661	0
609	.	.	Mikel, 2006	Included	Mo17	0.0122	0.5946	0.1501	0.2385	0.0046
610	.	.	Gerdes et al., 1993	Included	B73	1	0	0	0	0
611	.	.	Gerdes et al., 1993	Included	B73	0.4359	0.0112	0.0944	0.3634	0.0951
612	.	.	Gerdes et al., 1993	Included	A321	0.0334	0.0892	0.2528	0.5973	0.0272
613	.	.	Gerdes et al., 1993	Included	B73	1	0	0	0	0
614	.	.	Gerdes et al., 1993	Included	B73	0.7327	0.001	0.0024	0.1759	0.088
615	.	.	PVPA Certificate	Missing markers	.	.	.	.	.	.
616	.	.	Gerdes et al., 1993	Included	Mo17	0.001	0.983	0.0124	0.0028	0.0008
617	.	.	UM Records	Included	Oh43	0.016	0.0674	0.4601	0.3099	0.1466
618	.	.	UM Records	Included	A321	0.0718	0.0836	0.3373	0.3958	0.1114
619	.	.	Gerdes et al., 1993	Included	B73	0.5799	0.0042	0.1588	0.2151	0.042

No.	Year developed	Year released	Pedigree source	Status in study	Model-based cluster	B73	Mo17	Oh43	A321	PH207
620	.	.	Gerdes et al., 1993	Included	A321	0.0394	0.0254	0.3442	0.5389	0.052
621	.	.	PVPA Certificate	Included	B73	0.862	0.0002	0.0638	0.0732	0.0008
622	.	.	Mikel, 2006	Included	Mo17	0.0006	0.7732	0.0891	0.1299	0.0072
623	.	.	Mikel, 2006	Included	B73	1	0	0	0	0
624	.	.	Mikel, 2006	Included	B73	0.4242	0.1044	0.1847	0.2819	0.0048
625	.	.	Mikel, 2006	Included	B73	1	0	0	0	0
626	.	.	Mikel, 2006	Included	B73	0.7391	0.0028	0.0092	0.2465	0.0024
627	.	.	Mikel, 2006	Included	B73	0.6158	0.0068	0.1502	0.1454	0.0818
628	.	.	Mikel, 2006	Included	Mo17	0.1976	0.2909	0.1816	0.2131	0.1168
629	.	.	Mikel, 2006	Included	PH207	0	0.001	0.0594	0.0334	0.9062
630	.	.	Mikel, 2006	Included	A321	0.0082	0.0626	0.412	0.515	0.0022
631	.	.	Mikel, 2006	Included	Mo17	0.001	0.5272	0.2716	0.1752	0.025
632	.	.	PVPA Certificate	Included	Mo17	0.001	0.56	0.0906	0.3475	0.001
633	.	.	Flint-Garcia et al., 2005	Included	A321	0.0218	0.1838	0.3317	0.3961	0.0666
634	.	.	Gerdes et al., 1993	Included	A321	0.0302	0.141	0.3599	0.3794	0.0894
635	.	.	Gerdes et al., 1993	Included	A321	0.0808	0.1444	0.314	0.3674	0.0934
636	.	.	Mikel, 2006	Included	B73	1	0	0	0	0
637	.	.	Gerdes et al., 1993	Included	Oh43	0.044	0.1374	0.4212	0.3549	0.0424
638	.	.	PVPA Certificate	Included	PH207	0.2299	0.002	0.0554	0.0392	0.6735
639	.	.	PVPA Certificate	Included	PH207	0	0.0046	0.0008	0.0006	0.994
640	.	.	PVPA Certificate	Included	PH207	0	0	0	0	1
641	.	.	PVPA Certificate	Included	PH207	0	0	0.2545	0.1804	0.5652
642	.	.	Mikel, 2006	Included	Oh43	0	0	0.6	0.4	0
643	.	.	Mikel, 2006	Included	Mo17	0	1	0	0	0
644	.	.	Mikel, 2006	Included	Mo17	0	1	0	0	0
645	.	.	Mikel, 2006	Included	Mo17	0.0014	0.7569	0.05	0.1905	0.0012
646	.	.	Mikel, 2006	Included	Mo17	0	1	0	0	0
647	.	.	Mikel, 2006	Included	PH207	0.0014	0.006	0.041	0.4521	0.4995
648	.	.	Mikel, 2006	Included	A321	0.0052	0.0128	0.3309	0.5329	0.1182
649	.	.	Mikel, 2006	Included	A321	0.0578	0.1744	0.3075	0.3699	0.0904
650	.	.	Mikel, 2006	Included	B73	1	0	0	0	0

No.	Year developed	Year released	Pedigree source	Status in study	Model-based cluster	B73	Mo17	Oh43	A321	PH207
651	.	.	Mikel, 2006	Included	Mo17	0.0618	0.3379	0.3646	0.2209	0.0148
652	.	.	PVPA Certificate	Included	Mo17	0.0694	0.6016	0.1819	0.1119	0.0352
653	.	.	PVPA Certificate	Included	Mo17	0.0036	0.8182	0.0228	0.1332	0.0222
654	.	.	Mikel, 2006	Included	B73	0.6075	0.0016	0.16	0.2241	0.0068
655	.	.	Mikel, 2006	Included	B73	0.984	0.001	0.0088	0.0052	0.001
656	.	.	Mikel, 2006	Included	A321	0.0662	0.1009	0.2572	0.5589	0.0168
657	.	.	PVPA Certificate	Included	Mo17	0.0076	0.5057	0.2273	0.255	0.0044
658	.	.	PVPA Certificate	Included	B73	1	0	0	0	0
659	.	.	PVPA Certificate	Included	B73	0.998	0	0.0004	0.001	0.0006
660	.	.	PVPA Certificate	Included	B73	0.8485	0	0.003	0.0084	0.1401
661	.	.	PVPA Certificate	Included	B73	1	0	0	0	0
662	.	.	PVPA Certificate	Included	B73	1	0	0	0	0
663	.	.	PVPA Certificate	Included	B73	1	0	0	0	0
664	.	.	PVPA Certificate	Included	B73	0.9246	0.001	0.0012	0.001	0.0722
665	.	.	PVPA Certificate	Included	Mo17	0.001	0.7371	0.1141	0.1318	0.016
666	.	.	Nelson et al., 2008	Included	Oh43	0	0.0702	0.5618	0.367	0.001
667	.	.	PVPA Certificate	Included	Oh43	0	0.0032	0.5974	0.3978	0.0016
668	.	.	PVPA Certificate	Included	Oh43	0.0006	0.1476	0.4163	0.4141	0.0214
669	.	.	Gerdes et al., 1993	Included	Mo17	0	1	0	0	0
670	.	.	Gerdes et al., 1993	Included	A321	0.0706	0.0366	0.3479	0.5159	0.029
671	.	.	Gerdes et al., 1993	Included	B73	0.7997	0.001	0.0826	0.0931	0.0236
672	.	.	Gerdes et al., 1993	Included	Oh43	0.1509	0.0988	0.3613	0.2912	0.0978
673	.	.	Gerdes et al., 1993	Included	A321	0.037	0.0014	0.4004	0.555	0.0062
674	.	.	Mikel, 2006	Included	Mo17	0	1	0	0	0
675	.	.	Mikel, 2006	Included	B73	1	0	0	0	0
676	.	.	Mikel, 2006	Included	A321	0.0706	0.1134	0.3091	0.4798	0.027
677	.	.	Mikel, 2006	Included	B73	1	0	0	0	0
678	.	.	Mikel, 2006	Included	A321	0.2622	0.1523	0.1233	0.3942	0.068
679	.	.	Mikel, 2006	Included	Mo17	0	1	0	0	0
680	.	.	Gerdes et al., 1993	Included	Oh43	0	0	0.6	0.4	0
681	.	.	PVPA Certificate	Included	PH207	0.1166	0.005	0.001	0.0016	0.8758

No.	Year developed	Year released	Pedigree source	Status in study	Model-based cluster	B73	Mo17	Oh43	A321	PH207
682	.	.	Gerdes et al., 1993	Included	A321	0.0136	0.0796	0.2515	0.6499	0.0054
683	.	.	Mikel, 2006	Included	PH207	0	0	0	0	1
684	.	.	Mikel, 2006	Included	B73	0.4993	0.0678	0.1703	0.1688	0.0938
685	.	.	PVPA Certificate	Included	Oh43	0.0012	0.2763	0.3255	0.2764	0.1206
686	.	.	Mikel, 2006	Included	PH207	0	0	0	0	1
687	.	.	Mikel, 2006	Included	A321	0.0334	0.1312	0.3436	0.4322	0.0596
688	.	.	Mikel, 2006	Included	PH207	0	0	0.0002	0	0.9998
689	.	.	Mikel, 2006	Included	B73	0.4391	0.2739	0.0798	0.1322	0.075
690	.	.	Mikel, 2006	Included	PH207	0.0014	0.2012	0.1798	0.3085	0.3091
691	.	.	Mikel, 2006	Included	B73	0.988	0	0.0104	0.0016	0
692	.	.	Nelson et al., 2008	Included	PH207	0	0	0	0	1
693	.	.	PVPA Certificate	Included	PH207	0.0036	0.3049	0.0602	0.069	0.5623
694	.	.	PVPA Certificate	Included	A321	0.065	0.0682	0.287	0.4548	0.125
695	.	.	PVPA Certificate	Included	PH207	0.001	0.0024	0.1263	0.0706	0.7997
696	.	.	Mikel, 2006	Included	B73	0.7114	0.1166	0.0054	0.0682	0.0984
697	.	.	PVPA Certificate	Included	B73	0.877	0.1202	0.001	0.0006	0.0012
698	.	.	Mikel, 2006	Included	PH207	0	0	0	0	1
699	.	.	Mikel, 2006	Included	Mo17	0.0808	0.5909	0.1737	0.1144	0.0402
700	.	.	PVPA Certificate	Included	Oh43	0.012	0.0982	0.4206	0.395	0.0742
701	.	.	PVPA Certificate	Included	A321	0.0056	0.1419	0.3065	0.4058	0.1401
702	.	.	PVPA Certificate	Included	PH207	0.1202	0	0.1099	0.1809	0.589
703	.	.	Mikel, 2006	Included	PH207	0	0	0	0	1
704	.	.	PVPA Certificate	Included	PH207	0.4447	0.0008	0.003	0.0022	0.5493
705	.	.	PVPA Certificate	Included	PH207	0.0016	0.0046	0.127	0.1128	0.754
706	.	.	PVPA Certificate	Included	B73	0.5595	0.1708	0.1784	0.0856	0.0058
707	.	.	PVPA Certificate	Included	PH207	0	0.0006	0	0	0.9994
708	.	.	PVPA Certificate	Included	PH207	0.001	0	0	0	0.999
709	.	.	PVPA Certificate	Included	A321	0.0384	0.0466	0.4103	0.4877	0.017
710	.	.	PVPA Certificate	Included	PH207	0.0004	0.0004	0.0769	0.0286	0.8937
711	.	.	PVPA Certificate	Included	B73	0.8788	0.115	0.0018	0.0018	0.0026
712	.	.	PVPA Certificate	Included	B73	0.6239	0.145	0.057	0.1658	0.0082

No.	Year developed	Year released	Pedigree source	Status in study	Model-based cluster	B73	Mo17	Oh43	A321	PH207
713	.	.	PVPA Certificate	Included	A321	0.0112	0.0664	0.3912	0.4566	0.0746
714	.	.	Mikel, 2006	Included	A321	0.0024	0.119	0.1644	0.376	0.3382
715	.	.	PVPA Certificate	Included	A321	0.2204	0.1648	0.2896	0.3182	0.007
716	.	.	PVPA Certificate	Included	A321	0.0058	0.1898	0.1844	0.3113	0.3087
717	.	.	PVPA Certificate	Included	Mo17	0.0014	0.4034	0.2296	0.2738	0.0918
718	.	.	PVPA Certificate	Included	PH207	0	0.0334	0.0532	0.0314	0.882
719	.	.	PVPA Certificate	Included	B73	0.9996	0	0	0.0004	0
720	.	.	PVPA Certificate	Included	PH207	0	0.1464	0.1413	0.0915	0.6208
721	.	.	Mikel, 2006	Included	B73	0.6153	0.163	0.0914	0.0726	0.0578
722	.	.	Mikel, 2006	Included	Oh43	0.0018	0.3108	0.354	0.2274	0.106
723	.	.	PVPA Certificate	Included	Oh43	0.001	0.0852	0.4575	0.3181	0.1382
724	.	.	Mikel, 2006	Included	PH207	0.001	0.3008	0.0821	0.1129	0.5031
725	.	.	PVPA Certificate	Included	B73	0.5078	0.1329	0.0965	0.2089	0.054
726	.	.	PVPA Certificate	Included	A321	0.1086	0.0418	0.4045	0.438	0.0072
727	.	.	Mikel, 2006	Included	B73	0.8182	0.0012	0.027	0.0962	0.0574
728	.	.	PVPA Certificate	Included	PH207	0	0.0915	0.1167	0.1418	0.65
729	.	.	PVPA Certificate	Included	PH207	0.0006	0.0046	0.3187	0.2997	0.3764
730	.	.	PVPA Certificate	Included	B73	0.7102	0.1762	0.1056	0.003	0.005
731	.	.	PVPA Certificate	Included	B73	0.9188	0.063	0.0042	0.014	0
732	.	.	Mikel, 2006	Included	PH207	0.001	0.2673	0.2575	0.1532	0.3209
733	.	.	Mikel, 2006	Included	Mo17	0.0072	0.3357	0.1914	0.2743	0.1914
734	.	.	Mikel, 2006	Included	A321	0.1032	0.0314	0.2523	0.4704	0.1427
735	.	.	Gerdes et al., 1993	Included	Mo17	0.0458	0.4032	0.2057	0.3387	0.0066
736	.	.	Gerdes et al., 1993	Included	A321	0.0558	0.2065	0.2647	0.4101	0.0628
737	.	.	Gerdes et al., 1993	Included	A321	0.0012	0.1962	0.0976	0.5843	0.1208
738	.	.	Nelson et al., 2008	Included	B73	1	0	0	0	0
739	.	.	PVPA Certificate	Included	B73	0.9758	0.0008	0.0008	0.0112	0.0114
740	.	.	PVPA Certificate	Included	A321	0.2615	0.0652	0.3097	0.3135	0.0502
741	.	.	PVPA Certificate	Included	Mo17	0	1	0	0	0
742	.	.	PVPA Certificate	Included	Mo17	0	1	0	0	0