

UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE PATENT TRIAL AND APPEAL BOARD

INARI AGRICULTURE, INC.,

Petitioner,

v.

PIONEER HI-BRED INTERNATIONAL, INC.,

Patent Owner

Case PGR2024-00025
U.S. Patent 11,707,033

DECLARATION OF PATRICK S. SCHNABLE

REFERENCES CITED

Exhibit Number	Description
1001	U.S. Patent No. 11,707,033
1002	Prosecution History of U.S. Patent No. 11,707,033
1003	Declaration of Dr. Ray Riley
1005	U.S. Patent No. 9,572,319 (“Ross”)
1006	U.S. Patent No. 9,706,732 (“Carlone”)
1007	U.S. Patent No. 10,653,095 (“Heffner”)
1012	Lee, E.A.; Tracy, W.F. <i>Modern Maize Breeding</i> , in Handbook of Maize: Genetics and Genomics; Bennetzen, J.L., Hake, S., Eds.; Springer: New York, NY, USA, 2009; pp. 141–160. ISBN 978-0-387-77863-1
1015	Andorf et al., “Technological advances in maize breeding: past, present and future,” <i>Theor Appl Genet.</i> , 132(3):817-849 (2019)
1018	Schnable et al., The B73 Maize Genome: Complexity, Diversity, and Dynamics, <i>Science</i> , 326:1112-1115 (2009)
1020	Geiger, “Doubled Haploids in Hybrid Maize Breeding,” <i>Maydica</i> 54:485-99 (2009)
2007	FAS.USDA.gov, “Production – Corn”, available at https://fas.usda.gov/data/production/commodity/0440000
2008	Duvick et al., “Long-term Selection in a Commercial Hybrid Maize Breeding Program,” in <i>Plant Breeding Reviews: Part 2: Long-term Selection: Crops, Animals, and Bacteria, Volume 24</i> (Jules Janick, ed.) (2004)
2009	Pioneer.com, <i>History of Pioneer</i> , available at https://www.pioneer.com/us/about-us/our-history.html
2013	Cooper et al., “Predicting the Future of Plant Breeding: Complementing Empirical Evaluation with Genetic Prediction,” <i>Crop & Pasture Science</i> , 65:311–336 (2014)
2017	Springer and Stupar, “Allelic Variation and Heterosis in Maize: How do Two Halves Make More than a Whole,” <i>Genome Research</i> , 17:264–75 (2007)

2020	Silverio Garcia-Lara and Sergio O. Serna-Saldivar, Corn History and Culture, <i>Corn Chemistry and Technology</i> (2019)
2021	Doebley, “The Genetics of Maize Evolution,” <i>Annu. Rev. Genet.</i> 38:37–59 (2004)
2022	Martinez and Fernandez, “Economics of Production, Marketing and Utilization,” <i>Corn Chemistry and Technology</i> , (2019)
2023	Hochholdinger and Baldauf, “Heterosis in Plants,” <i>Current Biology</i> , 28:R1075–95 (2018)
2024	Mikel and Dudley, “Evolution of North American Dent Corn from Public to Proprietary Germplasm,” <i>Crop Science</i> , 46:1193–1205 (2006)
2025	White et al., “Diversity and Heterotic Patterns in North American Proprietary Dent Maize Germplasm,” <i>Crop Science</i> , 60:100–114 (2020)
2026	Product Sheet for the MaizeLD BeadChip Kit, available at https://www.illumina.com/content/dam/illumina-marketing/documents/products/datasheets/maize-ld-data-sheet-1370-2015-007.pdf
2027	Rouselle et al., “Study on Essential Derivation in Maize: III. Selection and Evaluation of a Panel of Single Nucleotide Polymorphism Loci for Use in European and North American Germplasm,” <i>Crop Science</i> , 55:1170-80 (2015)
2028	Declaration of Jason Wheeler
2040	Product Sheet for the Maize ear display mount, monohybrid cross, 3:1 available at https://www.southernbiological.com/biology/botany/s5-5-maize-ear-display-mount-monohybrid-cross-3-1/

2041	Product Sheet for the Maize ear display mount, dihybrid cross, 9:3:3:1 available at https://www.southernbiological.com/biology/botany/s5-4-maize-ear-display-mount-dihybrid-cross-9-3-3-1/
2042	Broman, KW, “The Genomes of Recombinant Inbred Lines,” <i>Genetics</i> 169(2):1133–46 (2005)
2043	Vanhevel et al., “Breeding for Improved Digestibility and Processing of Lignocellulosic Biomass in <i>Zea mays</i> ,” <i>Frontiers in Plant Science</i> 15:1419796 (2024)

I, PATRICK S. SCHNABLE, hereby declare the following:

1. I have been retained on behalf of Pioneer Hi-Bred International, Inc. (“Patent Owner” or “Pioneer”), in a post-grant review before the Patent Trial and Appeal Board (“PTAB” or “Board”) of U.S. Patent No. 11,707,033 (“the ’033 patent”) (Ex. 1001). The Petitioner in this case is Inari Agriculture, Inc. (“Petitioner” or “Inari”).
2. I have been asked to opine on the validity of the claims of the ’033 patent.
3. My findings, as explained below, are based on my study, experience, and background in the fields discussed below. I have also relied on my review and analysis of the prior art, information provided to me in connection with this case, and information I have independently reviewed.
4. I am being compensated for my work as an expert on this matter, but my compensation is not contingent in any way on the content of my opinions or the outcome of this proceeding.

I. QUALIFICATIONS AND PROFESSIONAL EXPERIENCE

5. My curriculum vitae (CV) is attached as Appendix A.
6. I am currently a Professor at Iowa State University (“Iowa State”), where I serve as a C.F. Curtiss Distinguished Professor, the Iowa Corn Endowed

Chair in Genetics, the Baker Scholar of Agricultural Entrepreneurship, and the Director of the Plant Sciences Institute.

7. I received my B.S. in Agronomy from Cornell University in 1981 and my Ph.D. in Plant Breeding and Cytogenetics from Iowa State University in 1986. Following my graduate work, from 1986-1988, I was a National Institutes of Health postdoctoral fellow in the laboratory of Heinz Saedler at the Max-Planck-Institut für Züchtungsforschung (Plant Breeding Research) in Köln, Germany.

8. In 1988 I became an Assistant Professor at Iowa State University. In 1994 I was promoted to Associate Professor and in 1998 I became a full Professor. I have served as a founder or founding member of several research centers at Iowa State University during my tenure: first as a Founding Member of the Center for Bioinformatics and Biological Statistics in 1999 and as a Founding Director of both the Center for Plant Transformation & Gene Expression and the Center for Plant Genomics, both in 1999. I currently serve as the faculty lead of the Digital and Precision Ag Economic Development Platform.

9. Between 1988 and 2003 I received eleven research and training grants from Pioneer, each totaling less than \$250,000. They all expired as of eighteen years ago. I am also a Co-Founder and Managing Partner at Data2Bio LLC, which provides fee-for-service experimental design, high-throughput genotyping and data analyses of plant samples for our clients, including crop breeding companies;

EnGeniousAg LLC, an agricultural sensor development company; and a Co-Founder and CEO at Dryland Genetics Inc., which breeds proso millet, a water-efficient grain crop.

10. During my entire career as a crop geneticist, I have been interested in the study of maize, maize breeding, and maize genetics.

11. Specifically, I and my research collaborators use a wide array of approaches, including genetics, genomics, bioinformatics, phenomics, and artificial intelligence & digital twins to understand the genetic control of agronomically relevant traits in corn (e.g., root and canopy architecture). Additionally, I have studied fundamental biological processes such as genetic recombination that underlie the success of crop breeding and analyzed how corn phenotypes have been changed by decades of breeding. I have developed improved methods to increase the efficiency of breeding and have also collaborated with engineers and data scientists to develop new phenotyping tools and methods to analyze the resulting data. Finally, I contributed to the maize genome sequencing project which transformed the genetic research and breeding of this crop.

12. I and my collaborators have jointly been awarded nearly \$100M in competitive grants from Federal agencies (e.g., the National Science Foundation, the US Department of Agriculture, The Department of Energy) and other sources to conduct this research.

13. Over my career I have trained over 40 graduate students, most of whom have gone on to successful careers in crop breeding companies or academia.

14. As a co-founder and CEO of Dryland Genetics, Inc., I have overseen the development and commercialization of new, higher yielding varieties of proso millet.

15. During my career, I have authored more than 200 peer-reviewed articles, which have collectively been cited by other researchers over 29,000 times; and have been granted 15 patents by the United States Patent and Trademark Office, most of which relate to crop genetics. My CV contains a comprehensive list of publications, review panels, advisory boards, and editorial posts. I have also received a number of awards over the course of my career. I provide a list of those awards in my CV.

I. MATERIALS CONSIDERED

16. I have considered all the documents I cite in this Declaration and all the relevant documents cited in the Petitioner's Petition for Post-Grant Review ("Petition") of the '033 patent in forming my opinions. A list of references cited is set forth at the beginning of this Declaration.

II. TECHNOLOGY BACKGROUND

17. The '033 patent relates to a *Zea mays* L. (corn or maize) variety. The terms maize and corn are synonyms that I will use interchangeably. Specifically, an inbred corn variety ("1PNZQ23"). ('033 patent (Ex. 1001), Title and Abstract.) Below, I give a brief technology background, as well as a description of the incredible progress that U.S. agriculture (in general) and Pioneer (specifically) has made to increase in corn yields over the last hundred years through the development of its elite inbred varieties.

A. Corn Biology and Breeding

18. At the most basic level, a corn plant is made up of cells that, together, form the plant's structure. Each cell carries the genetic material (genotypes) that controls the resulting physical traits (phenotypes) of the plant. The environment also plays a role in determining a plant's phenotype.

19. Below I give an overview of the basic biology behind the development of inbred lines and their use as parents of commercial hybrid corn varieties.

1. Reproductive Physiology

20. Unlike most commercial cereal plants, corn has separate male and female flowers. The ear (the female inflorescence), which develops at the terminal

end of a lateral branch, is covered by husk leaves. Within the ear, about 600–1,000 individual ovules (potential kernels) each produce a fiber (silk) connected to the ovule and extending beyond the husk. The tassel (male inflorescence) develops at the top of the plant and produces between 2 and 5 million pollen grains per plant. Pollen (which carry male gametes), shed by tassels (of the same or a different corn plant), falls on (or is placed on) the silks and a single pollen grain grows down a pollen tube in the silk until an ovary (which contains the female gamete) is fertilized. Once fertilized, the kernels develop on the ear, going through several stages of development until they reach physiological maturity. A schematic of a corn seedling plant and a mature corn plant (Fig. 1.4 of Silverio García-Lara and Sergio O. Serna-Saldivar, “Corn History and Culture,” *Corn Chemistry and Technology*, (2019), (Ex. 2020), at page 7) is reproduced below.

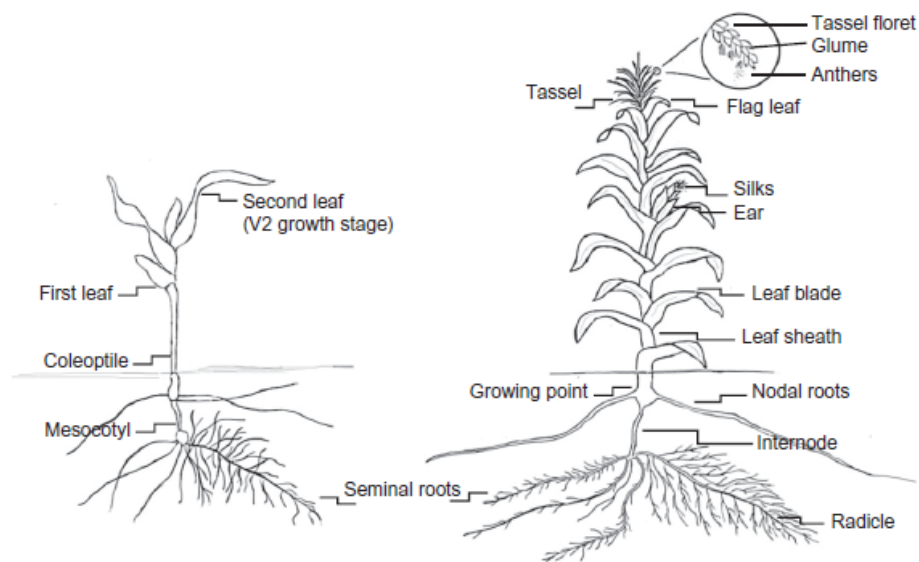


FIG. 1.4 Corn seedling plant and mature corn plant. (Source: Based on Benson, G.O., Reetz, H.F., 1984. *Corn Plant Growth-From Seed to Seedling*. National Corn Handbook, Purdue Univ. Coop. Ext. Serv., West Lafayette, pp. 1–240.)

2. Genetics and Breeding of Inbred Varieties and Commercial Hybrid Varieties

21. Typically, corn plants cells have nuclei with 20 total chromosomes—2 sets of 10 (referred to as “diploid”); 10 of the chromosomes come from the egg (female parent) and 10 from the sperm (male parent). Collectively, the 10 chromosomes are referred to as the “genome.” (Schnable et al., “The B73 Maize Genome: Complexity, Diversity, and Dynamics,” *Science*, (Nov. 20, 2009), (Ex. 1018), at page 1112.) The corn genome has been sequenced, and scientists use this published genome as a reference, which allows comparisons of genotypic data generated by different groups and from different genotypes to be compared directly. (*Id.*)

22. The total size of the genome is about 2.3 million gigabases of DNA and contains over 32,000 predicted genes. (*Id.*) At each gene / genetic segment or position in the genome, a diploid corn cell has two copies (one from the mother and one from the father, as a result of them having 10 chromosomes from each parent). Each of these copies is referred to as an “allele.” The two alleles at a gene or position in the genome may be the same (e.g., if they were the same in the parents), or they may be different (e.g., if they were different in the parents). When the two copies are different, the plant is “heterozygous” at that locus. When the two copies are the same, the plant is “homozygous” at that locus.

23. Plants that are homozygous at all or nearly all positions within the genome are referred to as “inbreds.” Inbreds, when selfed (i.e., self-pollinated), are expected to be the same both genotypically and phenotypically as the starting inbred line, differing only due to rare instances of random spontaneous mutations, which are the result of infidelity in replication common to all self-replicating organisms and other mutational processes. Because of their complete or near complete homozygosity, corn seed produced from selfed inbreds would be expected to be genetically (and, therefore, phenotypically) the same as the starting seed of the inbred line, both amongst the sibling seeds within a generation and over generations, aside from random spontaneous mutations.

24. When plants from two different inbred corn varieties are crossed as parents, each resulting progeny kernel (the “F1 generation” or “F1 hybrids”) will contain a 1:1 mixture of alleles from each parent. Because both parents were inbred (i.e., homozygous at all or nearly all positions within the genome), each F1 kernel (and, therefore, the resulting plants grown from those kernels) will share the same mixture of alleles (i.e., 50% from each parent). That is, they are both heterozygous (i.e., they don’t have the same two copies of alleles at each locus like inbred varieties) and homogeneous (i.e., they share the same mixture of alleles – 50% from each parent).

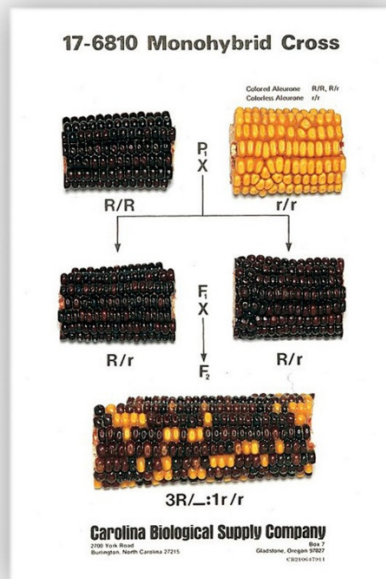
25. Because of their heterozygosity, however, even when these F1 hybrid plants are self-pollinated or crossed with their genetically identical F1 siblings (sib-pollinated), their progeny would be expected to have variable genotypes and phenotypes. There is no way to predict the exact combination of traits each progeny will inherit. The underlying biology is inherently unpredictable. Therefore, different inbred varieties, even when they originate from the same initial cross, are expected to be genotypically and phenotypically different, due to genetic segregation and genetic recombination.

26. This is illustrated, for example, by examining the cob of a F2 corn plant resulting from a monohybrid cross (a cross between two homozygous parents with different alleles at one particular gene). An educational display mount (available at <https://www.southernbiological.com/biology/botany/s5-5-maize-ear-display-mount-monohybrid-cross-3-1/>, Ex. 2040, photograph below) shows the phenotypes of such a cross between a parent homozygous for the red/purple (RR) color allele and a parent homozygous for the non-red/purple (rr) allele. The red/purple (R) allele is dominant. The non-red/purple (r) allele is recessive. The top row shows the parental phenotypes—red/purple and yellow (which results from the absence of the red/purple pigment), respectively. The second row shows the F1 phenotypes—all purple, as the red/purple allele is dominant, even though each F1 kernel carries one copy of each parental allele (i.e., are heterozygous R/r).

When the F1 (all heterozygous R/r) are self-pollinated to produce the F2 generation, there are 3 different possible genetic combinations giving rise to two different phenotypes (red/purple and yellow), as shown in the table below.

	R	r
R	R/R (red/purple)	R/r (red/purple)
r	r/R (red/purple)	r/r (yellow)

27. About 75% of progeny kernels in the F2 are red/purple (RR or R/r) and about 25% of progeny kernels are yellow (r/r), as depicted below.



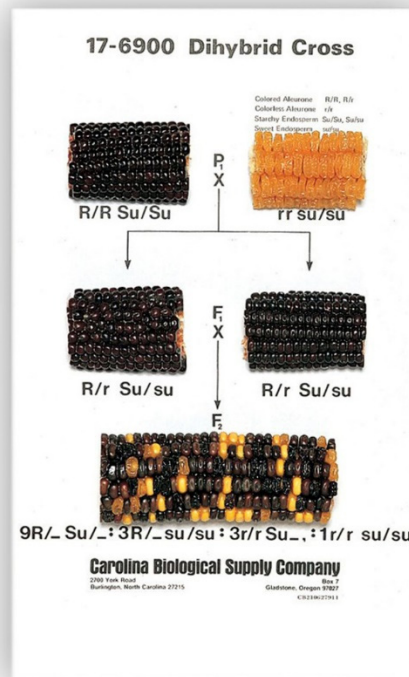
28. The monohybrid cross is the simplest example of Mendelian genetics. But considering more than just one gene, the possible genotypes and phenotypes are exponentially more complicated. The same type of display mount is available

for a dihybrid cross (similar to a monohybrid cross, but in this case the parents have different alleles at two genes). (Ex. 2041, <https://www.southernbiological.com/biology/botany/s5-4-maize-ear-display-mount-dihybrid-cross-9-3-3-1/>, photograph below). In this cross, the parents differ not only in their color allele, but also in their endosperm allele (starchy, Dominant *Su* vs. non-starch or sweet, recessive *su*).

29. In the dihybrid example, all the F1 progeny, again, have a uniform heterozygous genotype (*R/r* and *Su/su*) and a red/purple starchy phenotype. But in this case, there are nine different possible genetic combinations in the F2 that give rise to four different phenotypes (red/purple and starchy; red/purple and sweet; yellow and starchy; yellow and sweet), as shown in the table below.

	<i>R Su</i>	<i>R su</i>	<i>R Su</i>	<i>r su</i>
<i>R Su</i>	<i>R/R</i> <i>Su/Su</i> (red/purple, starchy)	<i>R/R</i> <i>Su/su</i> (red/purple, starchy)	<i>R/r</i> <i>Su/Su</i> (red/purple, starchy)	<i>R/r</i> <i>Su/su</i> (red/purple, starchy)
<i>R su</i>	<i>R/R</i> <i>Su/su</i> (red/purple, starchy)	<i>R/R</i> <i>su/su</i> (red/purple, Sweet)	<i>R/r</i> <i>su/Su</i> (red/purple, starchy)	<i>R/r</i> <i>su/su</i> (red/purple, v sweet)
<i>r Su</i>	<i>r/R</i> <i>Su/Su</i> (red/purple, starchy)	<i>r/R</i> <i>Su/su</i> (red/purple, starchy)	<i>r/r</i> <i>Su/Su</i> (yellow, starchy)	<i>r/r</i> <i>Su/su</i> (yellow, starchy)
<i>r su</i>	<i>r/R</i> <i>Su/su</i> (red/purple, starchy)	<i>r/R</i> <i>su/su</i> (red/purple, sweet)	<i>r/r</i> <i>su/Su</i> (yellow, starchy)	<i>r/r</i> <i>su/su</i> (yellow, sweet)

30. About 56% (9/16) of the progeny kernels in the F2 are red/purple and starchy, about 19% (3/16) are red/purple and non-starchy (sweet), another 19% (3/16) are non-red/purple (yellow) and starchy, and about 6% (6/16) are non-red/purple (yellow) and sweet.

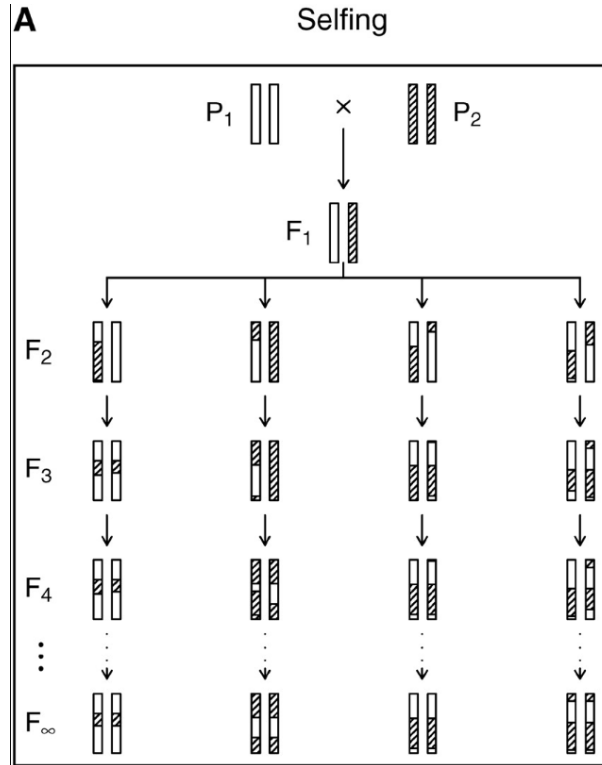


31. The one or two gene models of simple Mendelian inheritance illustrate how genetic segregation in the F1 leads to genetic and phenotypic diversity in the F2 generation. However, as described above, the maize genome contains over 32,000 predicted genes. And furthermore, many agronomically relevant traits are controlled by many genes and have more complex inheritance patterns.

32. Using one traditional method to create a homozygous inbred line, an F1 corn seed would be grown and self-pollinated for many generations. The F1 kernel from a starting cross would be grown into an F1 plant and selfed to produce the next generation (the “F2”). As described above, each of the F2 progeny is genetically and phenotypically distinct. The F2 kernels would be grown into plants, and those plants would be selfed again, for many generations. Through this process, approximately one-half of the heterozygosity across the genome is lost at each generation until the alleles are eventually fixed (i.e., homozygous for either the allele derived from the male parent or the allele derived from the female parent of the F1).

33. Furthermore, genetic recombination (i.e., meiotic crossing over) during the F1 generation leads to different patterns of inheritance that result in both genotypic and phenotypic differences in the F2 generation and beyond. So, the genomes of recombinant inbred lines (inbred lines “formed by crossing two inbred strains followed by repeated selfing or sibling mating”) are “mosaic[s] of the parental genomes.” (Broman, “The Genomes of Recombinant Inbred Lines,” *Genetics* 169(2):1133–46 (2005), Ex. 2042.) And, as illustrated in Broman’s, Figure 1, for example (reproduced below), different progeny inherit different patterns. Because of genetic segregation and recombination, there is no way to

predict the exact combination of traits each progeny will inherit, and the possibilities are enormous.



34. The inbreeding process is inherently stochastic (i.e., random) and, as such, if repeated, would be expected to produce an inbred variety with a different combination of alleles each time, even if the starting F₁ seed were identical. So, “parents” of new inbred varieties are not parents in the nuclear family sense, but ancestors from generations back.

35. Human intervention, however, can push the process in particular directions via “selection” (sometimes also called “artificial selection”). In that case, rather than randomly choosing any one of the F₂ seeds to start with (or which

seeds of later generations to use as parents of subsequent generations, i.e., “advance”), a breeder chooses which plants to self-pollinate or which seeds to plant in the next generation purposefully based on some specifically defined criteria. A corn breeder may select seeds based on genotype, phenotype, or both. But because of random genetic segregation and recombination (described above), that corn breeder must assess and select from an enormous number of unique progeny, but not all of the progeny are expected to be valuable. As described in Section II.C., below, almost all the lines resulting from an initial cross are discarded.

36. Historically, corn was selected based on phenotype alone. That is, after making a cross, the resulting seeds would be planted and the resulting plants measured phenotypically. The breeder would then select those plants with the most desirable traits and save those seeds (select them) to be bred again for the next generation.

37. Modern breeding, however, utilizes selection based on both genotype and phenotype. (Andorf et al., “Technological Advances in Maize Breeding: Past, Present and Future,” *Theoretical and Applied Genetics*, 132:817–49 (2019), (Ex. 1015), pages 820–24.) Corn is still planted and measured and selected based on phenotypes during the breeding process. However, because scientists now understand more about the genetic basis for certain traits, it is possible to estimate

what a plant's phenotype might be for those traits, based on its genotype alone.

(*Id.*) So, a corn breeder can make decisions about which plants to advance based on genotypes, without having to rely on phenotypic observations alone.

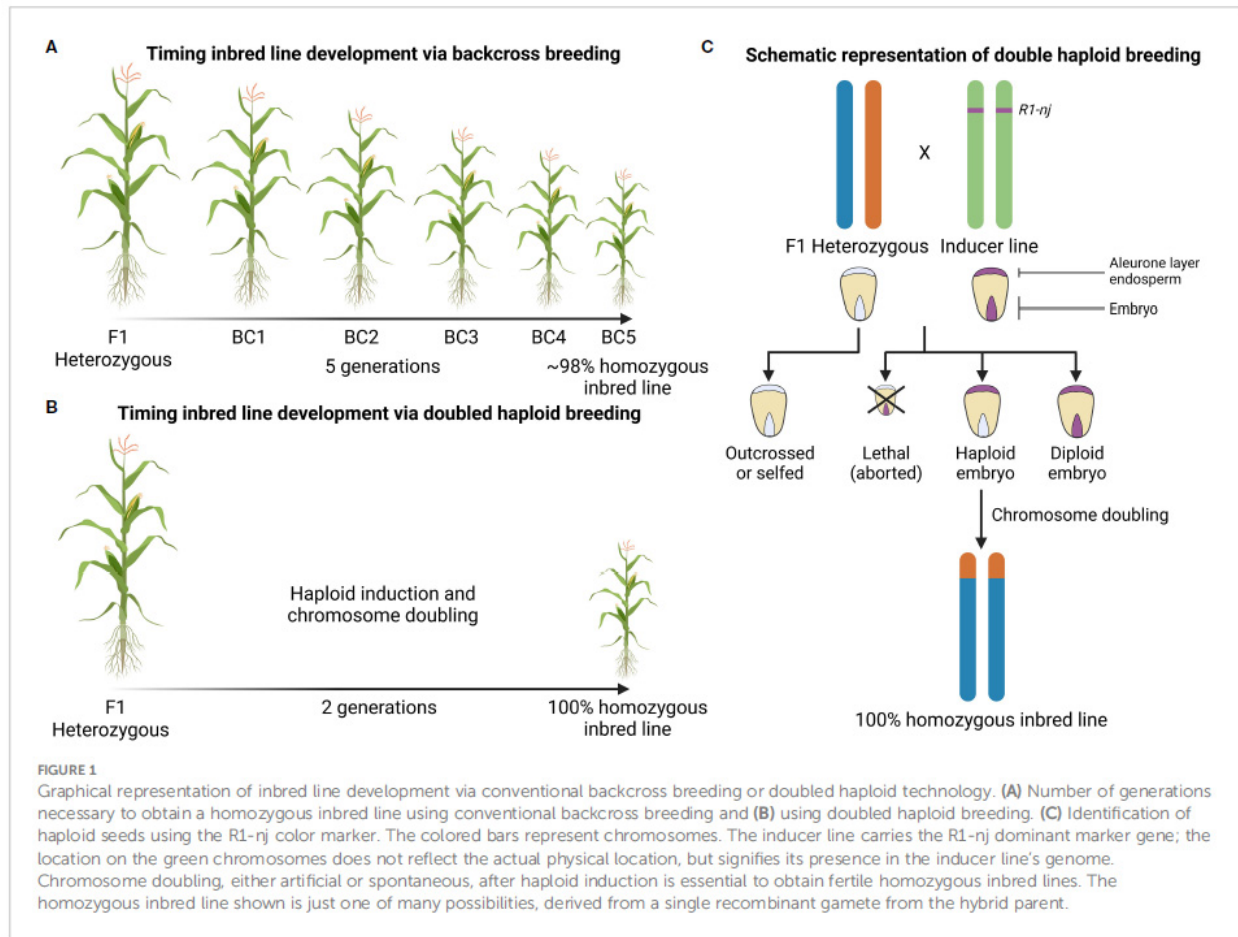
38. In some cases, the underlying genetics of a particular trait is known, and a breeder will select for that trait directly based on the presence or absence of the known genotype. In other cases, the underlying genetics of a particular trait is not known or is too complex to track directly by a single gene. Then, a breeder may select for genotypes that are associated with, but not necessarily causative of, a particular trait or traits. (*Id.*) As of August 2018, there were 13 sequenced corn genomes and a vast number of other genetic resources available in MaizeGDB (a publicly accessible database). (*Id.* at 824.)

39. Modern breeding is very sophisticated and genetic predictions have progressed to the point that corn breeders use genome-wide comparisons to predict performance and select candidates for advancement through the breeding process. (*Id.*) In corn breeding, it is possible to non-destructively sample tissue from a kernel to determine that seed's genotype even before planting it to predict the plant's phenotypes. That is typically done by sampling a portion of the endosperm off the seed, extracting DNA, and determining its genotype either across the genome or at specific locations. This technique allows breeders to conduct genetic

selection even before planting to reduce the number of plants to test phenotypically by orders of magnitude.

40. Another breeding technique that has been a boon to breeders is the doubled haploid (“DH”) procedure. As described above, development of inbred lines by conventional methods involves several generations of breeding. Alternatively, homozygous diploid lines (with—2 copies each of corn’s 10 chromosomes) can be produced from F1 corn by creating a haploid (with 1 copy each of corn’s 10 chromosomes) and then doubling that haploid content so that the resulting plant (the D1 plant) has two identical copies of each of the 10 chromosomes (i.e., is a homozygous inbred). D1 sibling plants, like F2 sibling plants described above, are genetically distinct due to genetic segregation and recombination in the F1. An advantage of using the doubled haploid procedure is reducing the overall number of generations required to produce a desirable and fully homozygous inbred line. (See H.H. Geiger and G.A. Gordillo, “Doubled Haploids in Hybrid Maize Breeding,” *Maydica*, 54:485–99 (2009) (Ex. 1020); see also Vanhevel et al., “Breeding for Improved Digestibility and Processing of Lignocellulosic Biomass in *Zea mays*,” *Frontiers in Plant Science* 15:1419796 (2024) (Ex. 2043)).

41. Vanhevel’s Figure 1 (reproduced below) illustrates the differences between traditional inbred development and doubled haploid inbred development.



42. Even with the new modern breeding techniques and advances in mechanization and farming practices, however, corn breeding is still a difficult and unpredictable endeavor. As described below, the entire process takes years. Arriving at one elite inbred line means discarding thousands or even millions of others along the way.

3. Phenotypes

43. A plant's phenotype (P) is the product of its genotype (G), its environment (E), and G and E interactions (GEI). So, $P = G + E + GEI$.

44. Environments differ in many ways—temperature, humidity, day length, pest pressures, just to name a few.

45. Genotypes and environment can interact (GEI) in complex ways to produce phenotypes, such that the relative performance of a set of genotypes can change depending upon the environment. For example, while one corn variety (having one set of genotypes) may have higher yield than another variety (having a different set of genotypes) in one environment (e.g., a hot dry environment), it may have lower yield in another (e.g., a cool wet environment).

46. Some phenotypes are more influenced by environment (E) than others, whereas some phenotypes are driven more influenced genotype (G) and are more stable across environments.

47. As a result, genetically identical plants will exhibit different phenotypes for many traits, when grown in different environments. Maturation and flowering time, for example, are highly dependent on environmental conditions such as temperature. This is an example of $G + E$.

48. Likewise, in some environments, genetically different plants may exhibit the same or similar phenotypes, while in other environments, they may exhibit different phenotypes. This is an example of GEI.

4. Heterosis (“Hybrid Vigor”)

49. Inbred corn lines, which have risen in prominence since the 1930s are primarily used as parents of hybrid varieties. (See Section II.B.) The reason why hybrid varieties are preferred in corn is because of the phenomenon of “hybrid vigor,” also called “heterosis,” in which certain “hybrid F1 offspring exhibit phenotypic characteristics that are superior to the mean of the two parents (mid-parent heterosis), or the better of the two parents (better parent heterosis).” (Springer & Stupar, “Allelic Variation and Heterosis in Maize: How do Two Halves Make More than a Whole,” *Genome Research*, 17:264–75 (2007) (Ex. 2017), at page 264.) The latter case (better parent heterosis) is “the underlying rationale for the widespread use of hybrids in many agricultural species.” (*Id.*) Springer and Stupar’s Figure 1 (reproduced below) demonstrates this effect.

50. As described below, the exploitation of hybrid vigor in corn breeding was revolutionary, allowing for substantial increases in yield since hybrids became prominent in the 1930s. (See Section II.B.; see also Riley Declaration (Ex. 1003 at page 24, ¶ 53).)

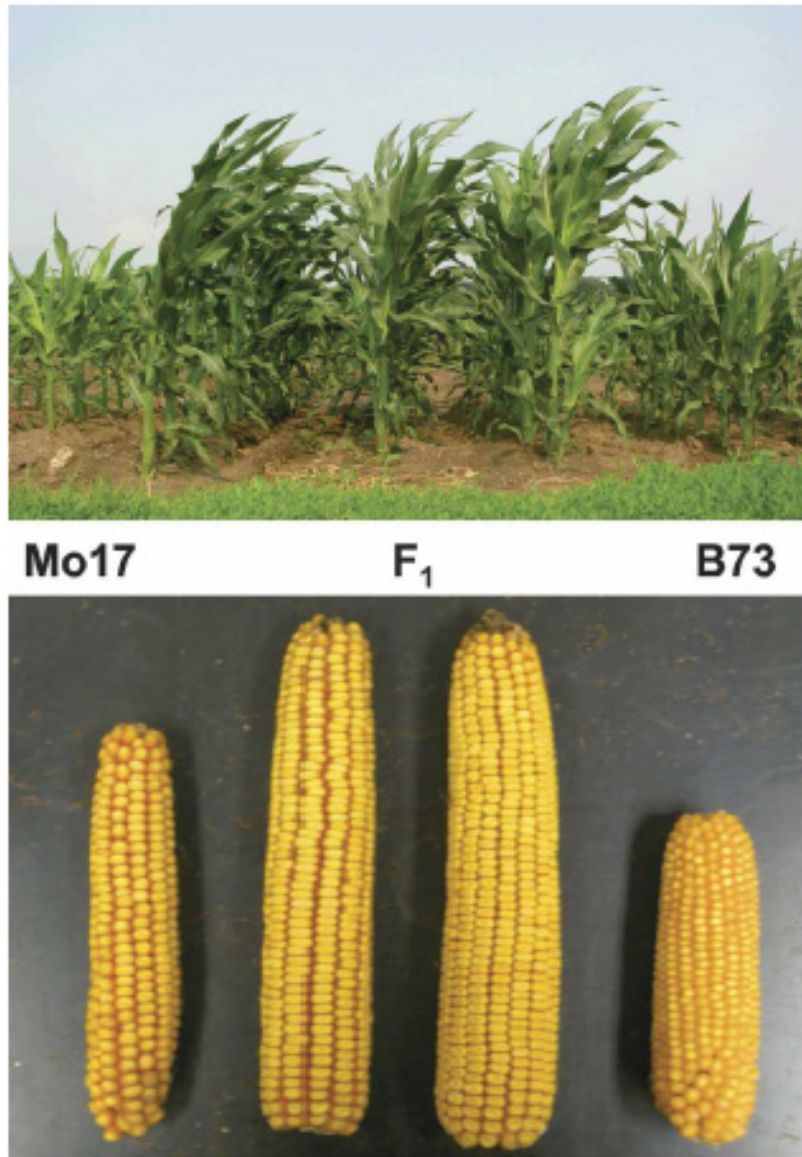


Figure 1. Phenotypic heterosis in the B73 $\times$ Mo17 hybrid. Representative B73, Mo17, and F₁ hybrid ears and plants are shown. Note the increased size of the two hybrid ears and three hybrid rows relative to the two inbred parents (left, Mo17; right, B73).

B. History of Corn and Corn Production

51. Modern corn was domesticated from the wild plant *Z. mays subsp. parviglumis* (teosinte) about 6,000 to 10,000 years ago. (Doebley, “The Genetics

of Maize Evolution,” *Annu. Rev. Genet.*, 38:37–59 (2004), (Ex. 2021), at page 39-40.) Teosinte still exists in the wild today but bears little resemblance to today’s modern corn varieties. Furthermore, modern corn varieties bear little resemblance to early domesticated corn. This is apparent from Doebley’s Figure 2 (reproduced below), showing both teosinte and a ‘reconstructed’ primitive maize.

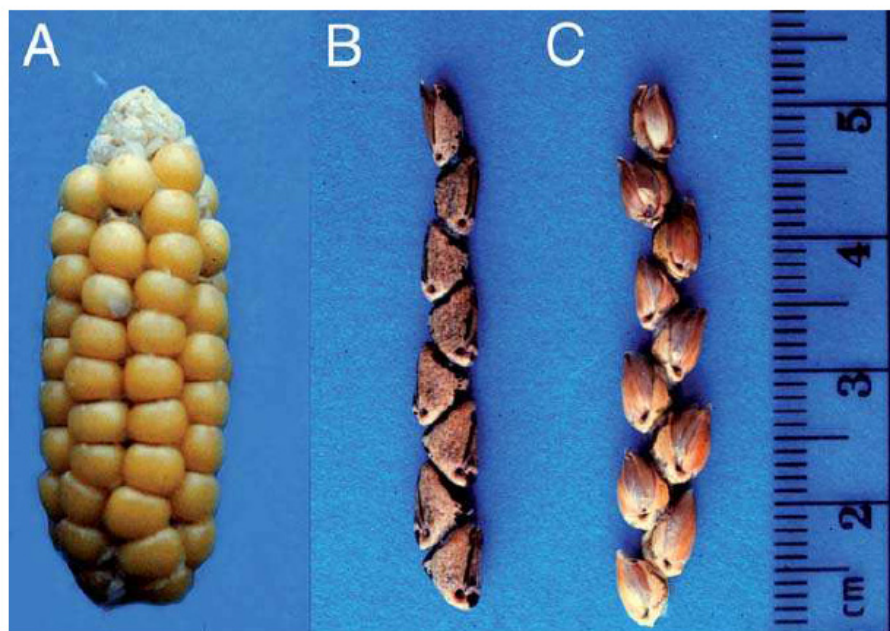


Figure 2 (A) A ‘Reconstructed’ ear of primitive maize (*left*). This small-eared form of maize was bred by George Beadle by crossing teosinte with Argentine pop corn and then selecting the smallest segregants (16). (B) Ear of pure teosinte (*Zea mays* ssp. *parviglumis*) composed of eight cupulate fruitcases. (C) Ear of teosinte carrying a segment of maize chromosome arm 4S including the maize allele of *tga1*. The effects of the maize allele of *tga1* include cupules that are less well-developed and shallower so that the kernels are visible. Photo by John Doebley.

52. Today, corn is “the most important cereal grain in terms of production,” surpassing rice and wheat in worldwide production about 10 years ago “due to the development of high-yielding regular and genetic-modified genotypes and its wider adaptation to different ecosystems.” (Silverio Garcia-Lara

& Sergio O. Serna-Saldivar, “Corn History and Culture,” *Corn Chemistry and Technology*, (2019) (Ex. 2020) at page 1). “Maize is the most extensively cultivated and consumed cereal in the world.” (*Id.*) “The U.S. Corn [sic] Belt produces 38% of the world’s total, followed by China (18%).” (*Id.*) Roughly “one third of the corn global trade comes from USA exports.” (Martinez & Fernandez, “Economics of Production, Marketing and Utilization,” *Corn Chemistry and Technology*, (2019), (Ex. 2022) at page 100.) China is also a top producer, but because its demand outpaces its production, China normally imports corn. (*Id.*)

53. The modern success of corn is “due to its adaptation to different ecosystems from coasts to mountains and the development of highly producing regular and biotechnological hybrids capable of yielding under commercial conditions up to 16 tons/Ha.” (Silverio Garcia-Lara & Sergio O. Serna-Saldivar, “Corn History and Culture,” *Corn Chemistry and Technology*, (2019), (Ex. 2020) at page 6.) “Corn is a crop with a remarkable genetic variability; therefore, many specialty genotypes are available.” (*Id.*)

54. Before the 1930s, corn production relied on open pollination. (Hochholdinger & Baldauf, “Heterosis in Plants,” *Current Biology*, 28:R1075–95 (2018) (Ex. 2023) at page R1090.) That is, farmers propagated an open-pollinated variety by saving the seed from the best ears of the best plants each season. The resulting seed had a known female parent (the plant that produced the ovule and

silk containing ears), but an unknown male parent (the plant that produced the pollen containing tassel). It could have been the same plant or a different plant, as there was no effort to control the pollen source.

55. Starting in the 1930s, however, and led by Henry Wallace and the founding of the Hi-Bred Corn Company in 1926 (see History of Pioneer, Pioneer, <https://www.pioneer.com/us/about-us/our-history.html>, Ex. 2009), production shifted to cross-pollinated hybrid varieties to exploit hybrid vigor. The production of hybrids relies not on open pollination, but rather on controlled crosses between pre-selected parental lines—in particular, inbred parental lines. This change allowed for the production of ever-improving inbred parental lines, resulting in rapid gains in average grain yields of hybrids from the 1930s to the 2020s (Frank Hochholdinger & Jutta Baldauf, “Heterosis in Plants,” *Current Biology*, 28:R1075–95 (2018), Ex. 2023), as reflected in Hochholdinger’s Figure 2, reproduced below.

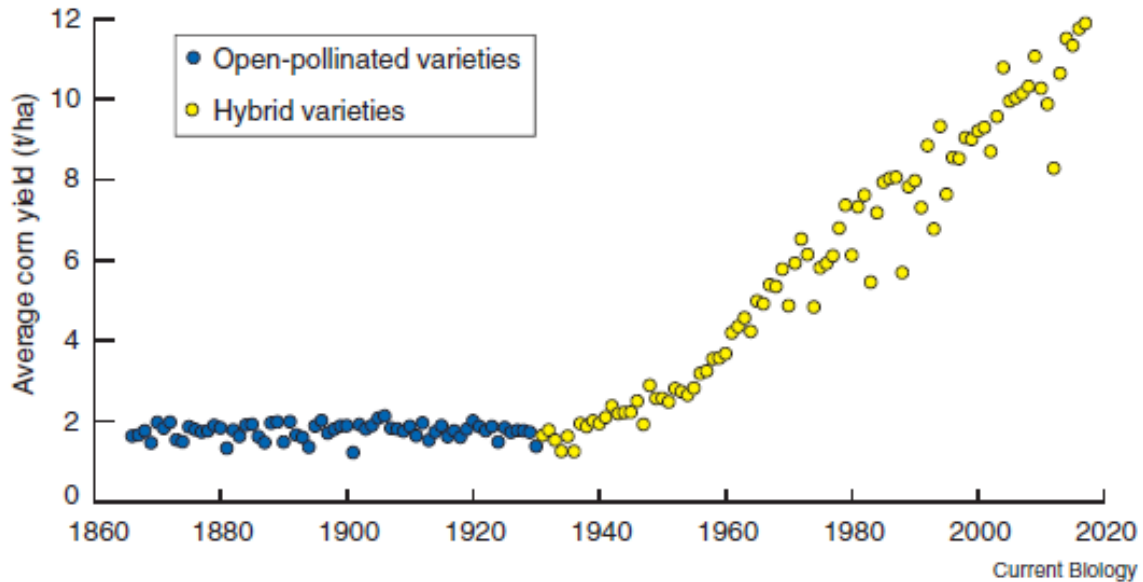


Figure 2. Average grain yield in tons per hectare for maize varieties in the United States. Yield of open-pollinated varieties (blue) from 1866 to 1930 and hybrid varieties (yellow) from 1931 to 2017. Data source: United States Department of Agriculture, National Agricultural Statistics Service (www.nass.usda.gov).

56. An example of a typical inbred line development scheme demonstrating the inbred line development process, generally, is set forth as Figure 3 of Lee et al. (Ex. 1012) on page 146 and is also reproduced below. E.A. Lee & W.F. Tracy, “Modern Maize Breeding,” in Handbook of Maize: Genetics and Genomics 141-60 (J.L. Bennetzen & S. Hake, eds.; 2009), (Ex. 1012). As described more fully below and shown in this figure, the entire process is recurrent. That is, successful inbred lines become part of the breeding pool to produce further inbred lines.

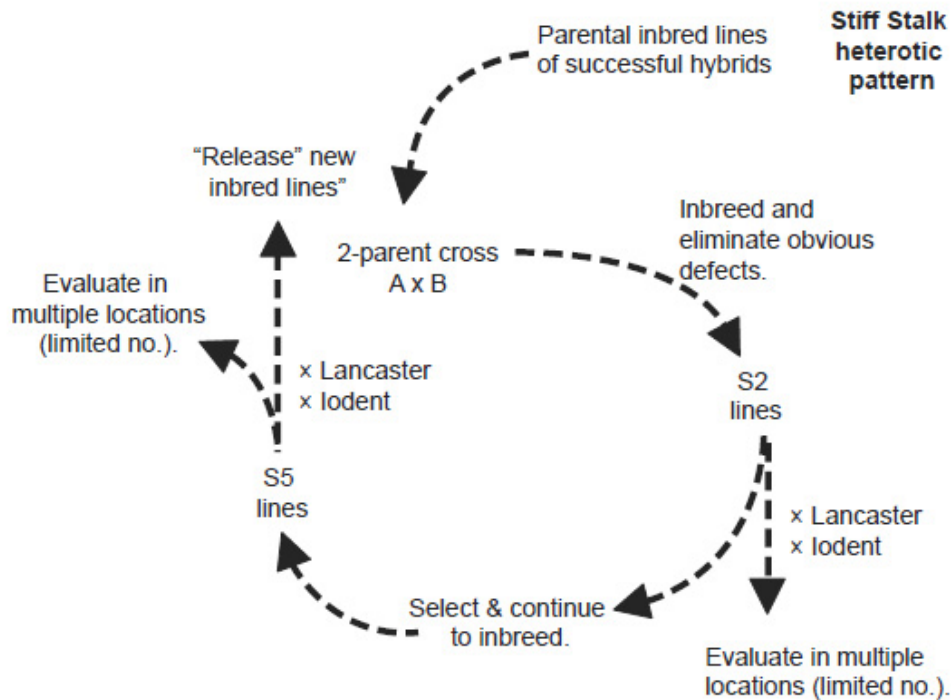


Fig. 3 An example of a typical inbred line development scheme, depicting a 2-parent breeding cross involving two inbred lines from the Stiff Stalk heterotic pattern. (From: Lee and Tollenaar 2007)

57. This entire process has resulted in modern corn varieties that are “adapted ‘to the broadest range of climactic conditions of all crops.’” (Andorf et al., “Technological Advances in Maize Breeding: Past, Present and Future,” *Theoretical and Applied Genetics* 132:817–49 (2019) (Ex. 1015).)

58. As discussed below, Patent Owner Pioneer’s own breeding efforts from the 1930s—using this type of breeding scheme—have resulted in the massive increase in yield year over year.

59. Furthermore, many of the inbred lines that led to this increase are now off patent and/or PVP protection and available to the public, with comparative

genotype and phenotype data available. Examples of publications describing them include Mikel & Dudley, “Evolution of North American Dent Corn from Public to Proprietary Germplasm,” *Crop Science* 46:1193–1205 (2006) (Ex. 2024) and White et al., “Diversity and Heterotic Patterns in North American Proprietary Dent Maize Germplasm,” *Crop Science* 60:100–114 (2020) (Ex. 2025).

C. Patent Owner Pioneer’s Germplasm Development

60. The United States’ corn production is the envy of the world. The U.S. is the largest producer, consumer, and exporter of corn, annually producing 390 million metric tons of corn grown (a third of all corn grown) on 30 million hectares of land. (Production – Corn, Foreign Agricultural Service, <https://fas.usda.gov/data/production/commodity/0440000>, (Ex. 2007); (Martinez & Fernandez, “Economics of Production, Marketing and Utilization,” *Corn Chemistry and Technology*, (2019), (Ex. 2022).) Hybrid corn varieties developed in the U.S. annually lead the world in production, and over the past hundred years have led a revolution in corn breeding that has helped feed a hungry world beyond agronomists’ wildest imagination. (See Duvick et al., “Long-term Selection in a Commercial Hybrid Maize Breeding Program,” in *Plant Breeding Reviews: Part 2: Long-term Selection: Crops, Animals, and Bacteria*, Volume 24 (Jules Janick, ed.) (2004), (Ex. 2008.))

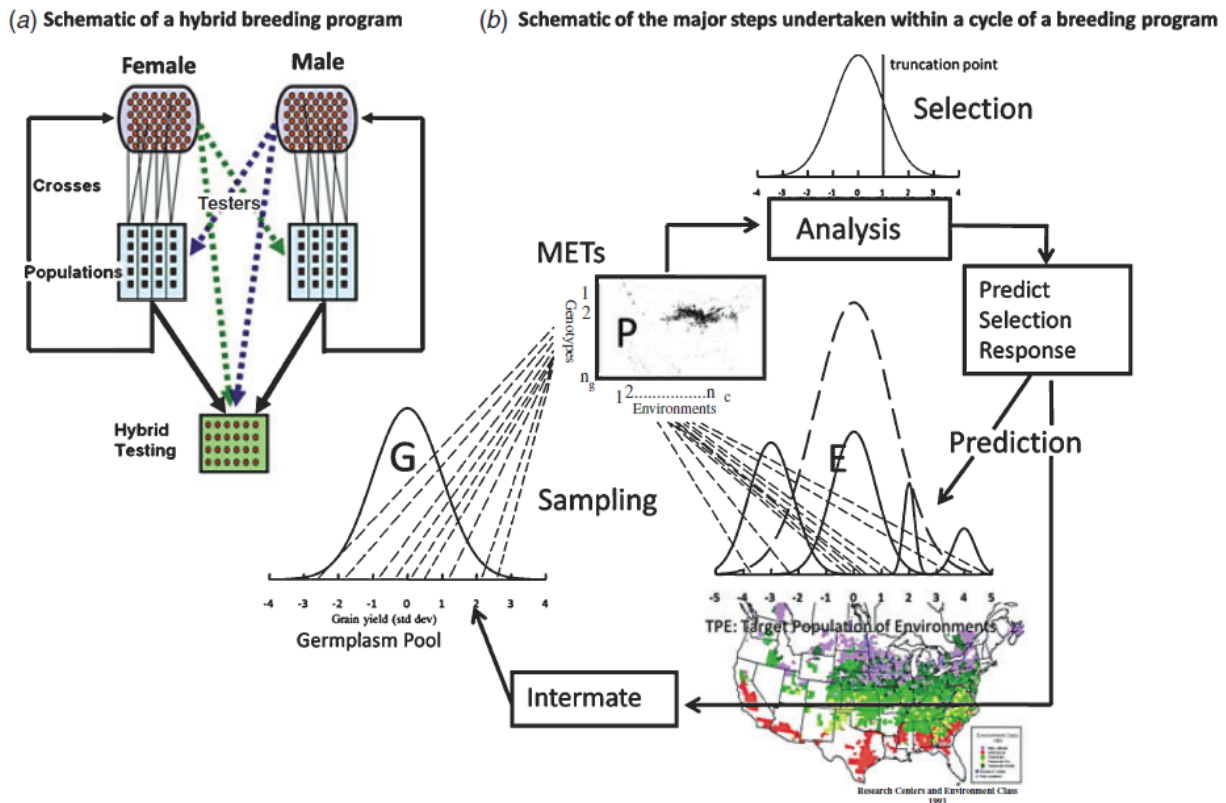
61. “Commercial plant breeders” like Pioneer, “have the same goal as plant breeders in the public sector—to produce improved cultivars that suit the needs of farmers who plant them.” (*Id.* at page 110.)

62. Pioneer’s “Intended Breeding Goals,” in particular, has been “[h]igher grain yield.” (*Id.* at 111.) But “from time to time various biotic and abiotic problems” such as severe drought, the onset of the European corn borer, higher plant densities and rates of nitrogen fertilizer, and no-till or minimum-till planting, “have necessitated the urgent implementation of additional goals.” (*Id.* at 111–112.) “Thus, one might say that the breeders’ constant goal has been to develop hybrids that produce higher yields in spite of the constantly enlarging array of biotic and abiotic stresses.” (*Id.*) Those stresses “were brought on in part by changing cultural techniques and in part by the increasing monoculture nature of maize production in the U.S. Corn Belt,” as well as climate change. (*Id.*) The development of commercial hybrids capable of withstanding these biotic and abiotic stresses requires the development of inbred varieties having beneficial and advantageous traits to confer to those hybrids. In pursuit of this goal, Pioneer has developed, over many decades, a collection of “elite germplasm” inbred varieties carrying advantageous traits that have the potential to produce agriculturally successful hybrids when crossed. Two elite maize inbreds having different, but

complimentary, traits are crossbred to create a maize hybrid—the crop seed that is planted by farmers to produce commodity grain to supply the market.

63. Over the past 100 years, Patent Owner has developed a sophisticated and robust process for developing the type of inbred maize varieties claimed in the '033 patent. As discussed in detail below, a program starting with millions of prospective genotypes involves the genetic and phenotypic characterization of tens of thousands prospective plant varieties with the goal of whittling those prospects down to just tens of new inbred varieties having potential for agronomic success. This process takes many years and involves multidisciplinary teams of hundreds of breeders, farmers, plant pathologists, geneticists, plant biologist, entomologists, meteorologists, data analyst and other specialists. The development teams are not only multidisciplinary but multinational. The development of a single inbred often requires several independent research groups spread across the globe to coordinate breeding, genotyping, planting, and evaluation activities to account for seasonal changes in different geographical regions.

64. A schematic of “the cyclical process followed in a typical, commercial maize breeding program” for the US corn-belt (as published by Pioneer authors) is excerpted below. (Cooper et al., “Predicting the Future of Plant Breeding: Complementing Empirical Evaluation with Genetic Prediction,” *Crop & Pasture Science*, 65:311–336 (2014) (Ex. 2013) at page 312-13, Figure 2).

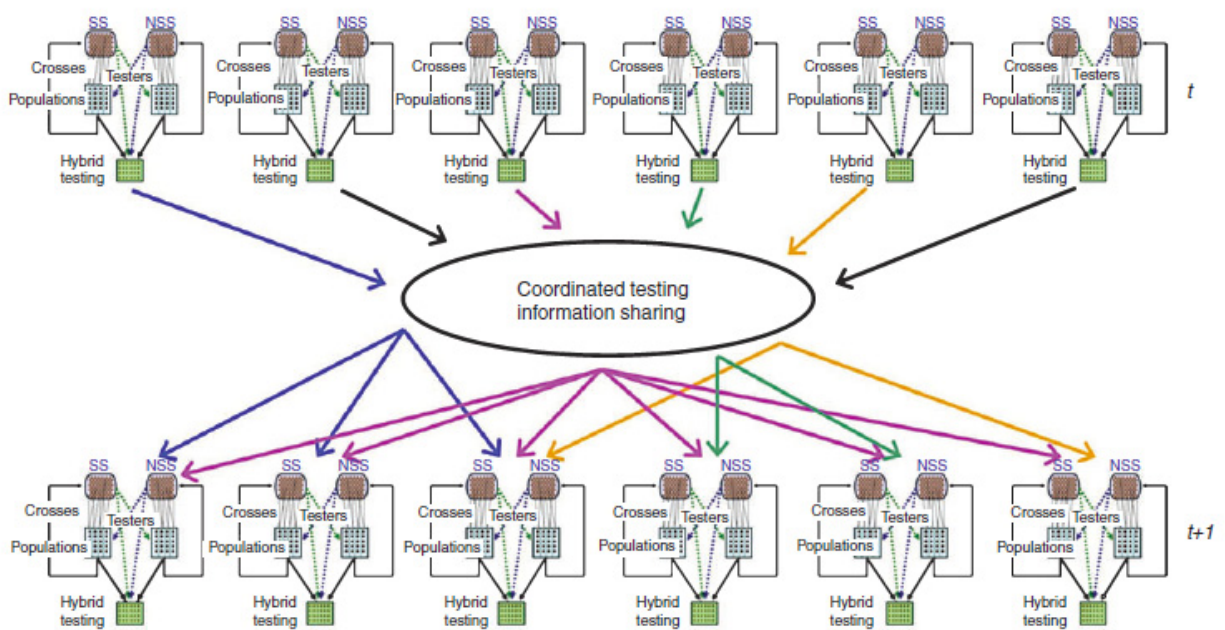


65. The top left panel (a) shows that the “maize germplasm pool is organised into two major heterotic groups.” (*Id.*) Heterotic groups refer to a group of plants that are classified according to their breeding requirements. This is somewhat analogous to the production of Labradoodle dogs, where two parents (a Labrador retriever and a poodle) are selected as mates to produce the labradoodle (like inbred corn varieties to produce hybrid corn), but dog breeders may also independently cross Labrador retrievers with each other and poodles with each other to improve the breeding stock of each individual breed. In Cooper’s example for a commercial corn breeding program, one heterotic group “is designated as the female pool, often referred to as Stiff-Stalks (SS),” while the “other is the male

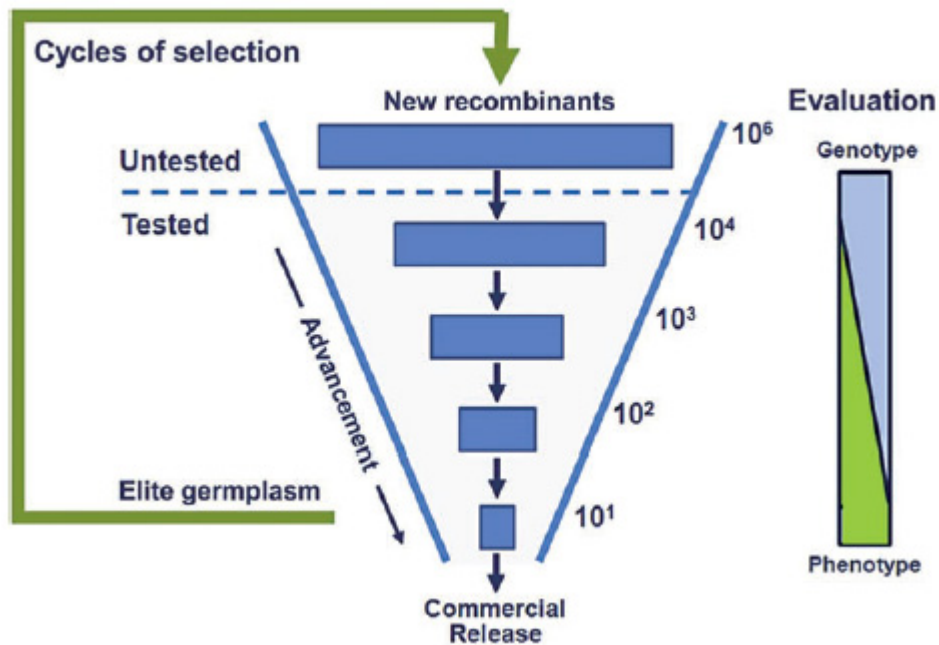
pool, often referred to as non-Stiff-Stalks (NSS). (*Id.* at 312-313.) These are two of the major North American field corn heterotic groups. However, not every inbred will perform as well as others as a hybrid parent. Therefore, those new inbreds are tested for yield and key agronomic traits “in hybrid combination[s] using appropriate testers from the complementary heterotic group[s].” (*Id.*) That is, they are crossed with a “stand in” second parent to test theoretical hybrid performance. That process builds up the potential pools of inbred lines to ultimately serve as parents for F1 hybrids while simultaneously generating more inbreds within the heterotic groups to use for further development. (*Id.*)

66. While this is occurring, and at each stage in the breeding program, potential new varieties are evaluated across many environments (e.g., in “multi-environmental trials (METs)”) to evaluate different traits across commercially representative environments, as depicted in panel (b). (*Id.*)

67. “Large-scale commercial breeding programs typically operate as a coordinated network of breeding programs.” (*Id.* at 314, Figure 3) (excerpted below). Novel inbred development is “not typically run as one large centralised breeding program,” but instead “operate[] more like an interconnected network of smaller breeding programs with multiple breeders applying distributed field testing to solve their local problems and exchanging improved germplasm.” (*Id.* at 314.) That is, this is all occurring at massive scale.



68. All of this results in a massive funnel, where the number of new recombinant inbred lines (inbred lines formed by crossing two inbred strains followed by repeated selfing or sibling mating) is winnowed down over the years from the starting F1 crosses to the elite germplasm varieties for commercial release using both genotypic and phenotypic evaluations. (*Id.* at 315.) Cooper’s Figure 4 depicts this “funnel” effect, where the starting germplasm includes 10^6 (millions) starting inbreds, of which 10^4 are “Tested,” and ultimately narrowed down by three orders of magnitude to just ten elite inbred varieties. (*Id.*)



69. As depicted in the figure, “[a]t the initiation of a cycle, new inbreds are generated from multiple crosses among elite inbreds available within the heterotic groups.” (*Id.*) Those “new inbreds represent new recombinants of the genetic variation available within the heterotic group.” (*Id.*) This is a result of the basic genetic processes that I describe above. As shown here, the early analyses are based on genotype of these newly created inbreds established soon after they are created. (*Id.*) I discuss genotypic and phenotypic analyses, generally, above. As the selected lines are advanced, “those that are retained are subjected to further rounds of phenotyping and the quantity of phenotypic information increases.” (*Id.*) Ultimately, commercialization decisions are made based on the performance of the resulting hybrids and market needs. (*Id.*)

70. In their “Era” study, Pioneer compared the performance of hybrids commercialized over a 70-year period to determine the importance of the contribution of their breeding program to overall yield increases of corn. (Duvick et al., “Long-term Selection in a Commercial Hybrid Maize Breeding Program,” in *Plant Breeding Reviews: Part 2: Long-term Selection: Crops, Animals, and Bacteria*, Volume 24 (Jules Janick, ed.) (2004), (Ex. 2008), at pages 113–14.) As noted in that publication, over the years “the breeders primarily, but not exclusively, have relied on pedigree breeding,” which “has been the most dependable method for producing inbred lines.” (*Id.*) “Germplasm for the most part came from inbred lines that had proven their utility in commercial hybrids.” (*Id.*) Pioneer’s inbred germplasm has been developed and improved since around the 1930s using its breeding program (e.g., as described above). (*Id.* at 111–13.) “Widespread on-farm performance of released hybrids was used to identify the top-performing inbreds, to winnow the best from merely average germplasm.” (*Id.* at 113–114.) “All of the hybrids were bred, produced, and sold by Pioneer Hi-Bred International.” (*Id.*)

71. The results of the study showed an increase in performance/yield resulting from an increase in genetic tolerance to environmental stresses and that the overwhelming increases observed year after year coming out of the breeding

program is directly attributed to the new inbred and hybrid varieties coming out of the massive breeding funnel year after year. (*Id.* at 141.)

72. “Formal breeding programs have allowed new diversity to be created by bringing together germplasms that otherwise would have been isolated in different regions of the country,” or the world, for that matter. (*Id.* at 147.)

Therefore, breeders “have continued to create and to test new combinations of diversity, a reality that differs from another misconception whereby breeders are said to have taken an initial small sample of corn inbreds and essentially then boiled away most of the diversity.” (*Id.*) The study of Pioneer’s breeding program “shows that the creation, testing, and incorporation of new diversity has accompanied the development of robust new hybrids that increasingly are tolerant of pests and stressful climatic conditions and that, consequently, can yield more per unit area of land.” (*Id.*)

73. Yet, further breeding will be needed as “new and presently unforeseen changes in agronomic practices (and probably in climate) will give tomorrow’s breeders new challenges and new opportunities to breed and select for enhanced yielding ability under new growing conditions.” (*Id.* at 149.)

74. Pioneer and other commercial corn breeders will continue to invest in these massive breeding efforts to developing tomorrow’s corn varieties if it is economically viable.

III. THE '033 PATENT—MAIZE INBRED VARIETY 1PNZQ23

75. The '033 patent is titled “Maize Inbred 1PNZQ23.” ('033 Patent, Ex. 1001 at cover page.) It issued on July 25, 2023. (*Id.*) It was filed as U.S. Patent Application No. 17/366,121 on July 2, 2021. (*Id.*)

A. Overview of The Specification

76. The '033 patent describes a “new and distinctive maize inbred variety designated 1PNZQ23, which has been the result of years of careful breeding and selection in a comprehensive maize breeding program.” (Ex. 1001, 4:41–44.) It is an “elite corn inbred line originated from a cross between inbred line PH1VKM and inbred line PH2DYM.” (Ex. 1001, 37:60–64.) That is, these two inbreds were crossed to produce F1 plants (as described above). “Inbred 1PNZQ23 was developed by producing a doubled haploid from the F1 plants, selfing and using pedigree selection amongst the D1 lines, and selfing and bulking from the subsequent generations.” (Ex. 1001, 37:66–38:3.)

77. This entire breeding process is “time-consuming” and takes “from six to twelve years” from first cross to finished seed. (Ex. 1001, 1:18–26.)

78. Representative seed of the resulting inbred variety was deposited with the National Center for Marine Algae and Microbiota (NCMA) under NCMA Accession Number 202301024. (Ex. 1001, 37:31–36.) The '033 specification

states that “[u]pon issuance of any claims in the application, the Applicant will make the deposit available to the public pursuant to 37 C.F.R. § 1.808.” (Ex. 1001, 37:44–46.)

79. I understand, as explained to me by Pioneer’s counsel, the representative seed was accessible to both the U.S. Patent Office (including during examination of the application) and the Petitioner (for the purpose of comparing the phenotypic and genotypic differences over the prior art after the patent issued).

80. The variety was bred “with careful attention paid to uniformity of plant type to ensure sufficient homozygosity and phenotypic stability for use in commercial hybrid seed production.” (Ex. 1001, 15:7–11.)

81. The specification itself describes a number of phenotypic traits of the variety (grown in one environment). (Ex. 1001, Table 1 spanning columns 38–39; see also 15:1–14 (“Phenotypic Characteristics of 1PNZQ23”).) It also describes how to determine genotypic characteristics of the variety. (Ex. 1001, 15:15–35 (“Genotypic Characteristics of 1PNZQ23”).) For example, by “loci shown in a marker profile.” (Ex. 1001, 15:19–20.) Different marker profile techniques, which are well known in the art, are described in the ’033 patent as well. (Ex. 1001, 15:51–16:11.)

82. The claimed variety (1PNZQ23) is an inbred line and, therefore, is “substantially homozygous.” (Ex. 1001, 15:19.) As such, it “can be reproduced by

planting seeds of the variety [for example, the deposited seeds], growing the resulting maize plants under self-pollinating or sib-pollinating conditions with adequate isolation, and harvesting the resulting seed using techniques familiar to the agricultural arts.” (Ex. 1001, 38:4–9).

B. The Claims

83. The '033 patent has 20 claims. (Ex. 1001 at columns 39 and 40). Claims 1, 10, and 18 are independent. Claims 2–9 depend on claim 1. Claims 11–17 depend on claim 10. Claims 19 and 20 depend on claim 18.

84. Claim 1 recites:

1. A seed, plant, plant part, or plant cell of inbred maize variety 1PNZQ23, representative seed of the variety having been deposited under NCMA accession number 202301024.

85. Claims 2–9 depend from claim 1 and recite specific plant parts (claim 2), F1 hybrids produced using the plant/plant part of claim 1 (claims 3 and 4), methods for producing additional plants from the F1 hybrids (claims 5–7), methods for producing maize seed from the plant of claim 1 (claim 8), and methods for producing nucleic acids from the seed, plant, plant part, or plant cell of claim 1 (claim 9).

86. Claim 10 recites:

10. A converted seed, plant, plant part or plant cell of inbred maize variety 1PNZQ23, representative seed of the maize variety 1PNZQ23 having been deposited under NCMA accession number 202301024, wherein the converted seed, plant, plant part or plant cell comprises a locus conversion, and wherein the plant or a plant grown from the converted seed, plant part or plant cell comprises the locus conversion and otherwise comprises all of the physiological and morphological characteristics of maize variety 1PNZQ23 when grown under the same environmental conditions.

87. Claims 11–17 depend from claim 10 and recite a specific locus conversion (claim 11), seeds or plants produced by crossing the plant / plant part of claim 10 (claims 12 and 13), methods for producing additional plants from those seeds or plants (claims 14–16), and methods for producing nucleic acids from the seed, plant, plant part, or plant cell of claim 10 (claim 17).

88. Claim 18 recites:

18. An F1 hybrid seed of 1PNZQ23 produced by crossing a plant or plant part of inbred maize variety 1PNZQ23 further comprising a transgene, representative seed of the inbred maize variety 1PNZQ23 having been deposited under NCMA accession number 202301024 with a different maize plant, wherein the transgene is inherited by the F1 hybrid seed, wherein the transgene

was introduced into inbred maize variety 1PNZQ23 by backcrossing or genetic transformation.

89. Claim 19 recites a method of producing progeny seed by crossing a plant grown from the seed of claim 18. Claim 20 recites a method of making a commodity plant product from the plant or plant part of claim 18.

IV. PETITIONER’S ASSERTED REFERENCES

90. Each of Petitioner’s asserted references describes another of Pioneer’s inbred maize varieties. Two (Ross, Ex. 1005, and Carlone, Ex. 1006, Ground 1) are the parents of the claimed 1PNZQ23; one is a sibling (Heffner, Ex. 1007, Ground 2).

A. Ross (Ex. 1005)—Inbred Maize Variety PH1VKM

91. Ross (Ex. 1005) is a U.S. Patent (9,572,319) titled “Maize Inbred PH1VKM”, which issued on February 21, 2017, and which lists Pioneer Hi-Bred International, Inc. (Patent Owner) as the Assignee. (Ex. 1005, cover page.) Ross describes an inbred maize variety (PH1VKM), which was developed by crossing “inbred line PH12P0 and inbred line PHPCW,” then “selfing the F1 plants, selfing and using ear-to-row (pedigree) selection from the F2 to F11 generation, and bulking the F12 seed.” (Ex. 1005, 18:55-61.) The inbred line is “substantially homozygous.” (Ex. 1005, 18:62-63.) A deposit of “at least 2,500 seeds of Maize

Variety PH1VKM” was made “with the American Type Culture Collection (ATCC) . . . with ATCC Deposit No. PTA-123680.” (Ex. 1005, 43:14-18.)

92. Table 1 of Ross (Ex. 1005) contains a description of some of the variety’s phenotypic characteristics. (Ex. 1005, Table 1.) Table 2 contains a “general combining ability report” (Ex. 1005, Table 2, 23:33-34), Table 3 “compare[s] a specific hybrid for which PH1VKM is a parent with other hybrids.” (Ex. 1005, 23:50-51.)

93. Inbred Maize variety PH1VKM is one of the parents of the elite Inbred Maize variety 1PNZQ23, which is claimed in the ’033 patent (Ex. 1001), 37:60-38:3.)

B. Carlone (Ex. 1006)—Inbred Maize Variety PH2DYM

94. Carlone (Ex. 1006) is a U.S. Patent (9,706,732) titled “Maize Inbred PH2DYM,” which issued on July 18, 2017, and which lists Pioneer Hi-Bred International, Inc. (Patent Owner) as the Assignee. (Ex. 1006, cover page.) Carlone describes the inbred maize variety PH2DYM, which was developed by crossing “inbred line PHVNV and inbred line PHPCW” then “producing a doubled haploid from the F1 plants, selfing and using pedigree selection amongst the D1 lines, and selfing and bulking from the subsequent generations.” (Ex. 1006, 18:46-53.) A deposit of “at least 2,500 seeds of Maize Variety PH2DYM” was made

“with the American Type Culture Collection (ATCC) . . . with ATCC Deposit No. PTA-124094. (Ex. 1006, 43:16-20.)

95. Table 1 of Carlone (Ex. 1006) contains a description of some of the variety’s phenotypic characteristics. (Ex. 1006, Table 1, 43-45.)

96. Inbred maize variety PH2DYM is one of the parents of the elite Inbred Maize variety 1PNZQ23, which is claimed in the ’033 patent. (Ex. 1001, 37:60-38:3.)

C. Heffner (Ex. 1007)—Inbred Maize Variety PH487D

97. Heffner (Ex. 1007) is a U.S. Patent (10,653,095) titled “Maize Inbred PH487D,” which issued on May 19, 2020, and which lists Pioneer Hi-Bred International, Inc. (Patent Owner) as the Assignee. (Ex. 1007, cover page.) Heffner describes the inbred maize variety PH487D, which was developed by crossing “inbred line PH1VKM and inbred line PH2DYM,” and then “producing a doubled haploid from the F1 plants, selfing and using pedigree selection amongst the D1 lines, and selfing and bulking from the subsequent generations.” (Ex. 1007, 38:54-61.) A deposit of “at least 625 seeds of Maize Variety PH487D” was made “with the American Type Culture Collection (ATCC) . . . with ATCC Deposit No. PTA-126657. (Ex. 1007, 38:26-30.)

98. Heffner's Table 1 contains a description of some of the variety's phenotypic characteristics. (Ex. 1007, 39-40.)

99. Inbred Maize Variety PH487D was generated by crossing the same two inbred varieties (PH1VKM and PH2DYM) as 1PNZQ23, which is claimed in the '033 patent. (Ex. 1001, 37:60-38:3). Corn breeders refer to this as a "sibling" or "sib;" more specifically, a "full sibling" or "full sib," although, as I describe above in Section II, not in the nuclear family sense. (*See above*, Section II.A.2, describing the genetics and breeding of inbred varieties).

V. PERSON OF ORDINARY SKILL IN THE ART

100. I understand from counsel that Pioneer does not dispute Inari's definitions of the qualifications of a person of skill in the art ("POSA") at this time. I further understand that Pioneer had reserved its right to challenge Inari's definition of a POSA and provide its own, should the Board decide to institute further proceedings. I understand Inari defined the POSA as a person "with a doctoral degree in plant breeding or a related field, at least five years of experience with corn breeding, and additional experience interfacing with laboratory-side personnel (including a computational biologist as along with genetics specialists) as well as field-side personnel. Alternatively, additional experience could take the place of an advanced degree."

101. While I have based my analysis below on this description of a POSA and her level of skill, I have not been asked to offer an opinion as to whether I agree with Inari's definition nor have I been asked to offer my own description of the level of skill in the art at the relevant time. I reserve the right to offer my own description of the POSA and the requisite level of skill in the art if this proceeding is instituted.

VI. LEGAL STANDARDS

102. My understanding of the legal requirements for non-obviousness under 35 U.S.C. § 103, utility under 35 U.S.C. § 101, and definiteness under 35 U.S.C. § 112 as explained to me by Patent Owner's counsel, is set forth below.

A. Non-Obviousness

103. I understand the factual inquiries in determining obviousness include 1) the "scope and content of the prior art;" 2) the "differences between the prior art and the claims at issue;" and 3) "the level of ordinary skill in the pertinent art." A claimed invention is obvious if the prior art made obvious the invention as a whole, from the perspective of a POSA at the effective filing date (here, July 2, 2021). I further understand a finding of obviousness requires consideration of the claims in their entirety and ex post facto reasoning is not allowed. That is, the obviousness analysis must be carried out without the benefit of hindsight.

104. Also, a finding of obviousness requires a showing that a skilled artisan would have been motivated to combine the teachings of the prior art references to achieve the claimed invention, and that the skilled artisan would have had a reasonable expectation of success in doing so. I also understand for a single prior art reference to invalidate a patent claim, the prior art must show a suggestion or motivation to modify the teachings of the prior art reference to obtain the claimed invention. The prior art must also enable a POSA make and use the invention without undue experimentation.

B. Utility

105. I understand an invention has utility if it is if it is capable of providing some identifiable benefit. I also understand that it need not be the best or the only way to accomplish a certain result, but rather that it need only be useful to some extent and in certain applications. Furthermore, an invention does not lack utility if such utility is limited and only operable in certain applications. I understand all that is required is that the invention can provide some identifiable present benefit. A claimed invention must be totally incapable of achieving a useful result to fail the utility test.

106. I understand the utility inquiry is focused on the invention at hand, not the invention as compared to the prior art. In determining utility, the Patent Office

looks for a disclosure of utility sufficient to satisfy the requirement described above and does not question it unless there is a reason for a POSA to question its objective truth.

107. Finally, I understand from counsel it is not required that a patent provide something not previously available to the public. For example, counsel informs me that a new maize inbred has utility even if it provides the same benefits as other maize varieties.

C. Definiteness

108. I understand from counsel that a patent claim is definite if, when read in light of its specification and prosecution history, a POSA would understand, with reasonable certainty, what is claimed. I also understand from counsel that an invention may be described in surrogate form by a biological deposit, which is incorporated by reference into the patent's specification.

VII. DISCUSSION OF PATENTABILITY

109. Below I set forth my opinions on patentability with respect to Petitioner's Grounds 1 and 2 (obviousness), 3 (utility), and 4 (definiteness).

A. Obviousness (Grounds 1 and 2)

110. In my opinion, claims 1–20 would not have been obvious over the prior art and arguments that Petitioner has asserted. In short, as described more fully below, Inari and Dr. Riley disregard the claimed invention (maize variety 1PNZQ23), ignore the genetic differences between 1PNZQ23 and the prior art, base their entire analysis on an improper comparison (to the exclusion of a proper one), and have not identified any reason why, based on the asserted prior art alone, a POSA would have created 1PNZQ23, nor any reason why the POSA would have had a reasonable expectation of success in doing so. Simply identifying the parents (Ground 1) or a sibling (Ground 2) of 1PNZQ23 does not render 1PNZQ23 obvious.

111. As an initial matter, Dr. Riley opines (and Inari asserts) that POSAs would have had a reasonable expectation of obtaining *an inbred maize variety* with [the asserted prior art]¹ as [parents² | a parent³],” citing “(1) the [alleged] routine nature of the breeding techniques involved,” and (2) “the multiple other

¹ Ground 1: PH1VKM (Ross, Ex. 1005) and PH2DYM (Carlone, Ex. 1006);
Ground 2: PH487D (Heffner, Ex. 1007).

² Ground 1.

³ Ground 2.

instances already reported in which [the prior art]⁴ had been used as a parent to obtain other inbred lines.” (Ex. 1003 ¶¶ 100, 136, 151; Pet., 41, 54.) Dr. Riley offers no opinions, however, on whether it would have been obvious to obtain *the maize inbred variety* 1PNZQ23 (as claimed in the ’033 patent). I understand from counsel this is legally incorrect and not relevant to a determination of obviousness.

112. As both Dr. Riley and Petitioner acknowledge, and I describe in detail above (Section II), corn breeding is a highly complex endeavor, and the level of skill in the art is high. Yet, neither have argued that it would have been obvious to the POSA to develop the *claimed 1PNZQ23 maize variety* based on the phenotypic traits described by Ross and Carlone (Ground 1) or Heffner (Ground 2). I understand from counsel that POSA must have been 1) motivated by the prior art to develop *what is claimed* and 2) have had a reasonable expectation of doing so based on the disclosures of the prior art. In my opinion and as described in detail below, a POSA would not have been so motivated and would not have had a reasonable expectation of success in developing 1PNZQ23 based on the phenotypic traits disclosed in Ross and Carlone (Ground 1) or Heffner (Ground 2).

⁴ Ground 1: PH1VKM (Ross, Ex. 1005) and PH2DYM (Carlone, Ex. 1006);
Ground 2: PH487D (Heffner, Ex. 1007).

113. Instead, it appears Petitioner simply argues that a POSA would have a reasonable expectation of success in developing a hypothetical maize inbred having some phenotypic traits in common with 1PNZQ23. I understand from counsel this is not a legally proper analysis and that the POSA must be motivated to develop the claimed 1PNZQ23 variety, not something that shares some similarity with it. Even if this were legally correct, in my opinion, a POSA would not have had a reasonable expectation of developing 1PNZQ23 based on the incomplete list of phenotypic traits described by Ross and Carlone (Ground 1) or Heffner (Ground 2).

114. I further understand from counsel that Pioneer deposited representative seed with the NCMA that is an example of the claimed 1PNZQ23 variety. I also understand that representative seed is also available for the maize varieties described in Ross, Carlone, and Heffner. I understand that this seed deposit was available to Petitioner and that Petitioner, if it so chose, could have extracted the genomes from these varieties and performed genetic comparisons between them to determine obviousness for the purpose of Petitioner's petition. I also understand Petitioner could have planted the seeds and compared the complete set of phenotypic traits of the fully grown plants for its obviousness determination. In my opinion, these comparisons, at least, would help to determine whether the prior art varieties would render the claimed 1PNZQ23 variety obvious.

115. Petitioner has simply not provided any compelling evidence even suggesting that 1PNZQ23 would have been obvious.

1. Inari and Dr. Riley's Comparisons of the Claimed Variety and the Prior Art Ignore their Genotypes

116. An understanding of 1PNZQ23's genetic make-up is helpful to understand how and in what ways it is distinct (or not) from other maize varieties. As discussed above, a plant variety's phenotypic traits are the outward expression of its genotype (in addition to environmental factors affecting the phenotype). When phenotypic comparisons alone may be insufficient, a POSA could analyze the underlying genetics to provide greater resolution.

117. A POSA would have no expectation of developing 1PNZQ23 based on Ross and Carlone (Ground 1) or Heffner (Ground 2) simply because they have some phenotypic traits in common. As biological material, 1PNZQ23 is characterized by both its genotype and phenotype and a comprehensive understanding of its traits requires an understanding of both. Without understanding the genetics of the prior art varieties and specific guidance to select, a POSA could have no expectation of success in developing 1PNZQ23 using any of them as a starting point, even where two of the varieties, PH1VKM (Ross) and PH2DYM (Carlone), are its parents and another (PH487D, Heffner) is its sibling.

118. As I described above, the development of a new maize inbred is not a trivial matter and not as simple as breeding two plants that appear to have beneficial traits. 1PNZQ23's unique genome is the result of at least a decade of breeding and refinement in an effort to create a maize inbred having some potential of producing an agriculturally successful hybrid when crossed.

119. A POSA seeking to understand the distinctiveness between two (or multiple) maize inbreds would not rely on phenotypic similarities alone but would consider both genotype and phenotype. Although neither Dr. Riley nor Petitioner have provided any other type of suitable comparison, one very simple starting point for assessing similarities or differences between any two corn inbreds is to genotype them. For example, performing a genetic analysis with a commonly used and publicly available marker set like the set of 3,072 single nucleotide polymorphism (SNP) markers described in Rouselle et al., "Study on Essential Derivation in Maize: III. Selection and Evaluation of a Panel of Single Nucleotide Polymorphism Loci for Use in European and North American Germplasm," *Crop Science* 55:1170-80 (2015) (Ex. 2027), most of which are on the MaizeLD BeadChip Kit by Illumina®, which uses a set of 3,047 SNP markers to "provide even genomic coverage" across the maize genome. (*MaizeLD BeadChip Kit*, illumina, <https://www.illumina.com/content/dam/illumina-marketing/documents/products/datasheets/maize-ld-data-sheet-1370-2015-007.pdf>,

(Ex. 2026).) Although this would not give a complete picture of all the genetic similarities or differences between the two inbreds (although one could even sequence the entire genomes using modern technology), it is a much more reliable method of comparing corn inbreds than comparing a select number of phenotypic traits. Also, the resulting data can be used to better the understand the similarity between the inbreds.

120. Here, however, both Dr. Riley and Inari completely ignore the biological deposit and provide no evidence of why a POSA would have found it obvious based on the prior art. As described below, the only comparison they provide is ambiguous and suggests differences between the claimed variety and the prior art varieties, rather than similarities.

121. I understand from counsel that it was possible for Dr. Riley or Petitioner to perform the genetic analysis I described above for the purpose of comparing 1PNZQ23 to the prior art varieties because seed deposits are available for that purpose.

122. Because of the importance of genetics in determining whether varieties are truly distinct from one another, I do not agree with Dr. Riley that obviousness can be determined based on an incomplete description of phenotypes alone with no genetic analysis.

2. A POSA Would Not Have Had a Reasonable Expectation of Success in Developing 1PNZQ23

123. As described above (Section II), an inbred's genome is a combination of its parent's genomes with each parent contributing 50% of its genetic material to F1 that gives rise to the new inbred. And even if **both** parents and/or a sibling were known to POSAs during this time (as is the case here), without additional information, a POSA still would have no reasonable expectation of success in developing 1PNZQ23 due to the unpredictability of the breeding process (as described in Section II). Each progeny of an F1 plant is genetically and phenotypically distinct even when the F1 plant itself results from a cross of two inbreds. A POSA would not expect that a cross of the same parents will produce F2 or D1 progeny identical to 1PNZQ23. As described above (Section II.A.), the genome of a progeny plant is the result of genetic segregation and recombination in the F1 plant of the two parental genomes and the chance of the exact same child resulting from that initial biparental inbred cross is infinitesimally small. So, starting only from the parents (or a sibling), it would not have been obvious for a POSA to have produced 1PNZQ23.

124. As also described above in Section II, the phenotypic differences in the F2 generation are a result of genetic segregation and recombination in the F1 generation, and, therefore, separately bred maize inbred varieties would be

expected to have different genotypic and phenotypic characteristics. This is true whether they share the same parents (i.e., are siblings), share just one parent (i.e., are half siblings), or have different parents altogether. Just as two children born at different times to the same parents will not be genetically or phenotypically identical, neither will two corn inbreds. This is most evident, for example, when comparing two separately generated inbred varieties sharing the same parents. Indeed, as discussed above in Section II, the entire modern breeding pipeline is based on re-use of high performing “elite” inbreds to create new and different inbred varieties. For example, PH1VKM (Petitioner’s Ross, Ex. 1005) and PH2DYM (Petitioner’s Carlone, Ex. 1006) are the parents of 1PNZQ23. But, as noted by Petitioner, they are also separately the parents of at least nineteen other distinct inbred lines, including PH487D (Petitioner’s Heffner Ex. 1007). (Pet., 35.) Furthermore, regardless of how “routine” it may have been to breed a new inbred variety in general, having only the knowledge that other inbred varieties exist (even parents and siblings), it would not have been obvious: which progeny to select for further breeding and which specific combination of breeding techniques or testing environments to use for further development. The ultimate genotypic and phenotypic traits of the resulting inbred certainly would not have been obvious. Neither Dr. Riley nor Petitioner has articulated any arguments as to why they would have been. Inari and Dr. Riley simply point to the “routine nature of

breeding techniques” alongside a phenotypic comparison that they admit is inappropriate to the exclusion of any further analysis at all. (Ex. 1003 ¶¶ 100, 136; Petition, at 41, 54.)

3. Maize Inbred Development is Unpredictable

125. Corn inbred development is inherently unpredictable. While plant breeding may utilize some well-known techniques (such as described in the '033 patent), it is still a highly complex and unpredictable science. (*See* Section II.) Dr. Riley explains as much when describing the level of skill in this area. (Ex. 1003, ¶¶ 19-22.) Yet, neither Dr. Riley nor Petitioner suggest which of the nearly infinite number of complicated breeding options or testing environments a breeder would choose to start with the prior art varieties and arrive at 1PNZQ23.

126. Dr. Riley and Inari’s position that “POSAs were capable of breeding inbred lines to create essentially any desired inbred phenotypical trait in descendant inbred lines, at least within the ranges made possible by the existing gene pool as confirmed by the existence of the trait in one or more preexisting corn varieties” would render any newly developed corn variety obvious based on my understanding of the law. (Ex. 1003 ¶ 91; Pet., 38.) Dr. Riley’s position essentially boils down to no *combination* of traits can be novel because the *individual* traits existed in previously existing corn varieties, or because the parents were known.

This completely ignores the fact that the benefits provided by a new variety are a result of its full complement and combination of traits and how some phenotypes are determined by the combined expression of certain genes.

127. Further, under Dr. Riley’s standard for comparison (i.e., whether the differences in a small subset of phenotypic characteristics fall “within the mainstream of corn phenotypes observed [before the filing date of the claimed invention]”), every single one of those inbred maize varieties that has generated the massive fold-scale increase in yields that drives the U.S. corn economy would have been obvious. (Ex. 1003 ¶ 69.) As described more fully below, the differences that Dr. Riley bases his opinions on are not representative of each variety as a whole (i.e., considering its genotypes and its phenotypes for the applicable traits in the relevant environments), and therefore are not indicative of overall similarity between the claims and the prior art.

128. As described above, the general scheme for producing corn inbred varieties has been employed by Pioneer and others since at least the 1930s. But, since the 1930s the creation of *specific* inbred varieties (using the general scheme) has led to the overall increase in U.S. corn yields from ~ 2 tons per hectare to ~ 12 tons per hectare. (See Section II). In the last ~ 20 years alone, yield has increased ~ 4 tons per hectare. (*Id.*)

129. And, as described above in Section II, Pioneer's own efforts have resulted in massive yield gains year over year, attributable to its efforts in developing new inbred and hybrid varieties. The varieties that are ultimately successful represent a small fraction of the millions upon millions of varieties that did not make it through the breeding funnel. As discussed in Section II, at the F1 stage, progeny carry 50% of their genotype from each of their two inbred parents. As explained above, however, progeny from the subsequent generations (whether F2 or doubled haploid) are expected to differ from each other genetically; indeed, the specific genetic contributions from each parent in a given inbred are inherently unpredictable. A breeder must decide which progeny plant is suitable for further development as well as which specific combination of breeding techniques she will use for this development (such as which traits to select for and how). And even though there may be a general scheme for breeding inbreds (i.e., selecting two parents, generating progeny, selecting among those progeny), getting to any one specific inbred variety is a long, arduous, and highly unpredictable process.

4. Petitioner Ignores Pertinent Differences

130. Dr. Riley provided a single table of comparisons between certain phenotypic characteristics of the claimed maize inbred 1PNZQ23 (from Table 1 of '033 patent) and each of the prior art references, in the aggregate. (Riley

Declaration, Ex. 1003 at the table spanning pages 29–37 (which I will refer to as Dr. Riley’s “Table 1”).) This table allegedly demonstrates that the prior art varieties have “characteristics very similar to” those of the claimed 1PNZQ23. (Ex. 1003 ¶ 59.)

131. However, as Dr. Riley notes, “the specific measurement outcomes of many of the listed traits of any given inbred line will differ based on environmental conditions the plants are grown in.” (Ex. 1003 ¶ 67.) This is true. As I have described above (Section II), a plant’s phenotype is a manifestation of both genotype and environment. As such, based on the Petition, nothing conclusive can be said about the similarity of the four varieties, and the data presented in Dr. Riley’s chart are not informative to this question.

132. Further and more importantly, any observed similarity between varieties with respect to a single (or even several) phenotypic trait is not indicative of the level of the *overall* similarity between varieties. Dr. Riley’s Table 1 omits several agricultural and agronomically important traits a breeder would consider essential in determining whether an inbred has potential for commercial success. For example: resistance to biotic stresses such as disease and insect resistance and resistance to abiotic stresses such as drought, low and high temperatures are all agronomically important traits not included in Dr. Riley’s Table 1. Dr. Riley and Petitioner focus individually on a handful of select traits from Dr. Riley’s Table 1

but never compare the *combined traits* of 1PNZQ23 to the *combined traits* of the prior art varieties. And even if they had done so, Dr. Riley admits that those comparisons have limited usefulness. (Ex. 1003, ¶ 70.)

133. Importantly, Petitioner has not demonstrated the phenotypic traits disclosed by Ross, Carlone, or Heffner are sufficient to develop 1PNZQ23 as claimed in the '033 patent or that a POSA would have a reasonable expectation of doing so based on the references' inbreds. A proper phenotypic evaluation would require growing seeds for each variety under the same conditions and then comparing the combined expressed phenotypic traits. But even this comparison would be insufficient based on my understanding of obviousness because it would not take into account the important genetic differences between the varieties responsible for their phenotypic traits and the behavior of those traits across environments. (*See* Section VII.A.1.)

134. Many types of genotypic and phenotypic comparisons are possible when one has access to seed of a particular variety. I understand from counsel that Dr. Riley or Petitioner could have accessed the biological deposits representing the claimed and prior art maize varieties in the United States for the purpose of comparing them. But, even with this access, Dr. Riley did not perform a direct and fulsome phenotypic or genomic comparison of the varieties. Had he done so, he would have found that they are not similar at all. Below I describe the percent

similarity between the varieties based upon a genetic marker comparison provided to me by Pioneer.

135. Paradoxically, after reiterating that “the data for each variety is not directly comparable given the potentially different environmental conditions in which the varieties were grown” (Ex. 1003, ¶ 67), Dr. Riley goes on to base all his opinions that the ’033 claims are obvious on those very data. Moreover, he does so by comparing individual traits (rather than the full complement of the measured traits) to the ranges encompassed by all three asserted prior art varieties. He never compares 1PNZQ23 to the prior art varieties in the combinations asserted (Ross and Carlone in Ground 1 and Heffner in Ground 2). His assertion that “[f]rom a POSA’s perspective, any differences between the prior art and the claimed invention are insubstantial and insignificant” (Ex. 1003, ¶ 68) is based on an inherently flawed comparison.

136. As an additional matter, it is my opinion that the fact that, as Dr. Riley highlights, the patent specifications for the ’033 patent and the prior art patents share some similarities in formatting is of no importance with respect to whether a POSA would find the claimed 1PNZQ23 variety obvious. (Ex. 1003, ¶ 68 (“virtually all of the ’033 Patent’s specification is drawn verbatim from Heffner (as indicated in the above-noted comparison, EX1102) and is also highly similar to the disclosures in Ross and Carlone.”).) I understand from counsel that patent

specifications can be similar, but based on my reading, the claimed variety is distinct due to its pedigree and/or the necessarily different genotypic and phenotypic characteristics it possesses compared to the inbreds described in Ross, Carlone, and Heffner. The structure of the words may be similar, but the maize varieties they describe (and claim) are clearly different.

B. Ground 1: Claims 1–20 Would Not Have Been Obvious over Ross (Ex. 1005) and Carlone (Ex. 1006)

137. As described above (Sections IV.A and IV.B), Ross describes the inbred maize variety PH1VKM and Carlone describes inbred maize variety PH2DYM, which are the parents of 1PNZQ23 (as well as Heffner’s PH487D).

138. Ross and/or Carlone are the parent of at least nineteen distinct inbred lines, as recognized by Dr. Riley. (Ex. 1003, ¶ 87.) As I noted above, the fact that PH1VKM and PH2DYM are the parents of other inbred varieties illustrates the reality of breeding new maize inbreds—differently bred varieties, even those that share one or both parents, are expected to have different genotypic and phenotypic characteristics.

139. 1PNZQ23 is one of only the nearly limitless number of genetically and phenotypically distinct inbreds that could be created by crossbreeding Ross’s PH1VKM and Carlone’s PH2DYM (one of which is 1PNZQ23, another of which

is Heffner's PH487D). (*See* Section II.A.2, above.) Patent Owner's entire breeding process—not just crossing Ross's PH1VKM and Carlone's PH2DYM—resulted in 1PNZQ23. (*See* '033 patent (Ex. 1001) at 37:66–38:3; *see also* Section II.A.C. (describing breeding process)).

140. As a result, having only the knowledge that these other varieties exist (even if they share some similar characteristics), a POSA would have no motivation or reasonable expectation of success in creating the claimed 1PNZQ23.

141. Dr. Riley opines (and Petitioner adopts the position) that “[f]rom a POSA's perspective, any differences between the prior art and the claimed invention are insubstantial and insignificant.” (Ex. 1003, ¶ 68; Pet., 33.) I disagree. As an initial matter, as I noted above, Petitioner and Dr. Riley's obviousness analysis is based not on what is claimed (1PNZQ23), but rather on a hypothetical “inbred maize variety with PH1VKM and PH2DYM as parents.” A proper analysis would be to compare 1PNZQ23 to Ross's PH1VKM and Carlone's PH2DYM (and not, for example, Heffner—which Petitioner superficially compares to 1PNZQ23 in its Ground 1). And a proper analysis would consider both genotypic and phenotypic differences as a whole, as discussed above. (*See* Section VII.A.1.)

142. As I noted, Dr. Riley and the Petitioner have not assessed any of the genotypic differences between the varieties at all. Nor have they assessed the

phenotypic differences of the varieties as a whole, instead focusing on just a handful of traits (in Dr. Riley's Table 1). Dr. Riley does not address any of the differences between the varieties, let alone provide any explanation as to why they would be "insubstantial and insignificant." (Ex. 1003, ¶ 68.)

143. As described above (Section VII.A.1), one very simple starting point for assessing similarities or differences between any two corn inbred varieties is to genotype them. For example, considering a set of just 3,072 public markers, for example, for which Patent Owner provided me the genotypes of PH1VKM and PH2DYM, these two varieties differ at 356 out of the 3,009 markers from this set (about 12%) for which both were genotyped and homozygous. (Ex. 2007; Ex. 2008.) Inbred maize varieties bred from these two parents could have either the PH1VKM allele or the PH2DYM allele at each of the 356 loci that differ between the parents. Ignoring genetic linkage, this number of loci that differ between two parents could yield 356^2 (126,736) different possible genetic combinations *for just this set of markers*. 1PNZQ23 is just one of those thousands of combinations. Its sibling (Heffner's PH487D) is another. As described below, the two siblings are genetically quite different from each other. See Section VII.C.

144. Furthermore, the expectation, based on genetic differences between their parental inbreds (PH1VKM and PH2DYM, as described above), would be that 1PNZQ23 and PH487D would not only be genetically different (as confirmed

by the genetic analysis below), but also have phenotypic differences above and beyond those in Dr. Riley's Table 1. This is because, again, it is impossible to predict the genotypic and phenotypic characteristics of an inbred line based on just its parents.

145. Given all of the above, I cannot agree with Dr. Riley or the Petitioner that claims 1–20 (which all recite “maize variety 1PNZQ23”) would have been obvious based on the disclosures of Ross and Carlone alone. In my opinion, they would not.

C. Ground 2: Claims 1–20 Would Not Have Been Obvious Over Heffner (PH487D, Exhibit 1007)

146. As stated above (Section IV.C), Heffner describes the inbred maize variety PH487D, which is a sibling of 1PNZQ23.

147. As stated above with respect to Ground 1, I disagree with Dr. Riley's opinion that from a POSA's perspective, any differences between the prior art and 1PNZQ23 are “insubstantial and insignificant.” (Ex. 1003, ¶ 68.) Again, Petitioner's and Dr. Riley's obviousness analysis is not based on the claimed 1PNZQ23 variety. Instead, Dr. Riley opines “POSAs would have had a reasonable expectation of obtaining *an additional maize varieties* with PH487D as parent.” (Ex. 1003, ¶ 136.) A proper analysis would compare 1PNZQ23 to Heffner's

PH487D and that analysis would consider both the full scope of genotypic and phenotypic differences between the two varieties.

148. I understand from counsel the proper inquiry is not whether *an inbred* is obtainable using PH487D as a parent, but whether a POSA would be motivated to and have a reasonable expectation of success in obtaining 1PNZQ23 based on the disclosures of Heffner. A POSA would not have been so motivated or have such a reasonable expectation of success because 1PNZQ23 and PH487D are genetically and phenotypically distinct. As noted above, Dr. Riley and Petitioner have not assessed any of the genotypic differences between the varieties nor have they assessed the phenotypic differences of the varieties as a whole. Instead, Dr. Riley and Petitioner compare only a handful of traits that they allege are “insubstantially different.” (Pet., 24.) Dr. Riley does not address any of the phenotypic differences between the varieties, nor explain why they would also be “insubstantial and insignificant.” (Ex. 1003, ¶ 68.)

149. As discussed above in my opinions relating to Ground 1, a very simple starting point for assessing similarities or differences between any two corn varieties is to genotype them. Using, for example, the SNPs from Rouselle 2015 (Ex. 2027), as described above. Patent Owner provided me with the genotype results of the Rouselle 2015 SNP panel for both 1PNZQ23 and Heffner’s PH487D (Exhibit 2028). Using the provided genotypes, I calculated the percent markers

that differed in genotype between 1PNZQ23 and PH487D. Just looking at that comparison, it is apparent that PH487D is different, genetically, from its sibling. These two siblings differ genetically at approximately 5% of the genotyped genetic markers (i.e., sharing only 95% of the 3,010 markers genotyped and homozygous for both inbred varieties). These genetic differences are not surprising given the genetic segregation and recombination that occur during inbred line development. Additional genotyping would be expected to uncover additional genetic differences between 1PNZQ23 and its sibling.

150. Furthermore, the expectation, based on the varieties' different breeding would be that they would not only be genetically very different (as confirmed by the genetic analysis above), but also have phenotypic differences above and beyond those in Dr. Riley's Table 1. This is because, again, it is impossible to predict the genotypic and phenotypic characteristics of an inbred line based on its parentage alone.

151. Given all of the above, I cannot agree with Dr. Riley or the Petitioner that claims 1–20 would have been obvious based on the disclosures of Heffner alone. In my opinion, they would not.

D. Ground 3: Utility

152. The specification of the '033 patent itself discusses the utility of the claimed inbred variety. As Petitioner points out, the “Background” section of the '033 patent identifies 1PNZQ23 as “continuing [the] goal of maize breeders . . . to develop stable, high yielding maize varieties and hybrids that are agronomically sound with maximal yield over one or more different conditions and environments.” (Ex. 1001, 1:23-26; Petition at 37.)

153. The '033 patent also explains that “[a] variety such as 1PNZQ23 which exhibits good general combining ability may be used in a large number of hybrid combinations” and that “1PNZQ23 may be used to produce a single cross hybrid, a double cross hybrid, or a three-way cross hybrid.” (Ex. 1001, 19:19-25, 18:50-51.) Furthermore, “[t]he seed of maize variety 1PNZQ23, the plant produced from the seed, the hybrid maize plant produced from the crossing of the variety, hybrid seed, and various parts of the hybrid maize plant and transgenic versions of the foregoing, can be utilized for human food, livestock feed, and as a raw material in industry.” (Ex. 1001, 36:60-65.) Each of these is an example of the utility provided by 1PNZQ23.

154. Moreover, the importance of inbred lines in generating hybrids (e.g., as discussed above in Section II) is well known in the corn industry. As discussed above, the American corn industry was built on this hybrid technology. Even Dr.

Riley, attests to this very specific utility. (Ex. 1003, ¶¶ 150–154.) As he states, “[g]iven that the claimed maize variety is an inbred variety, POSAs would understand that any such utility would be in the form of generating beneficial hybrids when crossed.” (Ex. 1003, ¶ 150.)

155. Finally, as described in Section II, inbreds have utility in that they beget other new, improved, inbreds. Indeed, that process has contributed to the rapid gains in average grain yields of hybrids from the 1930s to the 2020s.

E. Grounds 4: Definiteness

156. Dr. Riley and Petitioner assert that the phrases “inbred maize variety 1PNZQ23” and “representative seed” are indefinite. (Ex. 1003, ¶ 173–199; Pet. 65–75). I disagree.

157. Dr. Riley and Petitioner argue that the term “‘inbred maize variety 1PNZQ23’ does not have any meaning to a POSA outside of the ’033 Patent itself” because it “appears to be an arbitrary codename.” (Ex. 1003, ¶ 176; Pet., 67). I cannot agree.

158. New varieties necessarily need new names. The claimed variety was named 1PNZQ23. Just as the different prior art varieties were named differently—PH1VKM, PH2DYM, and PH487D. Naming new varieties is a common practice

in crop breeding. As is depositing seed of new varieties, as Patent Owner has done here.

159. As I also describe above in Section II, when selfed (i.e., self-pollinated), inbred maize plants are expected to be the same both genotypically and phenotypically as the starting inbred plant, differing only due to rare instances of random spontaneous mutations, which are the result of infidelity in replication common to all self-replicating organisms and other mutational processes. (*Supra*, ¶ 23.) Because of their complete or near complete homozygosity, corn seed produced from selfed inbreds would be expected to be genetically (and, therefore, phenotypically) the same as the starting seed of the inbred, both amongst sibling seeds within a generation as well as over generations, aside from random spontaneous mutations. (*Id.*)

160. And because of the phenotypic and genetic variation that occurs when working with a self-replicating biological organism, the deposited seeds of the variety (or seeds obtained from growing plants from the deposited seeds and selfing them to produce additional seed of the variety) may not be 100% identical to each other, but they still “represent” the variety and are considered as the same variety.

161. Finally, if a POSA wanted to know more about a particular variety (including how it compared to another variety genotypically and/or

phenotypically)—it would be routine for a POSA to obtain seeds of the variety, genotype them and/or grow them under a range of environmental conditions and measure phenotypes.

162. This is all consistent with the '033 patent (*see, e.g.*, Ex. 1001, 15:1–18; 17:56–66; 37:31–59).

163. In sum, a POSA understands with reasonable certainty what is meant by both “inbred maize variety 1PNZQ23” and “representative seed.”

VIII. CONCLUSION

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patents issued thereon.

Respectfully submitted,

A handwritten signature in blue ink, appearing to read 'P. Schnable', with a small horizontal line above the first letter 'P'.

Date: August 22, 2024

PATRICK S. SCHNABLE

APPENDIX A

PATRICK S. SCHNABLE

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PROFESSIONAL EXPERIENCE

1981-1986	Graduate Research Assistant, Laboratory of Peter Peterson, Iowa State University
1986-1988	NIH Postdoctoral Fellow, Laboratory of Heinz Saedler, Max-Planck-Institut für Züchtungsforschung, Köln, Germany
1988-1994	Assistant Professor, Iowa State University
1994-1998	Associate Professor, Iowa State University
1998-present	Professor, Iowa State University
1999-present	Founding Member, Center for Bioinformatics and Biological Statistics
1999-2003	Founding Director, Center for Plant Transformation & Gene Expression
1999-2023	Founding Director, Center for Plant Genomics
2002-2006	Associate Chair and Chair, Interdepartmental Genetics Graduate Program
2005-2010	Associate Director, Plant Sciences Institute
2007-2013	Director, Center for Carbon Capturing Crops
2007-2013	Baker Professor of Agronomy
2013-present	Iowa Corn Promotion Board Endowed Chair in Genetics
2013-present	C.F. Curtiss Distinguished Professor
2014-present	Baker Scholar of Agricultural Entrepreneurship
2014-present	Director, Plant Sciences Institute
2017-present	Lead, Digital and Precision Ag Economic Development Platform
2010-present	Co-Founder and Managing Partner, Data2Bio LLC
2014-present	Co-Founder and Co-Managing Partner, Dryland Genetics Inc.
2017-present	Co-Founder and Managing Partner, EnGeniousAg LLC

HONORS

- ISU Department of Agronomy Plant Breeding Research Award, 1985

- Max-Planck-Institute Postdoctoral Fellowship, 1986
- Iowa State Research Excellence Award, 1986
- Gamma Sigma Delta Honor Society, 1986
- National Institutes of Health Postdoctoral Fellowship, 1987-1988
- Raymond and Mary Baker Agronomic Excellence Award, 2000
- Iowa State University, College of Agriculture Research Team Award, 2005
- Best Paper Award, IEEE International Parallel and Distributed Processing Symposium, 2006
- Finalist, Computerworld Honors Program, 2007
- Changjiang Scholar, China Agriculture University, 2009-2012
- Outstanding Achievement in Research Award, College of Agriculture and Life Sciences, Iowa State University, 2010
- Fellow, American Association for the Advancement of Science (AAAS), 2010

REVIEW PANELS, ADVISORY BOARDS and EDITORIAL POSTS

1990	DOE, Energy Biosciences Panel
2001	NSF Technical Review Team of Missouri MaizeDB
2001-2003	Scientific Advisory Board, NSF-funded Potato Genome Project
2003	Committee of Visitors, Training Cluster, NSF-DBI
2003-2004	Grant Review Panel, NSF Small Business Innovation Research, Agricultural Biotechnology
2003-2007	Scientific Advisory Board, NSF-funded Cell Wall Project
2003-2007	Scientific Advisory Board, NSF-funded Wheat SNP Project
2003-2008	Scientific Advisory Board, NSF-funded Maize Genomic Diversity Project
2005-2009	Elected Member-at-Large of the AAAS Section Committee, Agriculture, Food and Renewable Resources Section
2006	Grant Review Panel, NSF SEI-BIO
2006-2011	MaizeGDB Working Group
2007	Invited to testify to National Research Council Committee: "The National Plant Genome Initiative: Achievements and Future Directions"
2007	Invited to testify to National Research Council Committee: "A Study of Technologies to Benefit Farmers in Africa and South Asia"
2008-2011	Associate Editor, The Plant Genome
2008-Present	Editorial Board, PLoS Genetics
	2008-2015, Associate Editor
	2015-Present, Consulting Editor
2009	Grant Review Panel, Agriculture and Agri-Food Canada
2009	Grant Review Panel, NSF Bioinformatics
2009-2010	NextGen Sequencing Working Group, NSF iPlant Consortium
2009-2010	Steering Committee, "Functionality and the Corn Genome" workshop (NCGA)
2009-present	Organizer, Maize Genetics Workshop, Plant and Animal Genome Meeting
2009-2013	External Advisory Board, French wheat chromosome 3B genome sequencing project

2010-2012	International Scientific Advisory Board, 10th International Congress on Plant Molecular Biology 2012, Jeju, Korea
2011	Co-organizer, Banbury Conference (CSHL): “Genotype to Phenotype: Deriving Biological Knowledge from Large Genomic Datasets”, 16-19 October 2011, Cold Spring Harbor, NY
2011	Organizer “Genomics to Agronomics” Session, American Seed Trade Association, Chicago IL 8 December 2011
2011-2012	Organizing Committee, International Conference of Heterosis Utilization in Crops, 21-24 August 2012, Xian, China
2011-2016	Scientific Advisory Board, NSF-funded <i>Amborella</i> Genome Project
2013-2018	International Advisory Board, Centre for Biotechnological and Agricultural Research, Olomouc, Czech Republic
2013-2016	Scientific Advisory Council, GeneSeek
2013-2014	National Plant Science Council
2013-2017	Scientific Advisory Board, NSF-funded <i>Aegilops tauschii</i> Genome Sequencing Project
2013-present	Co-lead, Maize Genomes to Fields Initiative
2014-2023	Member, Scientific Advisory Board, Hi-Fidelity Genetics, Durham, NC
2014-2019	Member, Scientific Advisory Board, US-based crop breeding company
2014-2014	Member, CAST Board of Representatives (ASPB representative)
2015	Scientific Committee, EUCARPIA Maize and Sorghum conference, "Genomics and Phenomics for Model-Based Maize and Sorghum Breeding"
2016-present	Member, Scientific Advisory Board, CTC (a Brazilian sugarcane breeding company)
2017	Organizing Committee, Nebraska EPSCoR “Predictive Crop Design: Genome-to-Phenome”
2017-present	Member, Scientific Advisory Board, Kemin Industries, Des Moines, IA
2021-present	Member, Agronomy Department Advisory Council
2021-present	Member, Agronomy Department Baker Council

PROFESSIONAL AFFILIATIONS

- American Association for the Advancement of Science
 - “Golden Goose Award” Nominating Committee (ASPB Representative)
- American Society of Plant Biologists
 - Executive Committee, 2012-2016
 - Science Policy Committee, 2008-2016
 - Chair, 2012-2016
 - Pioneer Hi-Bred International Graduate Student Prize Committee, 2009-2013
- Genetics Society of America
 - Public Policy Committee, 2013-2016
- Maize Genetics Cooperative
 - Steering Committee, 1993-1996; 2002-2004
 - Maize Genetics Executive Committee

- Member, 2000-2004, 2006-2012, 2014-2018
- Chair, 2003-2004, 2007-2009

PUBLICATIONS (refereed; *invited author*):

<https://orcid.org/0000-0001-9169-5204>

Schnable has an h-index of 89 (as calculated by Google Scholar, <http://scholar.google.com/citations?user=UW4mNTW0nOkC&hl=en>, on 6/2024) with a total of over 30,000 citations and over 11,000 since 2019. Reflecting his interest in computational approaches to biology he has an Erdős number of 3.

- **Schnable PS**, PA Peterson (1986) Distribution of genetically active *Cy* elements among diverse maize lines. **Maydica (McClintock issue)** 31:59-81.
- **Schnable PS**, PA Peterson (1988) The *Mutator*-related *Cy* transposable element of *Zea mays* L. behaves as a near-Mendelian factor. **Genetics** 120(2):587-596.
- **Schnable PS**, PA Peterson (1989) Genetic evidence of a relationship between two maize transposable element systems: *Cy* and *Mutator*. **Mol Gen Genet** 215(2):317-321.
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- **Schnable PS**, RP Wise (1994) Recovery of heritable, transposon-induced, mutant alleles of the *rf2* nuclear restorer of T-cytoplasm maize. **Genetics** 136(3):1171-1185.
- Wen T-J, **PS Schnable** (1994) Analyses of mutants of three genes that Influence root hair development in *Zea mays* (*Gramineae*) suggest that root hairs are dispensable. **Am J Bot** 81:833-842.
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- Wise RP, **PS Schnable** (1994) Mapping complementary genes in maize: Positioning the *rf1* and *rf2* nuclear-fertility restorer loci of Texas (T) cytoplasm relative to RFLP and visible markers. **Theoretical & Applied Genetics**, 88: 785-795.
- **Schnable PS**, PS Stinard, T-J Wen, S Heinen, D Weber, L Zhang, JD Hansen, BJ Nikolau (1994) The genetics of cuticular wax biosynthesis. **Maydica (Robertson issue)**, 39:279-287.

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- Yandeau-Nelson MD, BJ Nikolau, **PS Schnable** (2006) Effects of *trans*-acting genetic modifiers on the rates and distribution of meiotic recombination across the *al-sh2* interval of maize. **Genetics**, 174:101-112. (Epub: 2006 Jul 2; “recommended” by the *Faculty of 1000 Biology*)
- Fu Y, TJ Wen, YI Ronin, HD Chen, L Guo, DI Mester, Y Yang, M Lee, AB Korol, DA Ashlock, **PS Schnable** (2006) Genetic dissection of intermated recombinant inbred lines using a new genetic map of maize. **Genetics**, 174(3): 1671-1683. (Epub 2006 Sep 1)
- Ohtsu K, H Takahashi, **PS Schnable**, M Nakazono (2007) Cell type-specific gene expression profiling in plants by using a combination of laser microdissection and high-throughput technologies. **Plant & Cell Physiology**, 48(1):3-7. (Epub: 2006 Dec 5)
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- Zhang X, S Madi, LA Borsuk, DS Nettleton, RJ Elshire, B Buckner, D Janick-Buckner, J Beck, M Timmermans, **PS Schnable**, MJ Scanlon (2007) Laser microdissection of narrow sheath mutant maize uncovers novel gene expression in the shoot apical meristem. **PLoS Genetics**, 3(6):1040-1052. (*Selected an Editors’ Choice by MaizeGDB, 7/07*).
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- 10,704,091 Genotyping by next-generation sequencing (issued 7 July 2020)
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- 9,951,384 Genotyping by next-generation sequencing (issued, 24 April 2018)
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- 6,060,644 Isolation and use of cuticular lipid genes (issued, 9 May 2000)
- 5,981,833 Nuclear restorer genes for hybrid seed production (issued, 9 November 1999)
- 5,684,242 Nuclear restorer genes for hybrid seed production (issued, 4 November 1997)