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 PGR2024-00020
U.S. Patent 11,666,020

DECLARATION OF PATRICK S. SCHNABLE

PIONEER 2004
Inari Agric. Inc. v. Pioneer Hi-Bred Int'l, Inc.
PGR2024-00020

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LIST OF EXHIBITS

Exhibit Number	Description
1001	U.S. Patent No. 11,666,020
1003	Declaration of Dr. Ray Riley
1005	U.S. Patent No. 8,759,636 ("Smalley")
1006	U.S. Patent No. 10,681,888 ("Longenberger")
1007	U.S. Patent No. 7,528,307 ("Hoffbeck")
1008	Plant Variety Protection Certificate No. 201200313
1009	Plant Variety Protection Certificate No. 202200416
1010	Plant Variety Protection Certificate No. 200700315
1012	Lee, E.A.; Tracy, W.F. Modern Maize Breeding, 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, Theor Appl Genet., 132(3):817-849 (2019)
2008	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)
2007	FAS.USDA.gov, "Production – Corn", available at https://fas.usda.gov/data/production/commodity/0440000
2009	Pioneer.com, *History of pioneer*, 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," *Crop & Pasture Science*, 65:311–336 (2014)
2017	Springer and Stupar, "Allelic Variation and Heterosis in Maize: How do Two Halves Make More than a Whole," *Genome Research* 17:264–75 (2007)
2020	Silverio Garcia-Lara and Sergio O. Serna-Saldivar, *Corn History and Culture*, in Corn Chemistry and Technology (2019)
2021	Doebley, "The Genetics of Maize Evolution," *Annu. Rev. Genet.* 38:37–59 (2004)
2022	Martinez and Fernandez, *Economics of Production, Marketing and Utilization*, in in Corn Chemistry and Technology, (2019)
2023	Hochholdinger and Baldauf, *Heterosis in Plants*, Current Biology 28:R1075–95 (2018)
2024	Mikel and Dudley, "Evolution of North American Dent Corn from Public to Proprietary Germplasm," *Crop Sci.* 46:1193–1205 (2006)
2025	White et al., "Diversity and Heterotic Patterns in North American Proprietary Dent Maize Germplasm," *Crop Science* 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," *Crop Science* 55:1170-80 (2015)
2028	Declaration of Jason Wheeler

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. 11,666,020 ("the '020 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 '020 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. Curtis 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; EnGenious Ag 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 '020 patent in forming my opinions. An Exhibit List is set forth at the beginning of this Declaration.

II. TECHNOLOGY BACKGROUND

17. The ’020 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 (“1PFHC43”). (’020 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 Garcia-Lara and Sergio O. Serna-Saldivar, *Corn History and Culture*, in Corn Chemistry and Technology, (2019) (Ex. 2020) at page 7) is reproduced below.

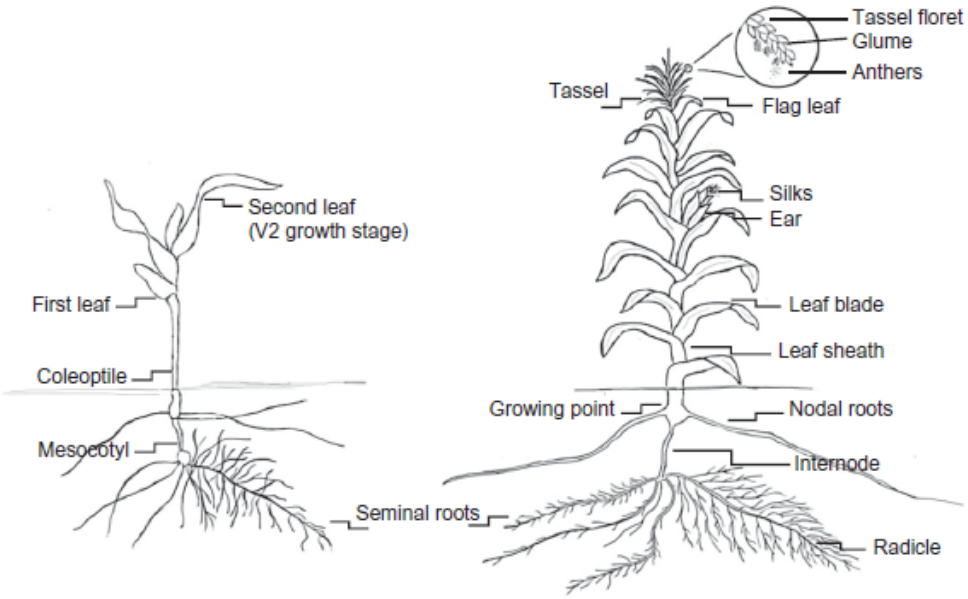


FIG. 1.4 Corn seedling plant and mature corn plant. *(Source: Based on Benson, G.O., Reetz, H.F., 1984. Corn Plant Growth-From Seed to Seedling. National Corn Handbook, Purdue Univ. Coop. Ext. Serv., West Lafayette, pp. 1–240.)*

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 (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 over 3 million gigabases of DNA (> 3 x 10^9) and contains over 32,000 predicted genes. (*Id.*) At each gene 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. However, 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.

26. Using one traditional method to create a homozygous inbred line, an F1 corn seed would be grown and selfed (or crossed with a sibling) 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, the F2

progeny are each genetically and phenotypically distinct. The F2 kernels would be grown into plants, and those plants would be selfed again, for many generations. (*Id.*) Through that process, some 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). (*Id.*) 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.

27. 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.

28. 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.

29. 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.

30. 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 of 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 842.)

31. 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.

32. 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. 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).)

33. 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

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

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

36. 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).

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

38. 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.

39. 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")

40. 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 and 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.

41. 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. (Section II.B.; *see also* Riley Declaration (Ex. 1003 at page 26).)

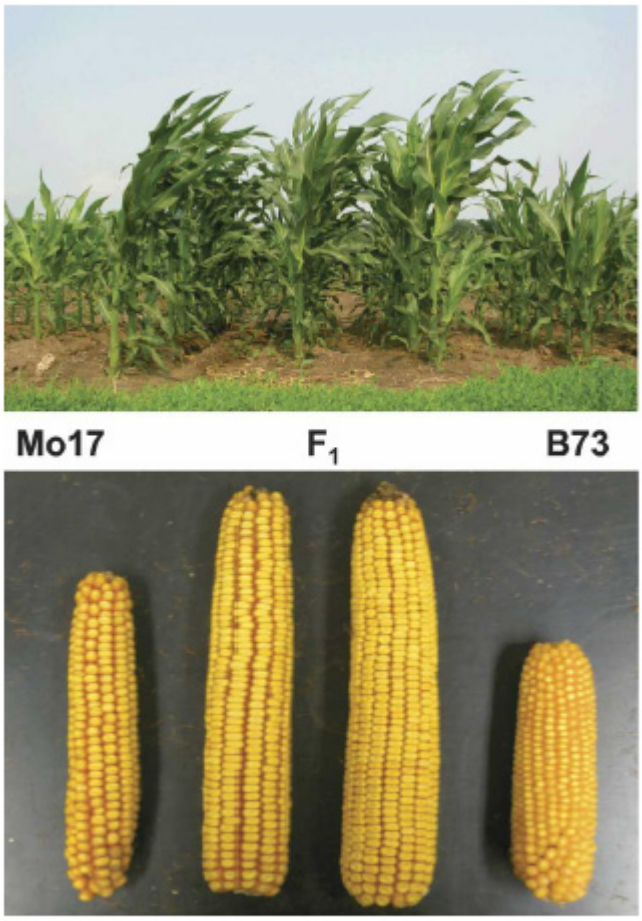


Figure 1. Phenotypic heterosis in the B73 × Mo17 hybrid. Representative B73, Mo17, and F_1 hybrid ears and plants are shown. Note the increased size of the two hybrid ears and three hybrid rows relative to the two inbred parents (*left*, Mo17; *right*, B73).

B. History of Corn and Corn Production

42. 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).) 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.

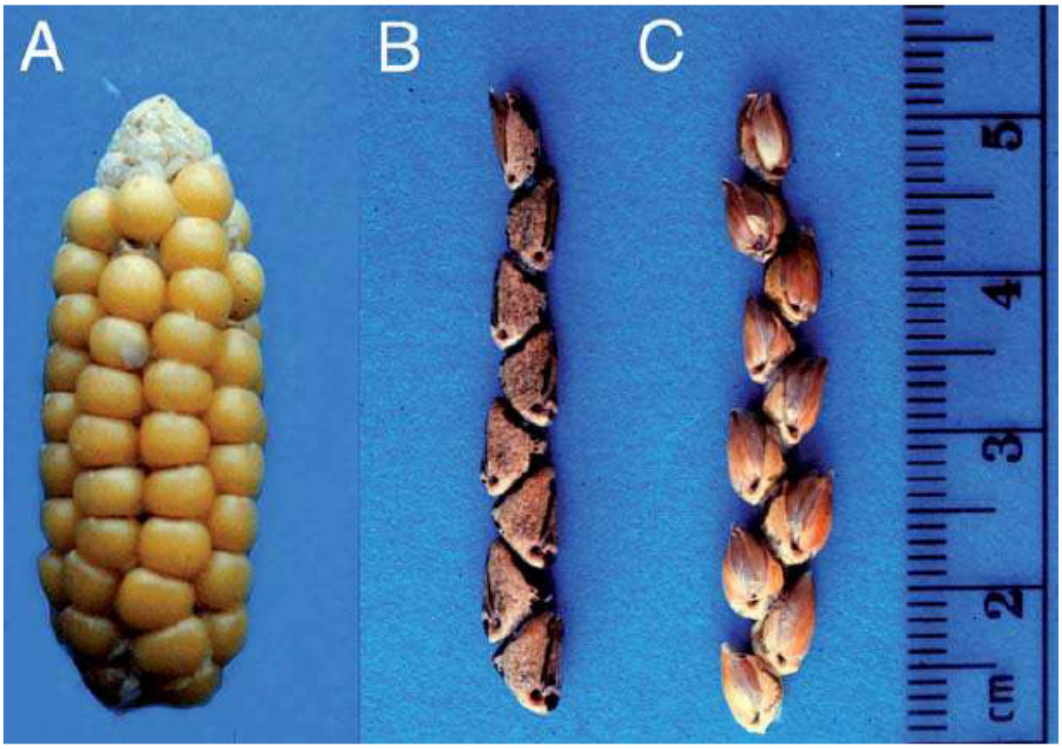


Figure 2 (*A*) A 'Reconstructed' ear of primitive maize (*left*). This small-eared form of maize was bred by George Beadle by crossing teosinte with Argentine pop corn and then selecting the smallest segregants (16). (*B*) Ear of pure teosinte (*Zea mays* ssp. *parviglumis*) composed of eight cupulate 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.

43. 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 and Sergio O. Serna-Saldivar, *Corn History and Culture*, in 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 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 and Fernandez, *Economics of Production, Marketing and Utilization*, in 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.*)

44. The modern success of corn is "due to its adaptation to different ecosystems from coasts to mountains and the development of highly productive regular and biotechnological hybrids capable of yielding under commercial conditions up to 16 tons/Ha." (Silverio Garcia-Lara and Sergio O. Serna-Saldivar, *Corn History and Culture*, in 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.*)

45. Before the 1930s, corn production relied on open pollination. (Hochholdinger and 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.

46. Starting in the 1930s, however, and led by Henry Wallace and the founding of the Hi-Bred Corn Company in 1926 (*see* 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 (Hochholdinger and Baldauf, *Heterosis in Plants*, Current Biology 28:R1075–95 (2018), Ex. 2023), as reflected in Hochholdinger's Figure 2, reproduced below.

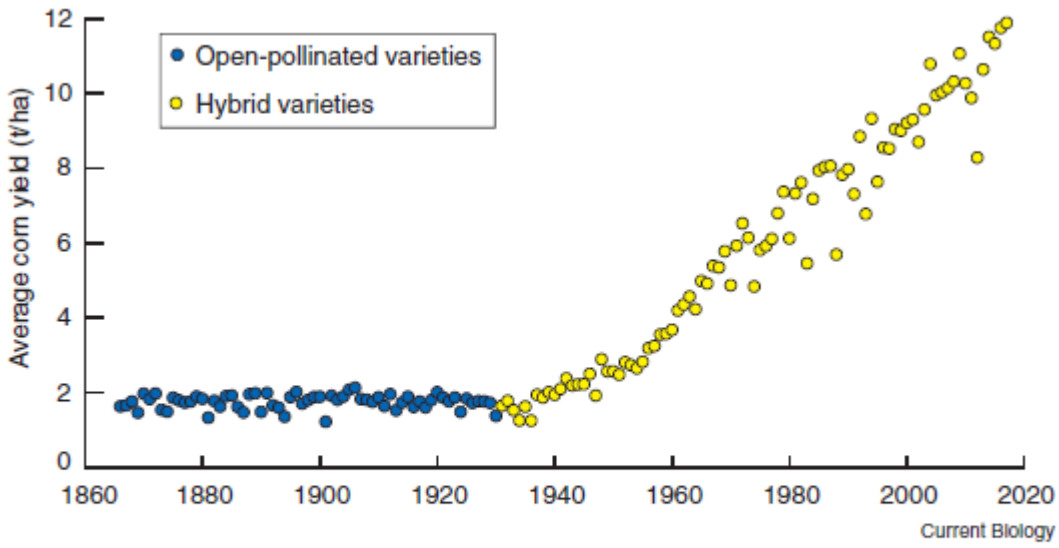


Figure 2. Average grain yield in tons per hectare for maize varieties in the United States. Yield of open-pollinated varieties (blue) from 1866 to 1930 and hybrid varieties (yellow) from 1931 to 2017. Data source: United States Department of Agriculture, National Agricultural Statistics Service (www.nass.usda.gov).

47. An example of a typical inbred line development scheme demonstrating the inbred line development process, generally, is set forth as Figure 3 of Lee (Ex. 1012) on page 146 and is also reproduced below. 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.

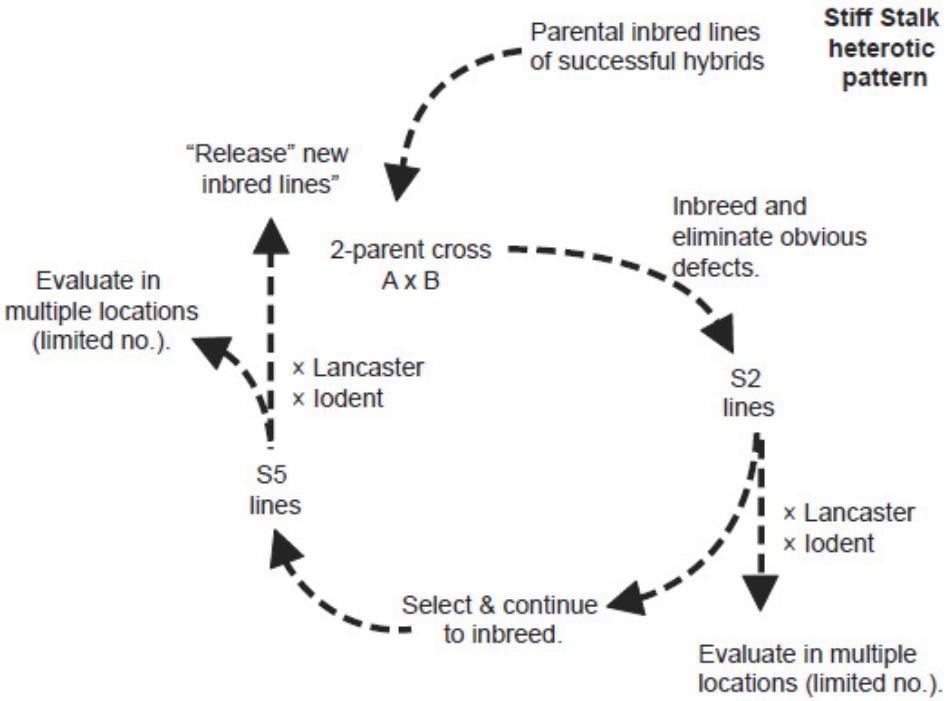


Fig. 3 An example of a typical inbred line development scheme, depicting a 2-parent breeding cross involving two inbred lines from the Stiff Stalk heterotic pattern. (From: Lee and Tollenaar 2007)

48. 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).)

49. 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.

50. 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 and Dudley, "Evolution of North American Dent Corn from Public to Proprietary Germplasm," *Crop Sci.* 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

51. 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 94 million acres of land. Ex. 2007;. 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* Ex. 2008.

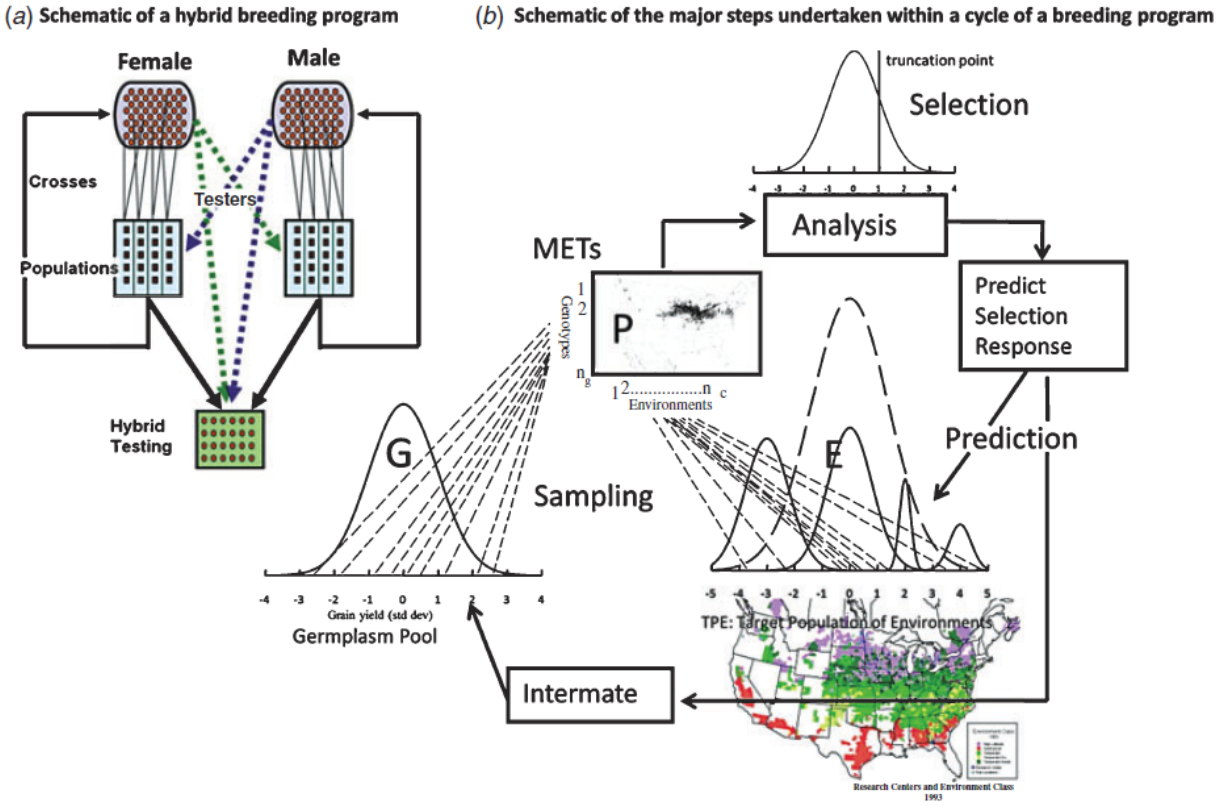
52. "Commercial plant breeders" like Pioneer, "have the same goal as plant breeders in the public sector—to improve cultivars that suit the needs of farmers who plant them." (Duvick et al., *Long-term Selection in a Commercial Hybrid Maize Breeding Program*, in Plant Breeding Reviews: Part 2: Long-term Selection: Crops, Animals, and Bacteria, Volume 24 (Jules Janick, ed.) (2004) (Ex. 2008), at page 110.)

53. 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.

54. 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

’020 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 analysist 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.

55. 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 313, Figure 2).

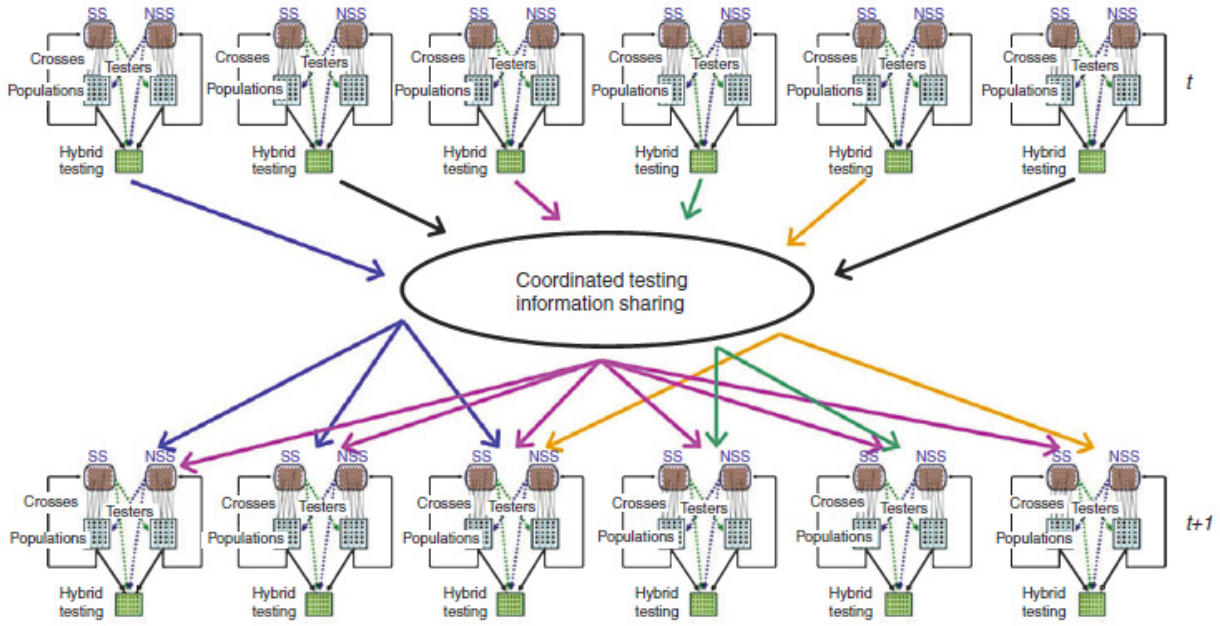


56. The top left panel (a) shows that the "maize germplasm pool is organized into two major heterotic groups." (*Id.*) Heterotic groups refer to a group of plants that are classified according to their breeding requirements. This is somewhat analogous to the production of Labradoodle dogs, where two 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 labradors 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

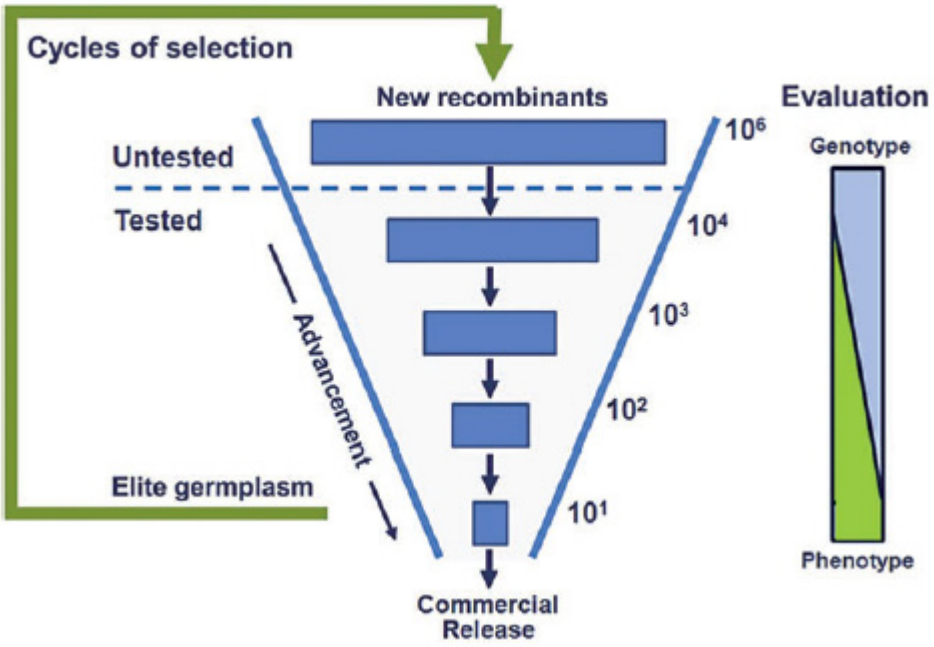
pool, often referred to as non-Stiff-Stalks (NSS). (Ex. 2013, 312-313.) These are two of the major North American field corn heterotic groups. However, not every inbred will perform well as a hybrid parent. Therefore, those new inbreds are tested for yield and key agronomic traits in hybrid combinations using appropriate testers from the complementary heterotic groups." (*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.

57. 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.*)

58. "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 centralized 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.



59. All of this results in a massive funnel, where the number of new recombinant inbred lines 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 (ten million) starting inbreds, of which 10^4 are "Tested," and ultimately narrowed down by three orders of magnitude to just ten elite inbred varieties.



60. 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 in Section II, 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, in Section II, 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*.)

61. 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 113–114.) 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 was built up since around the 1930s using its breeding program (e.g., as described above in Section XX). (*Id.* at 112–113.) "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*.)

62. 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.)

63. "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.*)

64. 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.)

65. 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 '020 PATENT—MAIZE INBRED VARIETY 1PFHC43

66. The '020 patent is titled "Maize Inbred 1PFHC43." ('020 Patent, Ex. 1001 at cover page). It issued on June 6, 2023. (*Id.*) It was filed as U.S. Patent Application No. 17/366,059 on July 2, 2021. (*Id.*)

A. Overview of The Specification

67. The '020 patent describes a "new and distinctive maize inbred variety designated 1PFHC43, 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 PH1VNA and inbred line PH1D84." (Ex. 1001, 38:25-28.) That is, these two inbreds were crossed to produce F1 plants (as described above). "Inbred 1PFHC43 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, 38:30–34.)

68. 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).

69. Representative seed of the resulting inbred variety was deposited with the National Center for Marine Algae and Microbiota (NCMA) under NCMA Accession Number 202212064. (Ex. 1001, 37:60-65.) The '020 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, 38:7-8.)

70. 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).

71. 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, 15:8–12.)

72. The specification itself describes a number of phenotypic traits of the variety (grown in one environment). (Ex. 1001, Table 1 at 38–40; 15:1–15 ("Phenotypic Characteristics of 1PFHC43").) It also describes how to determine genotypic characteristics of the variety. (Ex. 1001, 15:16–36 ("Genotypic Characteristics of 1PFHC43").) For example, by "loci shown in a marker profile." (Ex. 1001, 15:19–20.) Different marker profile techniques (well known in the art), are described in the '020 patent as well. (Ex. 1001, 15:51–16:11.)

73. The claimed variety (1PFHC43) 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, 38:36-40.)

B. The Claims

74. The '020 patent has 20 claims. (Ex. 1001, 40:25-42:27.) Claims 1, 10, and 18 are independent. Claims 2–9 depend on claim 1, claims 11–17 depend on claim 10, and claims 19 and 20 depend on claim 18. (*Id.*)

75. Claim 1 recites:

> 1. A seed, plant, plant part, or plant cell of inbred maize variety 1PFHC43, representative seed of the variety having been deposited under NCMA accession number 202212064.

76. 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). (*Id.*)

77. Claim 10 recites:

> 10. A converted seed, plant, plant part or plant cell of inbred maize variety 1PFHC43, representative seed of the maize variety 1PFHC43 having been deposited under NCMA accession number 202212064, wherein the converted seed, plant, plant part or plant cell comprises fewer than six locus conversions, and wherein the plant or a plant grown from the converted seed, plant part or plant cell comprises the fewer than six locus conversions and otherwise comprises the physiological and morphological characteristics of maize variety 1PFHC43 when grown under the same environmental conditions, and further wherein the fewer than six locus conversion confer a property selected from the group consisting of male sterility, a site for site-specific recombination, abiotic stress tolerance, altered phosphate, altered antioxidants, altered fatty acids, altered essential amino acids, altered carbohydrates, herbicide tolerance, insect resistance and disease resistance.

78. Claims 11–17 depend from claim 10 and recite specific locus conversions (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. (*Id.*)

79. Claim 18 recites:

> 18. An F1 hybrid seed produced by crossing a plant or plant part of inbred maize variety 1PFHC43, representative seed of the inbred maize variety 1PFHC43 having been deposited under NCMA accession number 202212064 with a different maize plant, wherein inbred maize variety 1PFHC43 further comprises a transgene and

> otherwise comprises all of the physiological and morphological characteristics of maize variety 1PFHC43 when grown under the same environmental conditions, wherein the transgene was introduced into inbred maize variety 1PFHC43 by back-crossing or genetic transformation.

80. Claim 19 recites a method of producing progeny seed by crossing a plant grown from the seed of claim 18 and claim 20 recites a method of making a commodity plant product from the plant or plant part of claim 18. (*Id.*)

IV. PETITIONER'S ASSERTED REFERENCES

81. Each of Petitioner's asserted references describes another of Pioneer's inbred maize varieties. One (Smalley, Ground 1) is one of the parents of the claimed variety. Another (Longenerger, Ground 2) is a half sibling of the claimed variety. The third (Hoffbeck Ground 3) is neither a parent or sibling to the claimed variety.

A. Smalley (Ex. 1005) and the Corresponding PVP Certificate (Ex. 1008)—Inbred Maize Variety PH1D84

82. Smalley is a U.S. Patent (8,759,636) titled "Maize Inbred PH1D84," which issued on June 24, 2014, and which lists Pioneer Hi-Bred International, Inc. (PO) as the Assignee. (Ex. 1005, cover page.) Smalley describes an inbred maize variety (PH1D84), which was developed by crossing "inbred line PHCCW and inbred line PHE4N," selfing the resulting F1 plants and "using ear-to-row

(pedigree) selection from the F3 to F9 generation, and bulking the F10 seed." (Ex. 1005, 12:34-40.) The inbred line is "substantially homozygous." (*Id.*) A deposit "of at least 2,500 seeds of Maize Variety PH1D84" was made "with the American Type Culture Collection (ATCC) . . . with ATCC Deposit No. PTA-121035." (Ex. 1005, 41:31-34.)

83. Table 1 of Smalley 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), Table 3 "compare[s] a specific hybrid for which PH1V5T is a parent with other hybrids," (Ex. 1005, Table 3, 15:63–16:14), and Table 4 contains a list of public genetic markers that can be used to genetic marker profile of a maize variety (Ex. 1005, Table 4, 34-35).

84. Exhibit 1008 is the PVP certificate for Inbred Maize Variety PH1D84. (Ex. 1008.)

85. As described in the PVP certificate (Exhibit 1008), Smalley's PH1D84 is "most similar" to (but "significantly different" from) its parent, PHE4N. It has "a greater average ear diameter," "a longer average kernel length," and "a shorter average plant height." (Ex 1008, 5.)

86. These (and other) differences between Smalley's inbred and its parent, PHE4N, are an expected result of meiotic recombination in the F1 plants and subsequent selection over twelve generations, as described above in Section II.

87. Inbred Maize variety PH1D84 is one of the parents of the elite Inbred Maize variety 1PFHC43, which is claimed in the ’020 patent. (Ex. 1001, 38:25-28.)

B. Longenberger (Ex. 1006)—Inbred Maize Variety PH47K2

88. Longenberger is a U.S. Patent (10,681,888) titled “Maize Inbred PH47K2” which issued on June 16, 2020, and which lists Pioneer Hi-Bred International Inc. as the Assignee. (Ex. 1006, cover page.) Longenberger describes the inbred maize variety PH47K2 which was developed by crossing “PH1D84” and “PH12K5,”and “developed by producing a double haploid from the F1 plants, selfing and using pedigree selection amongst the D1 lines, and selfing and bulking from the subsequent generations.” (Ex. 1006, 38:55-56.) The inbred line is “substantially homozygous.” (*Id.*) A deposit “of at least 625 seeds of Maize Variety PH47K2” was made “with the American Type Culture Collection (ATCC) . . . with ATCC Deposit No. PTA-126525.” (Ex. 1006, 38:29-33.)

89. Table 1 of Logenberger contains a description of some of the variety’s phenotypic characteristics. (Ex. 1006, 39-41.) Inbred Maize variety PH47K2 is not a parent of the elite Inbred Maize variety 1PFHC43, which is claimed in the ’020 patent. (Ex. 1001, 38:25-28.) It originated from a half-sibling of 1PFHC43’s,

as both were generated from crosses between PH1D84 and a second inbred variety (PH12K5 for PH47K2 and PH1VNA for 1PFHC43). (*Id.*; Ex. 1006 at 38:55-56.)

C. Hoffbeck (Ex. 1007) and the Corresponding PVP Certificate (Ex. 1010)—Inbred Maize Variety PHH5G

90. Hoffbeck is a U.S. Patent (7,528,307) which issued on May 5, 2009, and which lists Pioneer Hi-Bred International, Inc. as the Assignee. (Ex. 1007, cover page.) Hoffbeck describes the inbred maize variety PHH5G (Ex. 1001, cover page), which originated from a cross between PH6WA and PH4GP (Ex. 1010, 3). Hoffbeck is "substantially homozygous." (*Id.* 13:12-13.) A deposit "of at least 2500 seeds of Maize Variety PHH5G" was made "with the American Type Culture Collection (ATCC) . . . with ATCC Deposit No. PTA-9710." (Ex. 1007, 37:20–26.)

91. Hoffbeck's Table 1 contains a description of some of the variety's phenotypic characteristics. (Ex. 1007, 37-40.) Table 2 shows the "SSR genetic marker profile" for PHH5G. (*Id.* 14:52-56.) Tables 3A-3D shows comparisons between PHH5G and "other maize inbred varieties and hybrids." (*Id.* 40-45.) Table 4 shows the general combing ability of PHH5G. (*Id.* 45-46.) Table 5 "compare[s] a specific hybrid for which inbred PHH5G is a parent with other

hybrids." (*Id.* 46-48.) Table 6 shows the "numerous species of the genus F1 hybrids created with PHH5G." (*Id.* 49-51.)

92. Inbred Maize variety PHH5G is not a parent of elite Inbred Maize variety 1PFHC43, which is claimed in the '020 patent, nor is it a sibling. (Ex. 1001, 38:25-34; Ex. 1010, 3.)

V. PERSON OF ORDINARY SKILL IN THE ART

93. 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.

94. 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

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

A. Non-Obviousness

96. 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.

97. 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

98. 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.

99. 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.

100. 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.

VII. DISCUSSION OF PATENTABILITY

101. Below I set forth my opinions on patentability with respect to Petitioner's Grounds 1–3 (obviousness), 4 (utility), and 5 (question concerning information necessary for examiners to determine whether plant utility claims have the requisite specific utility under § 101).

A. Obviousness (Grounds 1–3)

102. In my opinion, claims 1–20 would not have been obvious over the prior art that Petitioner has asserted. In short, as described more fully below, Inari and Dr. Riley disregard the claimed invention (maize variety 1PFHC43), ignore the genetic differences between 1PFHC43 and the prior art, base their entire analysis on an improper comparison (to the exclusion of a proper one), and moreover, can only have come to their positions in hindsight (which I understand is improper).

103. 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 [PH1D84 | PH47K2 | PHH5G][1] as a parent," citing "(1) the routine nature of the breeding techniques involved," and "(2) the multiple other instances already reported in which [PH1D84 | PH47K2 | PHH5G][2] had been used as a parent to obtain other inbred lines." (Ex. 1003 at 64, 81, 88; Pet. at 42, 55, 62). Dr. Riley offers no opinions, however, on whether it would have been obvious to obtain ***the maize inbred variety 1PFHC43*** (as claimed in the '020 patent). I understand from counsel this is legally incorrect and not relevant to a determination of obviousness.

104. 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 1PFHC43 maize variety*** based on the phenotypic traits described by Smalley, Longenberger, and Hoffbeck. 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

[1] Ground 1: PH1D84 (Smalley, Ex. 1005); Ground 2: PH47K2 (Longenberger, Ex. 1006); Ground 3: PHH5G (Hoffbeck, Ex. 1007).

[2] Grounds 1 and 2: PH1D84 (Smalley, Ex. 1005); Ground 2 PH47K2 (Longenberger, Ex. 1006); Ground 3: PHH5G (Hoffbeck, Ex. 1007).

POSA would not have been so motivated and would not have had a reasonable expectation of success in developing 1PFHC43 based on the phenotypic traits disclosed in Smalley, Longenberger, or Hoffbeck alone.

105. 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 1PFHC43. I understand from counsel this is not a legally proper analysis and that the POSA must be motivated to develop the claimed 1PFHC43 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 1PFHC43 based on the incomplete list of phenotypic traits described by Smalley, Longenberger, or Hoffbeck alone.

106. I further understand from counsel that Pioneer deposited a "representative seed" with the NCMA that is an example of the claimed 1PFHC43 variety. I also understand that "representative seed" is also available for the maize varieties described in Smalley, Longenberger, and Hoffbeck. 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, are required to determine whether the prior art varieties would render the claimed 1PFHC43 variety obvious.

107. Petitioner has simply not provided any compelling evidence even suggesting that 1PFHC43 would have been obvious.

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

108. An understanding of 1PFHC43's genetic make-up is required to understand how and in what ways it is distinct (or not) from other maize varieties. From the perspective of a POSA, no useful comparison can be made between the varieties without an analysis of their underlying genetics. As discussed above, a plant variety's phenotypic traits are the outward expression of its genotype (in addition to environmental factors affecting gene expression).

109. A POSA would have no expectation of developing 1PFHC43 based on Smalley, Longenberger, or Hoffbeck simply because they have some phenotypic traits in common. As biological material, 1PFHC43 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 1PFHC43 using any of them as a starting point, even if one of the varieties, PH1D84 (Smalley), is one of its parents.

110. 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. 1PFHC43'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.

111. 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 3072 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 single nucleotide polymorphism (SNP) markers to "provide even

genomic coverage" across the maize genome. (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 (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.

112. 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.

113. 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 1PFHC43 to the prior art varieties because seed deposits are available for that purpose.

114. 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, especially given the differences in pedigree between the claimed inbred variety and the prior art inbred varieties.

2. A POSA Would Need Access to Both of 1PFHC43's Parent Varieties to Have a Reasonable Expectation of Success in Developing It

115. I understand from counsel one of 1PFHC43's parents, PH1VNA was not known to persons of skill during the relevant time period of July 2021. A POSA would have no reasonable expectation of success in developing 1PFHC43 without understanding both the genotypic and phenotypic characteristics of both its parents, PH1D84 and PH1VNA. 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. As such, 1PFLQ21's genome is derived from a mixture of both PH1V5T and PH2F7K and a POSA would have no "roadmap" to 1PFLQ21 based on the genotype and phenotype of PH1D84 alone.

116. Even if **both** parents were known to POSAs during this time, they still would have no reasonable expectation of success in developing 1PFHC43 due to the unpredictability of the breeding process (as described in Section II). Each progeny of an F1 plant resulting from a cross of two inbreds is genetically and

phenotypically distinct. A POSA would not expect that a cross of the same parents will produce the same child. The genome of a progeny plan is the result of the random recombination in the F1 plant of the two parental genomes and the chance of the exact same child resulting from that cross is infinitesimally small.

117. Relevant here, as described above in Section II, maize inbreds having different pedigrees would be expected to have different genotypic and phenotypic characteristics. This is true whether they share the same parents (i.e., are full 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, PH1D84 (Petitioner's Smalley, Ex. 1005) is the parent of 1PFHC43. But, as noted by Dr. Riley and Petitioner, it is also the parent of at least seven other distinct inbred lines. Pet. 73.

118. 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 other similar inbred varieties), it would not have been obvious:

1) which parents to combine; 2) which progeny to select for further breeding; and 3) 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.

119. In this case, Inari has not and cannot establish that it would have been obvious for a POSA to even have combined the parents of PH1D84 in the first place, as only one of the parents, PH1D84 (Smalley) was publicly available. Yet, even if both parents were publicly available (which is not the case here) and there had been a reason for a POSA to have selected those two parents (which Petitioner does not articulate), absent any evidence to the contrary, it would not have been obvious to produce 1PFHC43 as recited in the claims. Neither Dr. Riley nor Petitioner has articulated any arguments as to why it 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.

3. Maize Inbred Development is Unpredictable

120. Corn inbred development is inherently unpredictable. While plant breeding may utilize some well-known techniques (such as described in the '020 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, pages 9–11.) 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 1PFHC43.

121. Dr. Riley and Inari's position that "POSAs are capable of breeding inbred lines to incorporate essentially any desired inbred phenotypical trait in descendant inbred lines so long as it was within the scope of corn's 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. 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. 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.

122. 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. 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.

123. 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.*)

124. And, as described above in Section II.C., 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, 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

125. Dr. Riley provided a single table of comparisons between certain phenotypic characteristics of the claimed maize inbred 1PFHC43 (from Table 1 of '020 patent) and each of the prior art references, in the aggregate. (Riley Declaration, Ex. 1003 at Table 1, pages 30–37.) This table allegedly demonstrates that the prior art "disclose[s] inbred corn lines with characteristics very similar to those of the claimed 1PFHC43." (*Id.* at 30.)

126. 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." (*Id.* at 37.) This is true. As I have described above (Section II), a plant's phenotype is a manifestation of both genotype and environment. As such, 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.

127. 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 1PFHC43 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. Pet. 63.

128. Importantly, Petitioner has not demonstrated the phenotypic traits disclosed by Smalley, Longenberger, and Hoffbeck are sufficient to develop 1PFHC43 as claimed in the '803 patent or that a POSA would have a reasonable expectation of doing so based on their 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.

129. Many types of genotypic and phenotypic comparisons are possible when one has access to seed of a particular variety. I understand from counsel that nothing prevented Dr. Riley or Petitioner from accessing 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 comparisons 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.

130. 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)," Dr. Riley goes on to base all his opinions that the '020 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 1PFHC43 to the prior art varieties individually. 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, page 37) is based on an inherently flawed comparison.

131. As an additional matter, it is my opinion that the fact that, as Dr. Riley highlights, the patent specifications for the '020 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 1PFHC43 variety obvious. (Ex. 1003, page 37 ("virtually all of the '020 Patent's specification is drawn verbatim from Longenberger (as indicated in the above-noted comparison, Exhibit 1093) and is also highly similar to the disclosures in Smalley and Hoffbeck.")). 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 the necessarily different genotypic and phenotypic characteristics it possesses compared to the inbreds described in Gadlage, Smalley, and Chifflet. The structure of the words may be similar, but the maize varieties they describe (and claim) are clearly different.

5. Petitioner's Comparisons Must Have Been Made in Hindsight

132. Petitioner has identified three references that the maize variety 1PFHC43 would allegedly have been obvious over. However, Petitioner *must* have started from the perspective of the invention—looking at the traits in Table 1 of the

’020 patent and coming up with varieties that are allegedly similar or by looking at the disclosed Breeding History in the ’020 patent to find parents or siblings. There would have been no other way to choose the asserted prior art inbred lines out of the (at least) thousands of other inbred varieties.

B. Ground 1: Claims 1–20 Would Not Have Been Obvious over Smalley (PH1V5T, Exhibits 1005 and 1008)

133. As described above, Smalley describes the inbred maize variety PH1D48, which was developed by crossing “inbred line PHCCW and inbred line PHE4N.” (Ex. 1005, 12:34-40.) A deposit “of at least 2,500 seeds of Maize Variety PH1D48” was made “with the American Type Culture Collection (ATCC) . . . with ATCC Deposit No. PTA-121035.” (Ex. 1005, 41:31-34.) Exhibit 1008 is the PVP certificate for Inbred Maize Variety PH1D48.

134. As described in Exhibit 1008, Smalley’s PH1D84 is “most similar” (but “significantly different” from) its parent, PHE4N. (Ex. 1008 at page 5.) It has “a greater average ear diameter,” “a longer average kernel length,” and “a shorter average plant height.” (Ex 1008 at page 5.)

135. Inbred Maize variety PH1D48 is one of the parents of the elite Inbred Maize variety 1PFHC43, which is claimed in the ’020 patent. (’020 patent (Ex. 1001), 38:25-28) But it is also the parent of at least seven other distinct inbred

lines, as recognized by Dr. Riley. Pet. 73. As I noted above, the fact that PH1D48 is the parent 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.

136. 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." I disagree. As an initial matter, as I noted above, Petitioner and Dr. Riley's obviousness analysis is based not on what is claimed (1PFHC43), but rather on a hypothetical "inbred maize variety with PH1D48 as a parent." A proper analysis would be to compare 1PFHC43 to Smalley's PH1D48. And a proper analysis would consider both genotypic and phenotypic differences, as a whole, as discussed above.

137. 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."

138. As described above, one very simple starting point for assessing similarities or differences between any two corn inbred varieties is to genotype

them. For example, the SNPs from Rouselle 2015 (Ex. 2027), as described above could be used for this purpose. Patent Owner provided me with the genotype results of the Rouselle 2015 SNP panel for both 1PFHC43 and PH1D84 (Exhibit 2028). Using the provided genotypes, I calculated the percent markers that differed in genotype between 1PFHC43 and PH1D84. Just looking at that comparison, it is apparent that these are two very different varieties. They differ genetically at approximately 11% of genotyped genetic markers (i.e., sharing only 89% of the 2,990 markers genotyped and homozygous for both inbred varieties). This level of genetic differentiation is not surprising given the differences in pedigrees. Additional genotyping would be expected to uncover additional genetic differences.

139. Furthermore, the expectation, based on the inbreds' different parentages 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 just one parent (or both parents, for that matter).

140. Given all of the above, I cannot agree with Dr. Riley or the Petitioner that claims 1–20 (which all recite "maize variety 1PHC43") would have been obvious based on the disclosures of Smalley alone. In my opinion, they would not.

C. Ground 2: Claims 1–20 Would Not Have Been Obvious Over Logenberger (PH47K2, Exhibit 1006)

141. As stated above, Longenberger describes the inbred maize variety PH47K2 which was developed by crossing "PH1D84" and "PH12K5," (Ex. 1006, 38:55-56.). A deposit "of at least 625 seeds of Maize Variety PH47K2" was made "with the American Type Culture Collection (ATCC) . . . with ATCC Deposit No. PTA-126525." (Ex. 1006, 38:29-33.) Inbred maize variety PH47K2 is a half-sibling of 1PFHC43. (Ex. 1001, 38:25-28; Ex. 1006, 38:55-56.)

142. 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 1PFHC43 are "insubstantial and insignificant." Again, Petitioner's and Dr. Riley's obviousness analysis is not based on the claimed 1PFHC43 variety. Instead, Dr. Riley opines "POSAs would have had a reasonable expectation of obtaining ***an inbred maize variety*** with PH47K2 as a parent." A proper analysis would compare 1PFHC43 to Longenberger's 's PH47K2 and that analysis would consider both the full scope of genotypic and phenotypic differences between the two varieties.

143. I understand from counsel the proper inquiry is not whether ***an inbred*** is obtainable using PH47K2 as a parent, but whether a POSA would be motivated to and have a reasonable expectation of success in obtaining 1PHC43 based on the disclosures of Longenberger. A POSA would not have been so motivated or have

such a reasonable expectation of success because 1PFHC43 and PH47K2 are genetically and phenotypically distinct. As noted above, Dr. Riley and Petitioner have not assed 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." (Ex. 1003, ¶ 46; Pet., 23.) 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, ¶ 63.)

144. 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. 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 1PFHC43 and PH47K2 (Exhibit 2028). Using the provided genotypes, I calculated the percent markers that differed in genotype between 1PFHC43 and PH47K2. Just looking at that comparison, it is apparent that these are two very different varieties. They differ genetically at approximately 12% of the genotyped genetic markers (i.e., sharing only 88% of markers in common across the 2,785 markers genotyped and homozygous for both varieties). This level of genetic differentiation is not surprising given the

differences in pedigrees. Additional genotyping would be expected to uncover additional genetic differences.

145. Furthermore, the expectation, based on the varieties' different parentage 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.

146. 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 Longenberger alone. In my opinion, they would not.

D. Ground 3: Claims 1–20 Would Not Have Been Obvious Over Hoffbeck (PHH5G, Ex. 1007) and its Corresponding PVPA Certificate (Ex. 1010)

147. As stated above, Hoffbeck describes the inbred maize variety PHH5G (Ex. 1001, cover page), which originated from a cross between PH6WA and PH4GP (Ex. 1010, 3). A deposit "of at least 2500 seeds of Maize Variety PHH5G" was made "with the American Type Culture Collection (ATCC) . . . with ATCC Deposit No. PTA-9710." (Ex. 1007, 37:20-26.)

148. Inbred maize variety PHH5G is not a parent, sibling, or child of the claimed 1PFHC43 maize variety. (Ex. 1001, 38:25-28; Ex. 1007, 37:20-26.) While PHH5G is not a parent of 1PFHC43, it is a parent of at least one other maize variety as noted by Dr. Riley and Petitioner. (Pet. 61; Ex. 1003, ¶138). As I noted above, the fact that PHH5G is the parent of another, distinct inbred variety further illustrates a POSA would not have a reasonable expectation of developing 1PFHC43 based on the disclosures of Hoffbeck alone or using Hoffbeck's inbred, PHH5G, as a starting point without any additional context regarding its genetics or its full set of phenotypic traits. Differently bred varieties, especially where they have no parents in common, are expected to have different genotypic and phenotypic characteristics.

149. As stated above with respect to Grounds 1 and 2, I disagree with Dr. Riley's opinion that from a POSA's perspective, any differences between the prior art and 1PFHC43 are "insubstantial and insignificant." Again, Petitioner's and Dr. Riley's obviousness analysis is not based on the claimed 1PFHC43 variety. Instead, Dr. Riley opines "POSAs would have had a reasonable expectation of obtaining ***an inbred maize variety*** with PHH5G as a parent." A proper analysis would compare 1PFHC43 to Hoffbeck's PHH5G and that analysis would consider both the full scope of genotypic and phenotypic differences between the two varieties.

150. I understand from counsel the proper inquiry is not whether ***an inbred*** is obtainable using PHH5G as a parent, but whether a POSA would be motivated to and have a reasonable expectation of success in obtaining 1PFHC43 based on the disclosures of Hoffbeck. A POSA would not have been so motivated or have such a reasonable expectation of success because 1PFHC43 and PHH5G are genetically and phenotypically distinct. As noted above, Dr. Riley and the Petitioner have not assed 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." (Ex. 1003, ¶ 46; Pet., 23.) 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, ¶ 63.)

151. As discussed above in my opinions relating to Grounds 1 and 2, a very simple starting point for assessing similarities or differences between any two corn varieties is to genotype them. 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 1PFHC43 and PHH5G (Exhibit 2028). Using the provided genotypes, I calculated the percent markers that differed in genotype between 1PFHC43 and PHH5G. Just looking at that comparison, it is apparent that these are also two very different inbred varieties, that genetically

differ at approximately 12% of the genotyped genetic markers (i.e., sharing only 88% of markers in common across the 2,982 markers genotyped and homozygous for both inbred varieties). This level of genetic differentiation is not surprising given the differences in pedigrees. Additional genotyping would be expected to uncover additional genetic differences.

152. Furthermore, the expectation, based on the varieties' different parentage 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.

153. 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 Hoffbeck alone. In my opinion, they would not.

E. Ground 4: Utility

154. The specification of the '020 patent itself discusses the utility of the claimed inbred variety. As Petitioner points out, the "Background" section of the '020 patent identifies 1PFHC43 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; Pet., 14.)

155. The '020 patent also explains that "[a] variety such as 1PFHC43 which exhibits good general combining ability may be used in a large number of hybrid combination[s]" and that "1PFHC43 may be used to produce a single cross hybrid, a double cross hybrid, or a three-way cross hybrid." (Ex. 1001, 18:55-56.) Furthermore, "[t]he seed of maize variety 1PFHC43, 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, 37:21-26.) Each of these is an example of the utility provided by 1PFHC43.

156. 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, ¶¶ 154-167.) 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." (*Id.* at ¶ 161.)

157. Finally, as described in Sections II.B and II.C, 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.

VIII. CONCLUSION

158. 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,



Date: June 26, 2024

PATRICK S. SCHNABLE

APPENDIX A

PATRICK S. SCHNABLE

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EDUCATION

Cornell University, B.S., Agronomy, 1981
Iowa State University, Ph.D., Plant Breeding and Cytogenetics, 1986

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
- Changjang 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 *Amborella* 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 *Aegilops tauschii* 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*):

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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 Erdös number of 3.

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- 10,704,091 Genotyping by next-generation sequencing (issued 7 July 2020)
- 10,364,437 Plant genes involved in nitrate update and metabolism (issued, 30 July 2019)
- 9,951,384 Genotyping by next-generation sequencing (issued, 24 April 2018)
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- 8,779,233 QTL regulating ear productivity traits in maize (issued, July 15, 2014)
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