

Exploring Corn Inbred Line Grouping Using Cluster Analysis

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Abstract:

Most often, corn inbreds are grouped by looking at all ten chromosomes collectively and determining which inbred lines are similar in their genotyping (Figure 1). I wanted to compare the standard method of grouping inbreds to using individual chromosomes to determine groups. To do this, I compared groupings of off-patent inbred lines using the DNA segments from each chromosome. I found that some inbreds will switch groups when grouped by chromosome, primarily due to the inbred's parental grouping, but overall groupings stayed mostly consistent.

Introduction:

Groups that inbreds are in roughly estimate how an inbred will behave and determine how certain inbreds will be chosen to make hybrids. Looking at each individual chromosome to determine groupings would give a more specific level of detail, which may show important elements that were missed by looking at all of the chromosomes together.

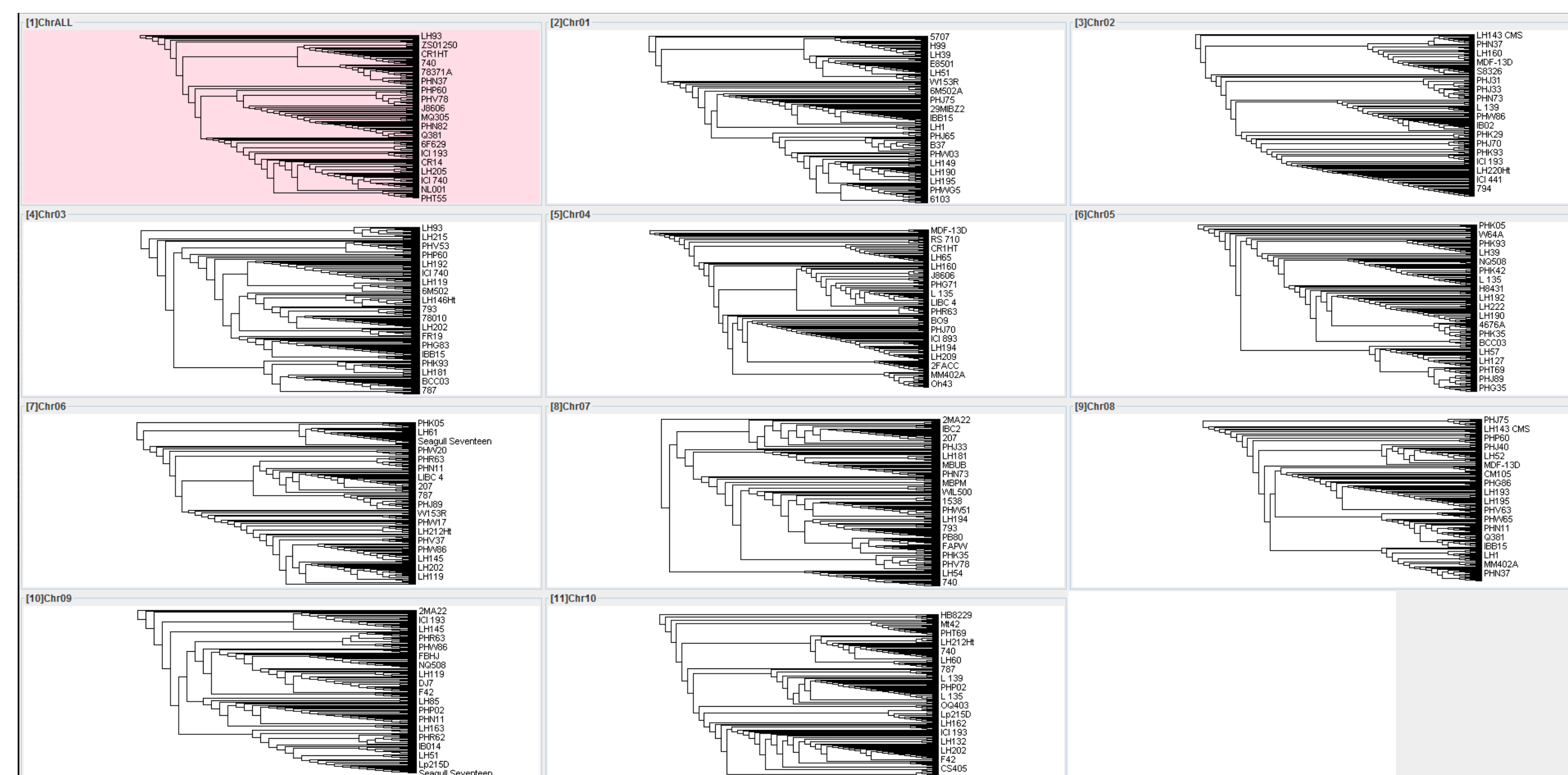


Figure 1. Phylogenetic trees showing grouping from all ten chromosomes and each individual chromosome using Dendroscope®

Materials and Methods:

Publicly available genotyping data was used to characterize inbred grouping (Romay et al., 2013). Data set was filtered to include off-patent lines with less than 5% missing values on every chromosome. Marker data was added by chromosome to R®, then “hclust” command was utilized to create the cluster information to generate phylogenetic trees. Information to draw the trees was extracted from R® using the “ctc” library in the Newick format and loaded into Dendroscope®. Tanglegrams were created in Dendroscope®, which allowed comparison of phylogenetic trees from each chromosome. Differences were calculated by taking the sum of the number of different markers between inbreds. Averages were then found for each group to determine different grouping distance. A significant difference in grouping was determined if the distance between groups was more than 75. Inbred parental information was obtained from PVP certificates (4).

Results and Discussion:

For the most part, inbreds stayed in the same general groupings across all ten chromosomes. Some even stayed exactly in the same group (ICI 441 and ICI 740 were in the same group throughout all chromosomes, as was PHP85 and PHWG5, among others). Some inbreds showed larger changes (see table 1). Some “jumps” between groups were expected due to wider parental crosses. Examining parental differences could prove helpful in determining how to evaluate an inbred line in hybrid combination. If one were studying a trait that maps to a certain chromosome which shows parental differences, it could impact interpretation of the trait. Also, when using inbred lines to make hybrids, examining the similarity of the inbred to each parent by chromosome could be important to examine appropriate combinations.

<u>Inbreds Compared:</u>	<u>PVP #'s</u>	<u>Pedigrees:</u>	<u>Similar Grouping on Chromosomes:</u>	<u>Different Grouping on Chromosome(s):</u>	<u>Significance:</u>
LH119 and LH132 (Figure 2)	8200064 8300148	LH119: H93 X (B73) ² LH132: H93 X (B73) ² H39: B37 X ?	1, 2, 3, 4, 5, 6, 8, 9, 10 (Grouped with B73)	7 (LH132 grouped with B37, LH119 stayed with B73)	LH119 could be used as a B73. LH132 has a strong B73 background but chromosome 7 is much more like B37.
PHK29 and PHVA9	8700214 9200096	PHVA9: PHK29 X ?	1, 2, 3, 4, 6, 7, 9, 10	5, 8 (PHVA9 jumps to another group similar to PHG47)	One can hypothesize that PHVA9's other parent is significantly different from PHK29 and more similar to PHG47.
B37 and FAPW	(no B73) 8200152	FAPW: B14 X B37	1, 2, 4, 5, 6, 7, 8	3, 9, 10 (FAPW grouped with B14)	FAPW has a strong resemblance to B37 but also strong resemblance to B14.
PHJ40 and PHT69	8600133 9200092	PHT69: PHJ40 X ?	1, 2, 3, 4, 5, 9	6, 7, 8, 10	One can hypothesize that PHT69's other parent is significantly different from PHJ40 and is fairly diverse because it clusters in a lot of different groups.

Table 1. Examples of inbred lines that changed grouping by chromosome

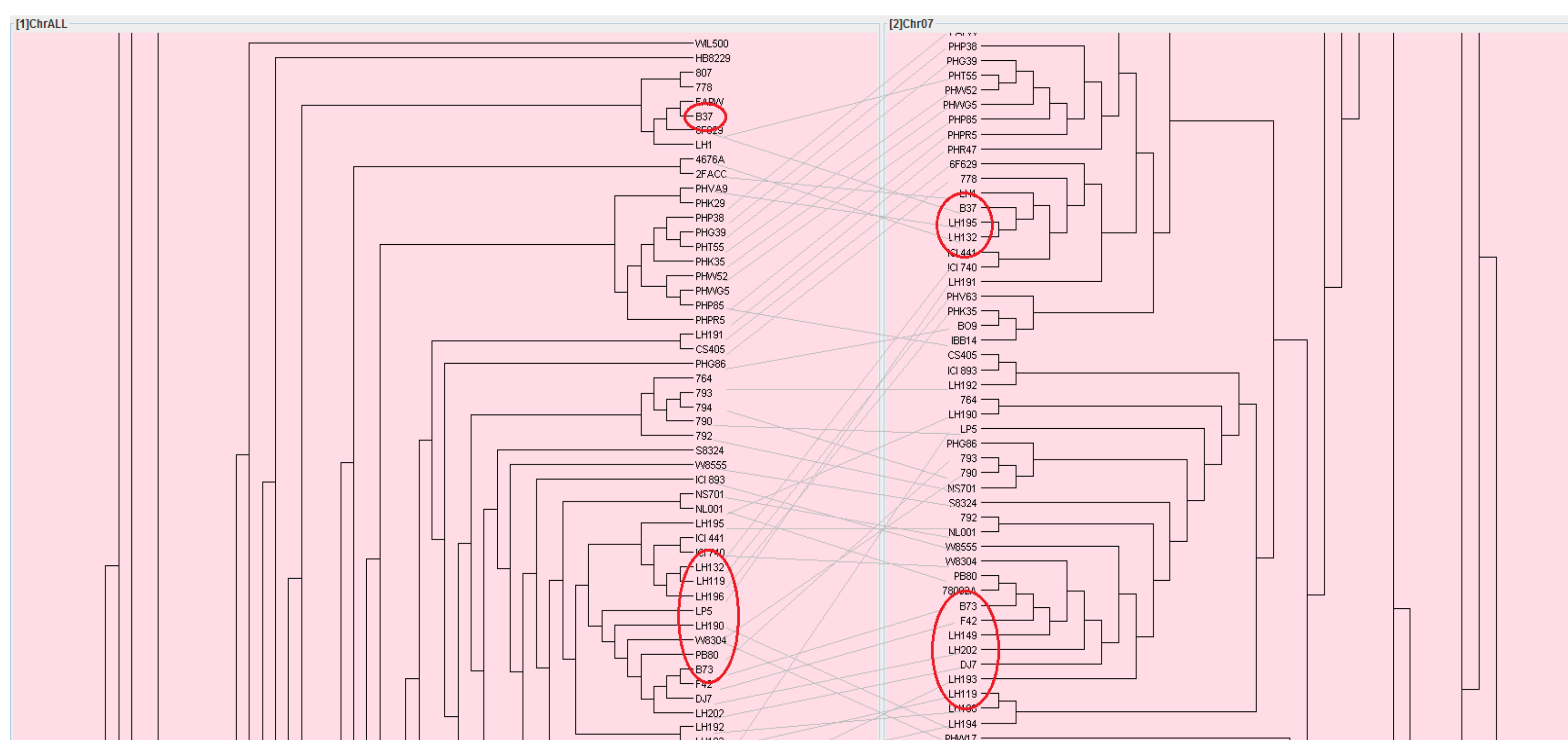


Figure 2. Difference of grouping of LH132 and LH119 on chromosome seven

Conclusion:

1. Grouping based on individual chromosomes instead of the whole chromosomal profile differs for some inbreds. Overall, grouping using the whole chromosomal profile is adequate to characterize a line.
2. The wider the cross is to create the inbred, the more one might want to consider the individual chromosome grouping to use the inbred to make a hybrid.

References:

- 1.) Comprehensive genotyping of the USA national maize inbred seed bank. Romay et al. Genome Biology 2013, 14:R55
- 2.) R Core Team (2013). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL <http://www.R-project.org/>.
- 3.) D.H. Huson and C. Scornavacca, Dendroscope 3- An interactive viewer for rooted phylogenetic trees and networks, Systematic Biology (2012); doi: 10.1093/sysbio/sys0624.
- 4.) Plant Variety Protection Office: <http://www.ars-grin.gov/cgi-bin/npgs/html/pvplist.pl>

Thank you to Beck's Superior Hybrids for their support and funding.