ARTICLE

Productivity Growth from Genetic Improvement: Evidence from Illinois Soybean Trial Data

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Abstract

In 2023, the United States produced 28% of the world's soybeans, making understanding yield trends in the United States important for understanding global price trends. We estimate yield growth due to genetic change in soybeans using Illinois variety trial data with a modified approach. Specifically, our approach uses the yield from "check varieties" that are planted consistently from 1997 to 2020 as a control variable to identify the gain in yield across years using only yield variation within the plot and year. Ours are the first estimates of genetic gain in commercial soybean varieties after 2010 and we find that soybean yields increased between 25 and 26 kg/ha (0.37–0.38 bu/acre), or 0.7%, per year at a roughly linear rate in the past two decades. We find mixed evidence that the yield of genetically engineered soybeans grew faster than conventional varieties: In many years, conventional varieties did just as well as genetically engineered ones. We also find that adding the check variety's yield as a control variable significantly impacts how models in the literature estimate the average annual yield gain from genetics in these data. Our findings suggest that genetic change continued to be a consistent driver of yield change in soybeans over the past two decades.

KEYWORDS
agriculture, innovation, soybeans, technological change

JEL CLASSIFICATION
D24, I23, Q16, Q18, O43

Soybeans are one of the most important crops to global agriculture due to their variety of uses: as a processed food ingredient, as an ingredient in animal feed, and, increasingly, as an ingredient in bio-based diesel. In the face of this potentially increasing demand, soybeans continue to be affordable only if the productivity of the soybean sector continues to rise to keep prices steady. Studies often focus on explaining trends in yield, that is, changes in the single-factor productivity measure of output per acre of land, to understand trends in soybean productivity. In 2023, the United States produced 28% of the world's soybeans, making understanding yield trends in the United States important for understanding global price trends.

One important question is how much changes in genetics have driven yield growth in soybeans. Measuring the role of genetic change in yield, however, is complicated by the fact that weather and climate also drive yield trends (Butler et al. 2018; Lusk et al. 2019; Ortiz-Bobea and Tack 2018; Tack et al. 2015b). Understanding the exact contribution of genetic change to yield trends is critical because, unlike weather and climate, genetic change is an economic process resulting from firm innovation. As climate change impacts become more severe and frequent, it is becoming increasingly important to understand how firm innovation contributes to yield growth independent of weather and climate.

Our analysis estimates yield growth from genetic change in US soybeans using soybean trial data from the University of Illinois State Agricultural Experiment Station (SAES). The University of Illinois SAES accepts soybean varieties from companies in order to grow them on experiment plots and determine their relative yield advantage. Of the extensive economics literature using yield trial data, ours is the first analysis to study genetic change in soybeans. Previous analyses of these sorts of yield trial data for other crops estimate the genetic contribution to yield for each variety by pooling yield data from across years and locations (Ramsey and Rejesus 2021; Tack et al. 2015a). When varieties are not planted consistently enough, this approach risks confounding genetic variation with weather impacts. We build on previous approaches with these data by including a crucial control variable to explain a variety's yield: the yield of a consistently planted "check variety" in the same location and year as the submission. We accomplish this by taking the difference between the yield of a submission and the yield of a variety that is planted in each location every year across the sample. This approach fits the experimental design of the Illinois SAES plots by only comparing varieties to other varieties in the same location and year.

We calculate the linear rate of annual genetic improvement to be 25–26 kg/ha (0.34–0.4 bushels per acre) or roughly 0.7% per year, an estimate that is a little lower than previous estimates of soybean yield growth from genetic improvement (Specht and Williams 1984; Xu et al. 2013). Without controlling for weather, the yield trend in the Illinois SAES over the same period was 47–54 kg/ha or 1.2%–1.4% per year. This suggests that genetic improvement explains roughly half of the yield improvements in these trials independent of management. We also find that previous methods that do not use the check variety yield as a control lead to substantially different conclusions about yield growth from genetic change. Using the fixed-effects approach from previous analyses, we do not see any yield gains from genetics in the first decade of the sample despite seeing gains in our main approach. When the check variety yield control is included, the fixed-effects approach predicts a yield trend much more similar to our method. We produce the first estimates of genetic gain in private soybean varieties post-2010 and find that yield gain from genetics grew at a roughly linear rate from 1997 to 2020.

Apart from newer estimates of yield gain from genetics, our analysis makes two contributions to the literature on estimating yield growth from genetic innovation in agriculture. First, we show that using the yield of another consistently planted variety as a control variable can have a large impact on the estimation of trends in yield growth from genetics from university yield trial data (Nalley et al. 2016; Ramsey and Rejesus 2021; Tack et al. 2015b). We compare our method to two alternative methods. One approach measures the average yield changes over time in the trials independent of observed characteristics. This approach assumes that, after covariates like weather and location characteristics are controlled for, the remaining variation is entirely driven by the genetic differences

between varieties. The second approach attempts to attribute the variation to the varieties themselves by estimating fixed effects for each variety. In the second stage of this approach, the fixed effects are used as the outcome variable and the year of release as the explanatory variable. In these data, neither of these methods predict yield gain from genetics for a decade, in stark contrast to what our method finds. However, adding the control variable aligns the variety-fixed-effects estimate with our approach. Previous analyses that did not use this control may have missed a vital control variable that can greatly affect our understanding of how genetics contribute to changes in yield.

Our second contribution is being able to provide more evidence of how GE varieties have contributed to yield growth from genetics in soybeans (Chavas et al. 2014; Nolan and Santos 2012; Shi et al. 2013). Previous analyses using on-farm data have the limitation that adoption of GE soybean seeds may be correlated to other management decisions that are unobserved, thus biasing estimates (Lusk et al. 2019; Xu et al. 2013). We find mixed evidence that soybeans with herbicide resistance had higher rates of improvement than conventional varieties. In many years, conventional varieties performed just as well as GE varieties, indicating that the underlying seed genetics in both groups are of approximately equal quality from a yield perspective.

Our results have significant implications for Illinois agriculture and for areas of the world with similar climates and soils. Given Illinois's importance to the US soybean market, our results are also important for understanding the pace of innovation in seed genetics in the United States. In contrast to other studies, we find that with a constant management regime, about 50% of the yield growth in the past two decades is explained by changes in genetics rather than changes in weather patterns (Butler et al. 2018; Rizzo et al. 2022; Taylor and Schlenker 2023). Firms testing their soybeans in Illinois have maintained a roughly linear rate of yield growth in their seed genetics. This suggests that other nonlinearities in yield trends are likely explained by weather and management rather than innovations in seed genetics.

1 | LITERATURE REVIEW

Crop science and economics have taken two approaches to estimating yield gains from genetics in seed varieties. Crop science has typically used experimental "heritage studies" to study genetic improvement. In contrast, economics has used either data from multiple years of yield trials or on-farm data on seed adoption and yields. In heritage studies, varieties released from multiple past years are grown together under the same experimental conditions in one plot to isolate the contribution of genetics from management and weather. Soybean heritage studies tend to find a rate of genetic improvement between 22 and 30 kg/ha per year from 1930 to 2008. The rate of improvement has not been uniform, as it increased in 1940 and after 1960. For example, Specht and Williams (1984) analyze cultivars from 1902 to 1978 and find an average growth rate of 18 kg/ha per year. A recent heritage study suggests this rate increased in the past three or four decades. Rincker et al. (2014) studies 80 years, from 1923 to 2008, and estimates the rate of genetic improvement to be around 22 kg/ha per year. They find that the rate of improvement was about 30 kg/ha per year from 1968 to 2008.

An advantage of heritage studies is that they control for one of the most important confounding factors: weather. Mourtzinis et al. (2015) finds that above-average temperatures depressed soybean yields in the United States by as much as 30% between 1994 and 2013. Some studies of corn yield find that weather has instead helped corn yield in the United States even more than changes in genetics have. Butler, Mueller, and Huybers (2018) find that about 25% of improvement in corn yield since 1981 can be attributed to favorable weather rather than technological innovation. Rizzo et al. (2022) study corn yield in Nebraska and finds that only 13% of growth is from genetics, while 48% is from climatic trends. This literature questions whether the robust growth in soybean yields in the US Midwest is due to favorable weather or changes in genetic technology.

Apart from being costly to run, heritage studies have the disadvantage of selecting seed varieties ex-post, which may only select the varieties that did the best in those years and bias estimates of yield gain from genetics upward. Using observational data reduces the cost of conducting the research at the expense of introducing potentially confounding variables like weather and management. The simplest way to estimate yield growth in soybeans with observational data is to estimate the unconditional time trend of soybean yields in a given location. For example, using USDA data and not correcting for any confounding factors, we can estimate that average soybean yields in Illinois grew at about 53 kg/ha (0.8 bu/acre) per year from 2000 to 2020 (Schnitkey et al. 2021). Two notable studies focus primarily on estimating the effect of adopting GE seeds on on-farm yield. Xu et al. (2013) uses county-level data from the Central Corn Belt over the years 1964 to 2010 and calculates an annual growth of rate of 31 kg/ha per year, which is similar to what Rincker et al. (2014) finds. They also find that GE adoption played a relatively minor role in soybean yield growth compared to corn.[1] Lusk et al. (2019) hypothesizes that weather may depress yields in observational studies, thus making it appear that adopting GE varieties has no yield impact. After introducing controls for weather, they find that adoption of GE corn correlates with a 17% increase in corn yield at the county level. Table 1 summarizes the genetic improvements for soybeans from three studies, only one of which is an observational study (Xu et al. 2013). Rincker et al. (2014) and Xu et al. (2013) appear to measure about the same rate of genetic improvement: 30 kg/ha per year from the 1960s to 2010.

While these studies have the advantage of examining the actual returns to technology on-farm, many confounding factors can bias these estimates. Most studies have robust weather controls, but data on other management decisions that may accompany seed adoption are usually lacking. Our approach joins other economics studies by using data from variety yield trials to take advantage of an experimental design that controls for management and also has multiple years of company varieties. Companies use these yield trials to test and advertise their new seeds, so analyzing the data provides a picture of how genetic technology changes year after year among the firms that participate. Since some varieties do not make it to market after being tested, these trials will not suffer from the same sample selection problem of a heritage study, which tends to select popular varieties that have already done well.

Thus far, there have been no analyses of variety trial data in economics focused on US soybeans despite their importance to US agriculture. However, several studies have analyzed variety trial data for wheat (Tack et al. 2015a), corn (Nolan and Santos 2012), sorghum (Tack et al. 2017), peanuts (Ramsey et al. 2021), and tobacco (Ramsey and Rejesus 2021). Of these studies, a few focus specifically on estimating the same basic parameter as the heritage studies: the average annual yield gain from changes in genetics. Most of these approaches do this by estimating variety-level intercepts in a

TABLE 1   Estimates of rates of yield gain from genetics in soybeans (kg/ha per year.)

Study	MG III growth	MG II growth	Time period	Location
Specht and Williams (1984)	17.2	29.1	1902–1977	Nebraska
	12.5, all MGs		1939–1977	Nebraska
Rincker et al. (2014)	22.8	23.1	1923–2008	US and Canada
	29.4	31.1	1968–2008	US and Canada
Xu et al. (2013)	30, all MGs		1964–2010	Central Corn Belt, US

Note: Maturity group II (MG II) and maturity group III (MG III) are groups of soybean varieties that thrive in different agro-ecological zones. In Illinois, MG II soybeans tend to be planted in the north of the state whereas MG III soybeans are planted in the center band.

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[1]The study even finds that GE adoption has a *negative* impact on soybean yields, which they theorize is because soybeans only have herbicide-tolerant traits, and insect-resistant traits are more conducive to yield increases. However, the study is using observational data where the precise variety and GE trait is not identified, and the authors note that further data are needed before making that conclusion.

regression model and then, in a second step, estimating how the variety intercepts are related to the year of release.

What often differs across studies is the assumption about the variety intercept. Tack et al. (2015a) assumes that the variety intercept is fixed. This approach has the advantage of allowing arbitrary correlation between the variety-fixed effects and the other covariates, which random effects cannot allow (Wooldridge 2010). However, other studies point out that fixed effects can be skewed by outliers in unbalanced panels and so model the variety intercept as a random draw from a distribution. In particular, Ramsey and Rejesus (2021) and Ramsey et al. (2021) model the random intercept with a Bayesian approach and afterward analyze how the variety intercepts are correlated to the year of their release. The disadvantage of this approach, as Nolan and Santos (2012) point out, is that varieties are often grown in specific locations by companies based on weather or soil, violating the random effects assumption of independence of the covariates. Other studies overcome this limitation by modeling not just random intercepts across varieties but also random slopes on weather variables, thus allowing the impact of a variety to differ across some covariates (Nolan and Santos 2012; Tack et al. 2017).

Our approach builds on this literature by recognizing that yield trials typically are designed to only make comparisons within one plot and year. Much like a heritage study, the yields of the varieties are only supposed to be compared if they are grown in the same location and year. In this circumstance, fixed effects and random effects estimation works by pooling yield observations for different varieties regardless of when or where they occur. If submitted varieties are tested for several years, this presents less of an issue since there will be enough variation to disentangle the genetics from the weather that might have occurred when it was planted.

However, the soybean yield trials at the University of Illinois have very few varieties that have been planted for more than one year. Rather than using an approach that imposes assumptions on the correlation between the variety's impact and the other covariates, we test an innovation of the fixed-effects approach, which can produce more robust analyses of yield change from genetic gain without imposing distributional assumptions. This study joins economic studies that use these data to not only analyze the contribution of genetics to yield gain but also the yield impact of GE traits (Nolan and Santos 2012; Shi et al. 2010; Shi et al. 2013) and the value of extension information (Lee and Moschini 2022).

2 | DATA

Our data set is collected from annual reports from the State Agricultural Experiment Station (SAES) soybean trials in Illinois from 1995 to 2020 (University of Illinois 2022).[2] During this period, 9430 varieties were tested from 206 companies at 18 locations, providing 85,761 yield records in total. The data include the variety name and yield, maturity date, lodging score, and height for each variety tested. Companies pay a flat fee per location to test a variety at the Illinois SAES and can choose a region to test the variety. Once that region is selected, the variety is planted at two to three locations in that region. Figure 1 shows all five regions in Illinois and where the three plots are located from 1995 to 2020.[3] The table below Figure 1 cross-tabulates where varieties were planted and their maturity group. The location where the variety is tested is highly correlated to the maturity group: Region 1 is usually used to test Maturity Group (MG) I and II, Region 2 tests MG II and III, etc. Maturity Groups II and III have the largest numbers of varieties in the trials since these groups grow the best in Illinois (Nafziger 2021).[4]

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[2]These reports are publicly available and can be accessed at http://vt.cropsci.illinois.edu/soybean.html.

[3]Two locations, Fenton and Harrisburg, are not included in the analysis because they are only used in a few years.

[4]More details about the variety trial setup can be found in Online Appendix S1. Each trial used a 30-inch row and a seeding rate of 166,000 ppa.
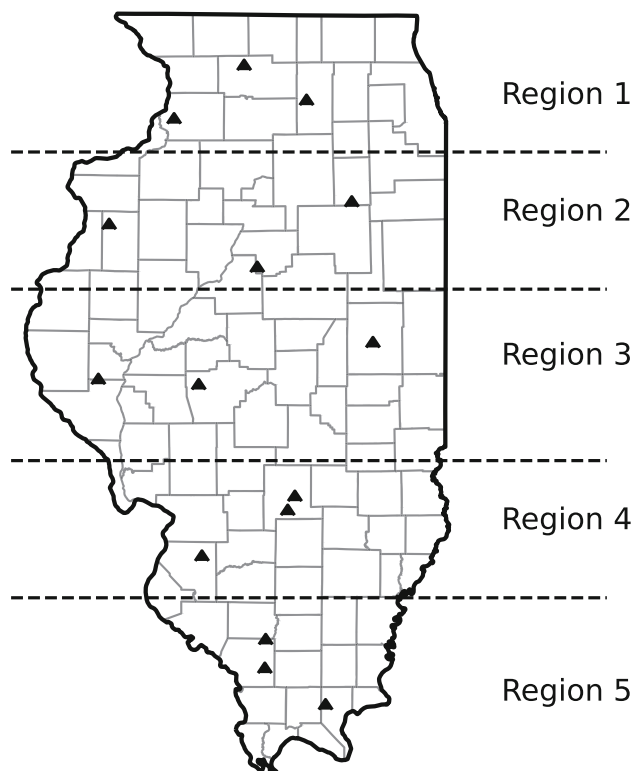
	Submissions in each maturity group				
	MG I	MG II	MG III	MG IV	MG V
Region 1	52	2071	408	0	0
Region 2	3	1252	1909	31	0
Region 3	3	486	2434	280	0
Region 4	1	54	1283	1314	0
Region 5	0	0	561	1341	107

FIGURE 1   Plots and Maturity Groups by Region.

The Illinois SAES yield trials test both public varieties (varieties developed by the University of Illinois or another public institution) and private varieties (varieties developed by private companies and submitted to the trials). During this period, three public varieties, Jack, Dwight, and Williams 82, were planted in at least one location every year to compare to private sector varieties. Jack is a cross of two public varieties, Fayette and Hardin, that was released in 1990 and is resistant to soybean cyst nematodes (SCN), one of the most widespread pests in US soybeans (Lee & Moschini 2022; Nickell et al. 1990). Dwight is a fourth-generation cross from Jack, released in 1997 (Nickell et al. 1998). Jack and Dwight belong to MG II, meaning they mature relatively earlier. Williams 82 is a strain of an older public variety, Williams, released in 1981. It was developed from Williams to be resistant to phytophthora rot though backcrossing disease resistance into Williams and belongs to
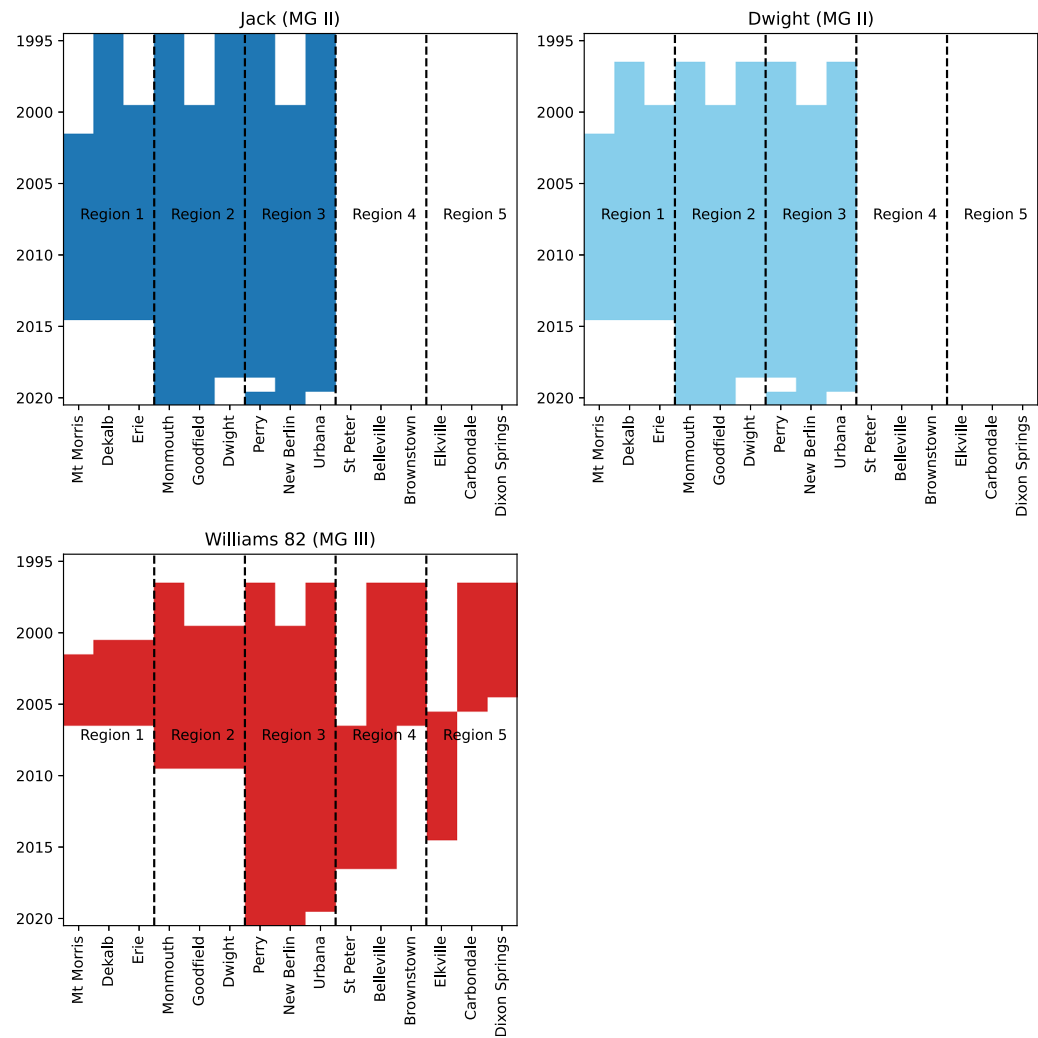
FIGURE 2 Public Variety Participation Across Locations. Each point on the x-axis is a testing location, and each filled-in block is where the public variety is planted. The locations are sorted from north to south, meaning locations closer to the graph's origin are in the north of Illinois.

MG III, meaning it matures relatively later (Bernard and Cremeens 1988). All three varieties were created and released at the University of Illinois SAES.

Figure 2 shows where Jack, Dwight, and Williams 82 were planted in each year. All three varieties were planted consistently at the Urbana and Perry plots in Region 3 since 1997. Because Jack and Dwight are MG II soybeans, they are also consistently tested in Region 2. Williams 82 is only consistently planted in Region 3 and inconsistently in other regions. Given these patterns, Jack and Dwight are a consistent comparison to MG II varieties submitted to Regions 2 and 3 and Williams 82 is a consistent comparison to MG III beans submitted to Region 3. As the table in Figure 1 shows, each public variety is consistently grown in the region where many of the submissions in their maturity group are grown.

Figure 3 plots the number of companies participating in the trials and the number of varieties submitted annually. Starting in 2005, participation in the Illinois SAES began to decrease. From 2005 to 2020, the number of varieties and companies dropped by more than 50%. There are two
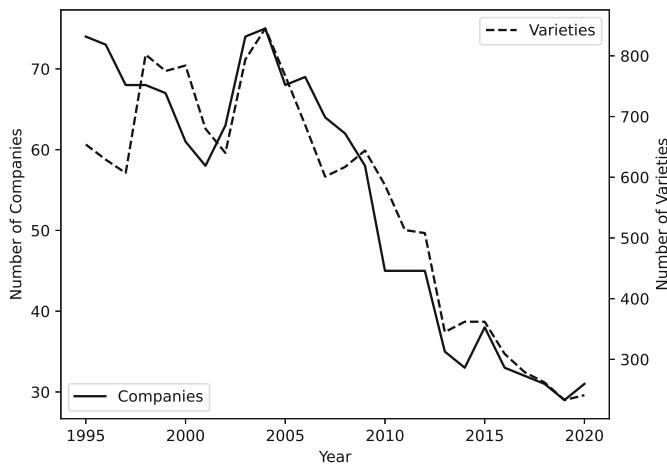
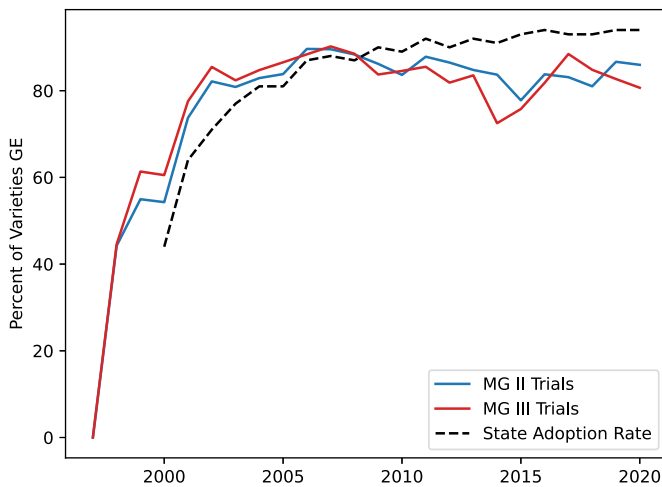**FIGURE 3**   Company participation and variety submissions.

FIGURE 4   GE adoption rates.

possible explanations for declining participation in the SAES. First, there are fewer seed companies today than in 2005 due to consolidation. Since the mid-1990s, waves of mergers and acquisitions have drastically reduced the number of seed companies (Howard, 2015; Shi et al., 2013). A second explanation may be that consolidation has reduced demand for SAES services. Historically, many seed companies engaged in breeding were too small to conduct extensive yield tests on their own. As companies have become larger, they are now more than capable of running their own trials and providing farmers with information from these trials. If farmers view yield information from SAES and the companies themselves as equivalent, then companies running their own experiments could crowd out demand for the SAES yield trials.

Figure 4 shows the percentage of varieties in the trials that are GE versus the percentage of acres planted to GE soybean seeds in Illinois (USDA ERS 2021). Until 2008, the adoption rate at the state level was lower than the percentage of GE varieties in the trials and experienced about the same growth rate. After 2008, the percentage of GE seeds in the trials decreased slightly. In 2020, the Illinois trials contained a slightly higher percentage of conventional seeds than those planted on farms
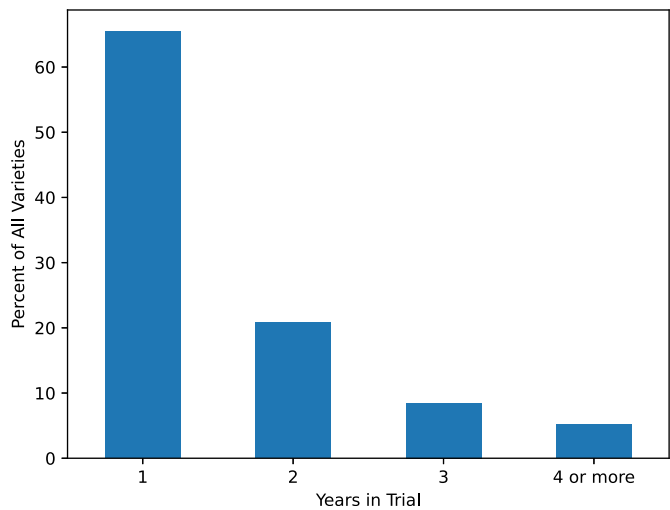
FIGURE 5 Number of years in the trials, private varieties.

in the state. One explanation is that several smaller, regional companies still participate in the Illinois trials and produce non-GE seeds. This means our data has a higher percentage of conventional seeds than the USDA survey on GE seeds (USDA ERS, 2021). Having more conventional seeds in the data allows us to analyze the contribution of GE and avoid the problems of selection bias pointed out by Shi et al. (2013).

In the Illinois soybean trials, companies tend to test a variety for only one year. Figure 5 shows that over 60% of the private varieties in our sample are only tested one year.[5] On average, each submission is tested at 4.47 locations and 1.74 regions across the entire sample, a number that stays relatively consistent over time. In nearly all cases, a variety has at least two yield observations in each year.[6]

3 | METHODOLOGY

The literature uses three broad categories of approaches to understand how much changes in seed technology have increased yield in a crop like soybeans: heritage studies, variety-fixed effects, and variety random effects. Approaches using multiple years of yield trial data tend to focus on addressing the issues of estimability and confoundedness. Estimability is an issue when variety-level impacts cannot be estimated because there are not enough repeated plantings of varieties. Confoundedness is an issue when the genetic contribution of each variety can be estimated but may be biased. Our approach contributes to this literature by pointing out that the yield of a check variety is an important control variable often omitted from these approaches. We implement this correction by differencing with the check variety, which is equivalent to including the check variety's yield as a control variable. Adding this control variable is a way to help address confoundedness in the case that varieties are estimable but may still be biased by the weather that occurs during their testing.

The heritage study design is the cleanest way to control for confounding variation. In the heritage study design, varieties are chosen from multiple years and grown together in an experimental

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[5]As a point of comparison to Tack et al. (2015a), the 5th, 25th, 50th, 75th, and 95th percentiles of the number of years a variety is tested in our sample is 1, 1, 1, 2, and 4 compared to 1, 2, 4, 7, and 13 for the Kansas Performance Tests wheat trials from 1985 to 2011.
[6]A variety having only one yield observation occurs in 0.5% of the varieties.

plot at one point in time. Once yield data are collected, yield is compared to the year the variety was released on the market. The rate of yield gain from genetics can be estimated by running a regression that predicts yield using the year of release. In other words, heritage studies predict yield y_i of variety i with the year of release YoR_i:

$$y_i = \tau_0 + \tau YoR_i + \epsilon_i. \tag{1}$$

This regression model draws a linear trend line through the yield measurements across the year of release (YoR_i), described by the y-intercept τ_0 and slope τ. The coefficient τ is often the goal of estimation and is interpreted as a measure of the speed of innovation in soybean genetic yield potential. To consider nonlinearities, models are either fitted with squared and cubed terms or a "breakpoint" is chosen for the line. Since all varieties are grown in the same location and year, comparing yields would contain less confounding variation than on-farm data. Nevertheless, heritage studies are expensive and can only test a small subset of the varieties that have existed over time.

Experiment station yield trials, like heritage study trials, are designed to compare the yields of varieties within the same location and year. However, unlike heritage studies, experiment station trials contain hundreds of submissions that may not be selected for a heritage study. To understand how we would estimate yield change from genetics in the experiment station yield trials, first assume that the yield of variety i at location j in year t can be expressed as:

$$y_{ijt} = \beta_i + \alpha_j + \gamma_{jt} + \epsilon_{ijt} \tag{2}$$

where β_i is the effect of genetics, α_j is the permanent effect of the location (e.g., soil type), and γ_{jt} is the effect of time-varying shocks to location j (e.g., weather and changes in management). In on-farm data, the choice of a variety i and unobserved decisions ε_{ijt} are likely correlated, which makes an estimate of β_i potentially biased.

In an experiment station trial, we know that the choice of growing variety i is likely to be less correlated with management or location since it was grown as part of an experimental design. Thus, another approach to estimating the average yield gain over time from genetics (τ) is with a two-step method. In the first stage, the variety-fixed effects are estimated with a model like the following:

$$y_{ijt} = \beta_i + \mu_j + \upsilon Z_{jt} + \epsilon_{ijt} \tag{3}$$

where μ_j are the experimental plot-fixed effects, Z_{jt} is a vector of time-varying location controls (usually temperature and precipitation), and β_i are the variety intercepts for each i. In this approach, the estimates $\widehat{\beta}_i$ are equivalent to an average across the pooled yield data from each i after the location and weather impacts are removed. When the coefficients $\widehat{\beta}_i$ are recovered, the second stage is to draw a linear trend line through the data with the year of release:

$$\widehat{\beta}_i = \tau_0 + \tau YoR_i + \epsilon_i. \tag{4}$$

Alternatively, with a long enough time frame, it can be advantageous to estimate fixed effects for each level of YoR_i to allow the rate of change to be different in each year.

An issue with the above approach is that many varieties in the Illinois trials are only grown in one year. Since companies submit to a region that contains three locations in the state, a variety submitted in only one year in the Illinois trials has only two to three observations, all in different plots. In this case, $\widehat{\beta}_i$ averages these three observations across the plots after the observed characteristics Z_{jt} are netted out. If there is not sufficient variation in soil and weather in that one year, the fixed-effect estimate of β_i will be hard to separate from the plot-specific variation Z_{jt} that occurred when it was tested.

If a lack of yield observations prevents β_i from being estimated, a mixed model approach can estimate β_i as a random effect. Specifically, mixed and Bayesian methods model β_i as a draw from a prior distribution (e.g., a normal distribution). This variety random effects (VRE) approach makes it possible to estimate β_i with more limited data and will shrink estimates toward an average instead of estimating β_i solely from yield observations that may have occurred in unusual circumstances. In other words, this approach borrows variation from other β_i to help estimate the intercepts for varieties with fewer observations (Ramsey and Rejesus 2021). The disadvantage of this approach is that it requires specifying a prior distribution and making the assumption that β_i, as part of the error term, is not correlated to any other covariate in the model (Antonakis et al. 2021; Wooldridge 2010). If weather shocks coincide with certain varieties being planted, this would violate that independence assumption (Nolan and Santos 2012).

Our approach is motivated by the original design of the experiment station trials, which only makes comparisons within locations and years. In the variety-fixed-effects approach, the existence of a check variety is often only used to be an excluded category, essentially adjusting the $\widehat{\beta}_i$ so that they are interpreted as the average yield difference between each i and the check variety. However, in the trial design, the check variety is grown specifically to be compared to other varieties in that plot and year and not pooled across time and space. The check variety helps identify β_i by taking differences within the same plot and year. Call the check variety $i = 0$, which has yield in year t at location j:

$$y_{0jt} = \beta_0 + \alpha_j + \gamma_{jt} + \epsilon_{0jt}. \tag{5}$$

Subtracting Equation (5) from Equation (2) yields:

$$\begin{aligned} \Delta y_{ijt} &= y_{ijt} - y_{0jt} \\ &= \beta_i - \beta_0 + \epsilon_{ijt} - \epsilon_{0jt} \\ &= -\beta_0 + \beta_i + \Delta\epsilon_{ijt} \end{aligned}$$

which is β_i plus a constant term (β_0) and the difference in yield shocks for the private and base varieties ($\Delta\epsilon_{ijt}$). The linear impacts of management are gone from the yield difference since both i and 0 were exposed to the same conditions. Using the difference between y_{ijt} and y_{0jt} as the outcome is equivalent to including y_{0jt} as a covariate that has a coefficient fixed to 1. We can apply any of the above methods, including the VFE approach, but with an additional control variable that nets out variation in y_{0jt} that may shift the estimation of β_i. The term $\Delta\epsilon_{ijt}$ represents nonlinear reactions between the variety and its environment, usually called "genotype-by-environment" interactions ($G \times E$) (Sudarić et al. 2006). If the genetics in each variety interact with the environment, then there will be variation in Δy_{ijt} unrelated to genetic gain. We include variety control variables X_{ijt}, location control variables Z_{jt}, and location-fixed effects μ_j to control these confounding interactions. With the inclusion of control variables, the estimating equation becomes:

$$\Delta y_{ijt} = \mu_j + \tau YoR_i + \delta X_{ijt} + \upsilon Z_{jt} + \Delta\epsilon_{ijt}. \tag{6}$$

In this equation, YoR_i is the first year the variety i is in the trial, X_{ijt} is a vector of control variables for the private variety, which includes the height, maturity week, seed treatments, and lodging score of variety i and the base variety $i = 0$. The vector Z_{jt} contains the location-specific controls, growing season rainfall and temperature, and planting date for that plot. The location-fixed effects μ_j allow the base variety coefficient β_0 to differ across locations j.

The coefficient of interest in Equation (6) is τ, the average annual yield rate gain from genetics. Rather than doing two steps, this approach draws a trend line through the residual of Δy_{ijt} with the understanding that the residual only measures genetic gain. To more precisely estimate the residual's

relationship to genetic gain, we estimate a second version of the model that is more similar to the variety-fixed-effects approach to understand the impact of using the check variety's yield.

We choose to first fit the data with a linear time trend to compare our results to other studies in the literature, such as Rincker et al. (2014) and Xu et al. (2013). We also estimate a version of the model with year-of-release-fixed effects, τ_i, which does not require the trend to be linear. We also compare our method to three alternative specifications: a linear time trend with no controls ("Unadjusted"), a linear time trend with controls ("Unadjusted with Controls"), and the variety-fixed-effects approach ("Variety FE"). We use the same controls for the last two models as our main specification and use the three public varieties as the "base category" for the variety-fixed-effects approach.

4 | RESULTS

Figure 6 shows the difference in yields (Δy_{ijt}) averaged by year for MG II and MG III in all locations. We use Jack and Dwight as the check variety for MG II and Williams 82 as the check variety for MG
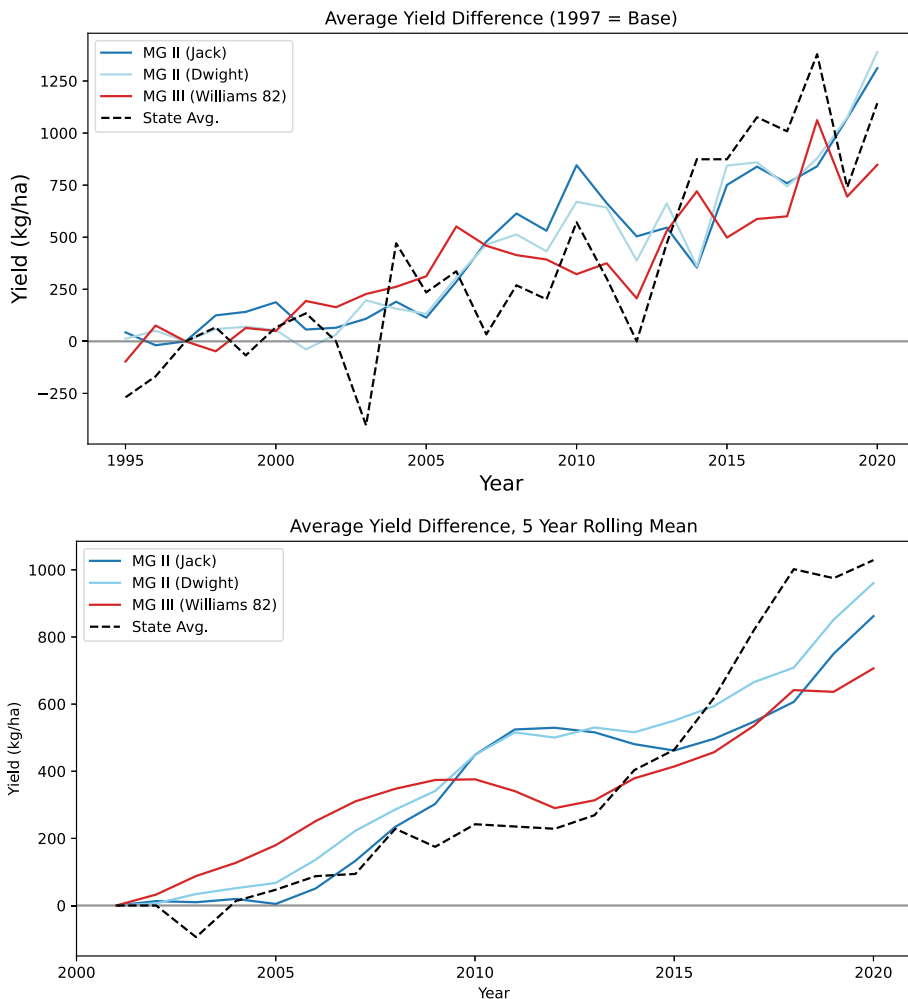

FIGURE 6 Average yield differences over time. All yield differences are relative to the 1997 or 2001 average. State average is reported by NASS.

III. We also show the average soybean yield in Illinois using data from the USDA as a black, dashed line. The top graph shows the annual average relative to each group's 1997 average, and the bottom graph shows the five-year average relative to each group's 2001 average. Yield differences are increasing throughout the period, though the increases are not constant. The state average does not increase meaningfully relative to 1997 until after 2012.

The bottom graph of Figure 6 shows these same data series but as a five-year rolling average. The state average keeps pace with the three lines until about 2013, when it grows much faster than any of the yield differences. This suggests that genetic improvement has fueled some of the yield growth in Illinois from 1997 to 2012 but may have played less of a role from 2013 onward. This is consistent with Butler et al. (2018) who find that favorable weather after 2010 drove a significant portion of corn yield growth in the Corn Belt.

In the following sections, we first present our main results: the average annual gain in soybean yield from genetics as measured by our approach. We measure this by estimating a linear time trend and then examining fixed effects for each year of release, which allows the trend to be nonlinear. We then analyze the influence of GE varieties by allowing GE and conventional varieties to have different trends. Finally, we compare our estimates to the variety fixed effects model and a combined approach where we estimate variety fixed effects while using the check variety's yield as a control variable.

4.1 | Estimates of yield gain from genetics

In the following analyses, we estimate Equation (6) and compare this to a simple time trend model with and without controls. Details on the control variables and their impact on estimation is discussed in detail in Online Appendix S1. Table 2 shows estimates of a linear time trend through the data with and without the check variety adjustment. Without subtracting the public variety's yield, our genetic improvement estimates would contain confounding weather and soil factors. Without using controls, MG II and MG III gain between 47 and 54 kg/ha (0.71 and 0.81 bu/acre) per year.

TABLE 2 Yield Gain from Genetics With and Without Differencing Adjustment, Kg/Ha.

	Maturity group II			
	Unadj. (1)	Unadj., Controls (2)	Differenced Jack (3)	Differenced Dwight (4)
Year Trend	47.784***	29.735***	25.226***	26.413***
	(0.697)	(7.936)	(3.534)	(3.069)
Observations	23,207	23,207	23,207	23,207
Adjusted R^2	0.168	0.534	0.449	0.455
	Maturity Group III			
	Unadj. (1)	Unadj., Controls (2)	Differenced Williams 82 (3)	
Year Trend	54.412***	35.926***	25.664***	
	(0.669)	(4.586)	(4.073)	
Observations	27,233	27,233	27,233	
Adjusted R^2	0.196	0.622	0.375	

Note: *$p < 0.1$; **$p < 0.05$; ***$p < 0.01$. Standard errors are clustered at the location level. Variety Controls: height of base and private variety, lodging score of base and private variety, maturity week of base and private variety, seed treatment, planting week, and SCN resistance. Weather Controls: monthly rainfall, monthly rainfall squared, mean monthly temperature, max monthly temperature, min monthly temperature (May, June, July, August, September).
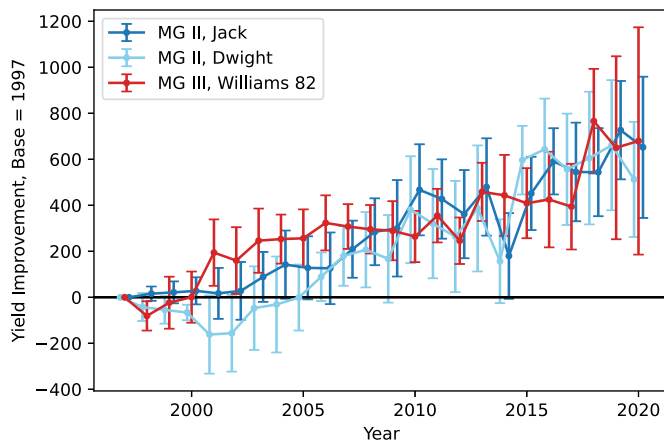
FIGURE 7 Yield improvements from genetics, year FE.

This is similar to the unconditional yield gain of Illinois on average, 53 kg/ha (0.8 bu/acre), as calculated from USDA estimates of the state average yield of soybeans (Schnitkey et al., 2021). After including controls, the linear time trend is significantly reduced: about 29 kg/ha for MG II and around 35 kg/ha (0.39 bu/acre) for MG III. This is much closer to the Rincker et al. (2014) estimates and demonstrates that not controlling for confounding factors during this period would have considerably overstated yield growth due to genetic change. Much like Butler et al. (2018) finds for corn, we find that confounding variables like weather make genetic yield growth in soybeans appear larger than they are in reality.

After our differencing adjustment, the rate of yield gain for MG III decreases to 25–26 kg/ha. Figure 7 shows the year-of-release-fixed-effects version of our model, which does not require the rate of gain to be constant across time. Both MG II and MG III grew at a roughly linear rate but experienced slowdowns at different times. For example, MG III (the red line) begins to stall in 2008 before picking up again after 2015. In contrast, MG II (the blue lines) has slower growth at first but grows consistently starting in 2010.[7]

4.2 | Conventional and GE varieties

A commonly studied question is whether GE varieties have higher yields than conventional varieties. Xu et al. (2013) finds that GE soybean varieties had lower yields and attributed this to yield drag in the genetics. We test whether this is true in our data by examining whether there are statistically different time trends for GE soybeans compared to conventional soybeans. Table 3 shows the model results where GE varieties have their own intercept and slope and Figure 8 shows year-of-release fixed effects for GE and conventional. For MG II, whether adjusted by Dwight or Jack, GE varieties have a higher growth rate than conventional. GE varieties in these groups have a more than 50% higher yield trend than conventional varieties. Interestingly, GE varieties did not double the growth in MG III. This appears to be larger than what Lusk et al. (2019) finds for GE corn (about 17% contribution to growth). This is likely driven by companies embedding their best genetics with GE traits since the herbicide-resistant traits put into soybeans do not necessarily impact yield (Shi et al. 2013). Instead, herbicide-resistant traits are most likely to reduce cost, a factor not captured here since all varieties experience the same management regime.

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[7]The year 2014 is one exception: the yield gain for MG II is smaller in only that year, whether adjusted by Dwight or Jack.

T A B L E 3 Yield Regression with GE Interactions, Kg/Ha.

	MG II		MG III
	Differenced, Jack (1)	Differenced Dwight (2)	Differenced, Williams 82 (3)
Year Trend	13.207***	13.546***	15.941***
	(3.231)	(3.805)	(3.551)
Year Trend X GE	23.104***	19.172***	13.337***
	(4.497)	(3.785)	(3.798)
Observations	23,207	23,207	27,233
Adjusted R^2	0.467	0.458	0.385

Note: $*p < 0.1$; $**p < 0.05$; $***p < 0.01$. Standard errors are clustered at the location level. Variety Controls: height of base and private variety, lodging score of base and private variety, maturity week of base and private variety, seed treatment, planting week, and SCN resistance. Weather Controls: monthly rainfall, monthly rainfall squared, mean monthly temperature, max monthly temperature, min monthly temperature (May, June, July, August, September).
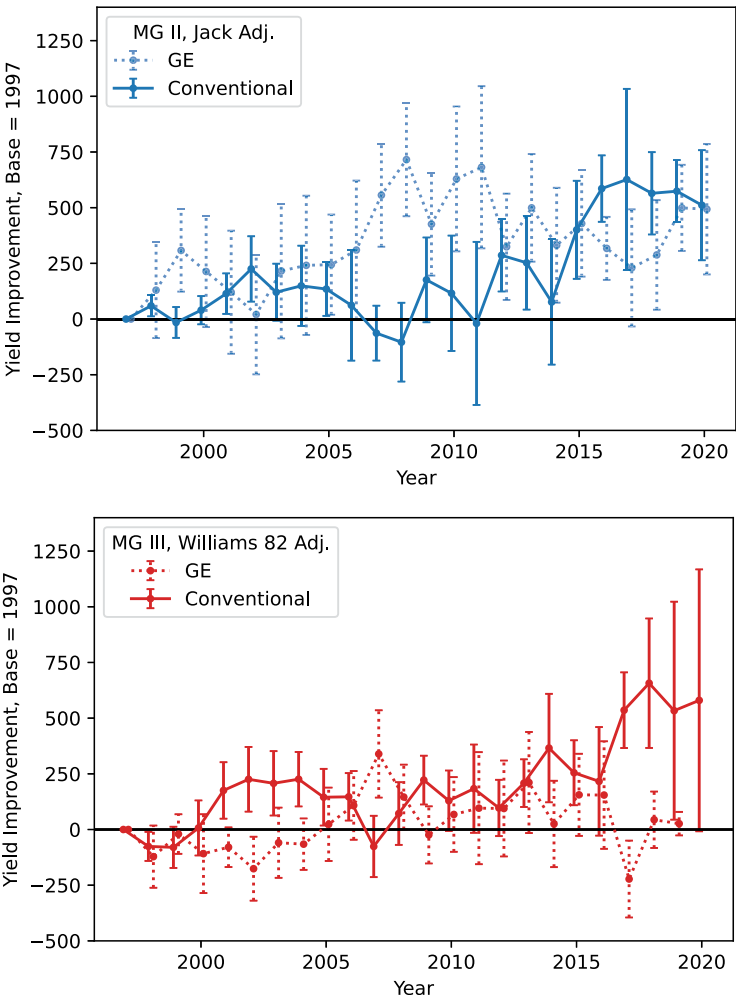

F I G U R E 8 GE versus conventional, Year FE.

In Figure 8, it is more apparent that the GE contribution to yield is not consistent. In some years, the GE effect for MG II is statistically insignificant while the conventional effect explains all of the growth in that year. In other years, GE drove all of the yield increases and conventional varieties explained none of the increase. For MG III, the conventional effect usually explains all the growth, and GE hardly any. At the very least, the GE impact is just as high in many years as the conventional impact. This suggests that, in contrast to what Shi et al. (2013) finds, the quality of the underlying genetics of many varieties is roughly the same whether the variety has GE traits or not.

4.3 | Variety-fixed-effects method

Next, we compare our method to the variety fixed effects (VFE) approach used in other studies. In the VFE method, β_i are estimated with cross-sectional and temporal variation in yield tests of that variety. After estimating these fixed effects, we estimate a linear regression of the year first tested in the trial on the variety's fixed effect as in Equation (1). More details on this estimation and some robustness checks can be found in Online Appendix B.2. We also estimate a simple random-effects version of this model in Online Appendix B.3.

Table 4 compares our results in Table 2 to the unadjusted model with controls and the variety fixed effects approach without using the check variety control variable. The rate of growth measured by the VFE is closer to the unadjusted model in the case of MG II relative to Jack and MG III relative to Williams 82. The VFE method calculates genetic improvement in yield as about 31 kg/ha for MG II using Jack as the check variety and 23 kg/ha using Dwight. The estimated genetic improvement in MG III is 28 kg/ha, more than our method but less than the unadjusted method with controls.

T A B L E 4   Comparison of Yield Regressions Using Different Methods.

	Maturity group II		
	Unadj., controls	**Differenced, Jack**	**Variety FE, Jack**
Year Trend	29.735***	25.226***	31.424***
	(7.936)	(3.534)	(0.989)
Observations	23,207	23,207	2814
Adjusted R^2	0.534	0.449	0.264
		Differenced, Dwight	**Variety FE, Dwight**
Year Trend		26.413***	31.463***
		(3.069)	(0.989)
Observations		23,207	2814
Adjusted R^2		0.455	0.265
	Maturity Group III		
	Unadj., Controls	**Differenced, Williams 82**	**Variety FE, Williams 82**
Year Trend	35.926***	25.664***	31.240***
	(4.585)	(4.073)	(0.864)
Observations	27,233	27,233	3257
Adjusted R^2	0.622	0.375	0.286

Note: *$p < 0.1$; **$p < 0.05$; ***$p < 0.01$. Standard errors are clustered at the location level. Variety Controls: height of base and private variety, lodging score of base and private variety, maturity week of base and private variety, seed treatment, planting week, and SCN resistance. Weather Controls: monthly rainfall, monthly rainfall squared, mean monthly temperature, max monthly temperature, min monthly temperature (May, June, July, August, September).
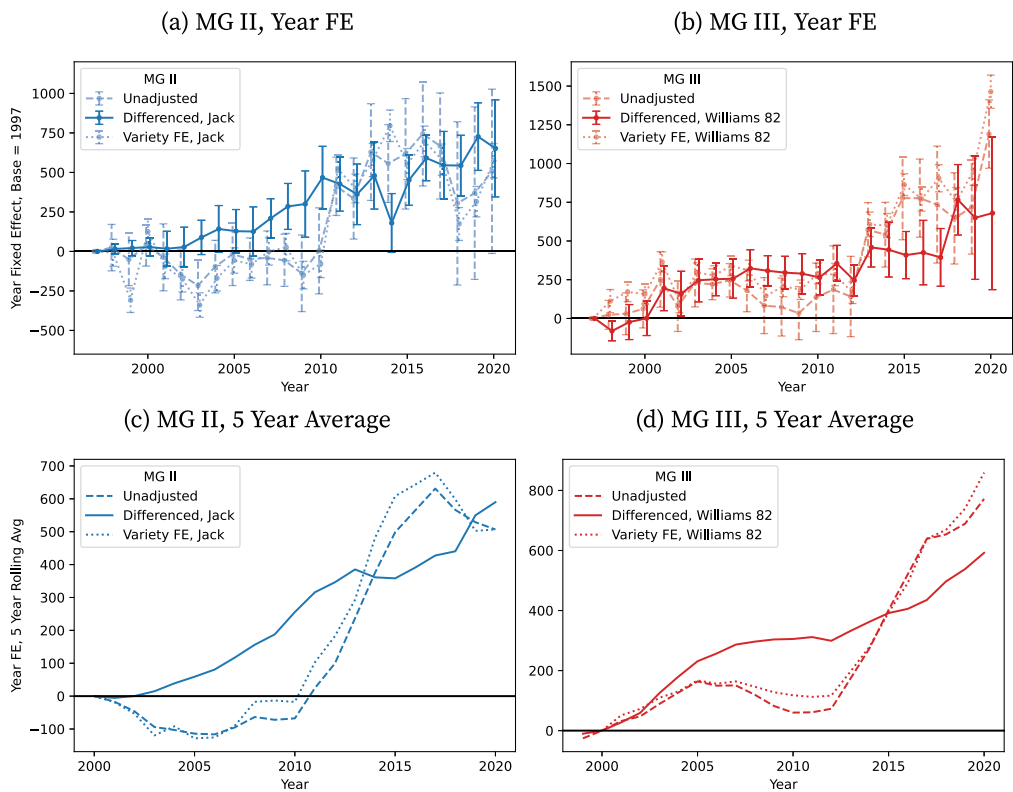
(a) MG II, Year FE   (b) MG III, Year FE

(c) MG II, 5 Year Average   (d) MG III, 5 Year Average

FIGURE 9   Comparison of three methods across years.

The top two panels of Figure 9 show the year-of-release fixed effects for all three methods. The main difference between our method and the other two methods is that our method estimates a roughly linear growth rate for genetics, while the other two methods suggest little growth before 2010 and high growth after 2010. The VFE and the unconditional method predict no genetic progress in MG II before 2010 and slightly slower growth in MG III before 2010.

The bottom two panels of Figure 9 show each model's rolling five-year averages of the year-of-release fixed effects. Both models predict very high growth rates after 2010, a period where Butler et al. (2018) finds that weather was a strong driver of corn yields in the Corn Belt. In contrast, our model using yield differences suggests a more linear growth rate in MG II (panel c) and MG III (panel d). While in Table 4 the linear trends of most of the models may appear similar, it is clearer in these plots that the unadjusted and VFE method gives trends that are more nonlinear than the differencing method. In general, the unadjusted and VFE methods follow each other closely.

To understand the impact of including the check variety control on estimation, we can compare the variety-fixed-effects approach with and without this variable. In this version, we allow the coefficient on the check variety's yield to vary and not be fixed to 1 by simply including it as a control variable in the regression model. In Online Appendix B.1, we show that allowing the check variety's coefficient to vary does not significantly impact the estimation of the trends.

Figure 10 plots the year-of-release fixed effects for yield improvement from genetics for our main model, the VFE model, and the VFE model with the check variety yield control. We use Jack as the check variety for MG II and Williams 82 as the check variety for MG III. After adding the control, the estimates of the VFE model become more similar to those of our main model, except that they have smaller standard errors. Rather than predicting no yield gain from 2000 to 2010, the VFE
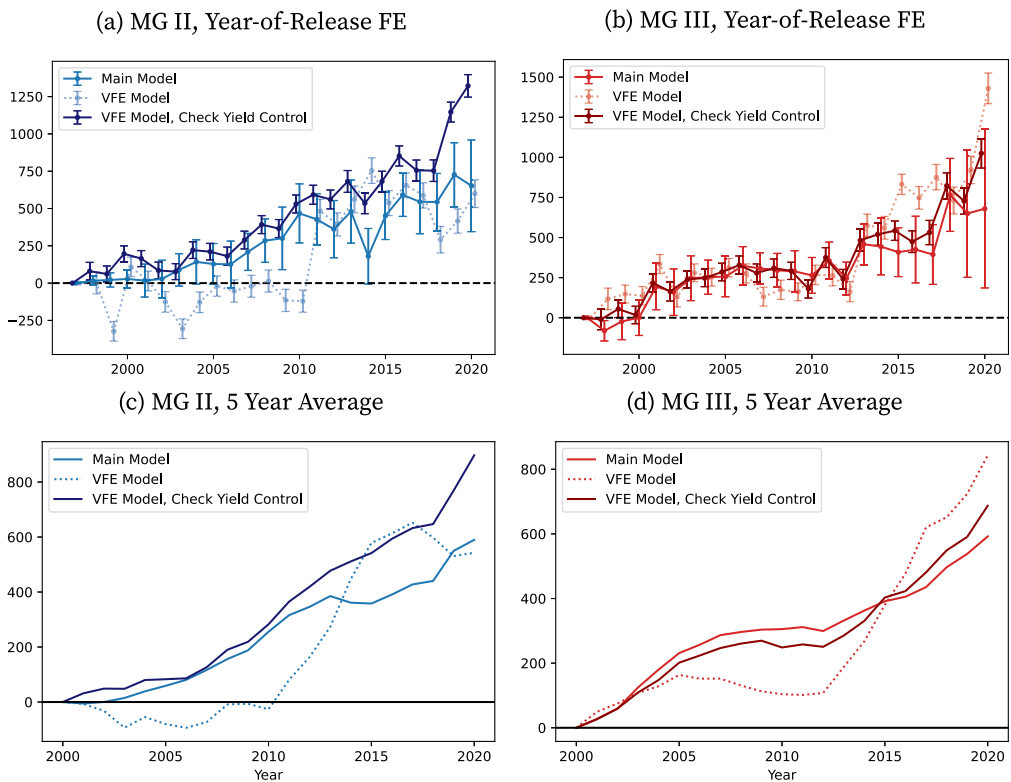
FIGURE 10   Yield changes with VFE model, with and without check variety control.

model now predicts yield gains similar to the main model in both maturity groups. Our main model estimates these fixed effects directly from the variation in Δy_{ijt}, which may make the main model estimates more noisy than the two-step approach of estimating year trends from a first-stage estimate of $\widehat{\beta}_i$.

In MG II, the estimates only begin to diverge when the VFE model without the control finds larger yield gains. This is around the same time that Butler et al. (2018) finds that weather drove yield trends for corn and where Figure 6 shows average soybean yields in Illinois increasing at a higher rate. The result is that the VFE model with the control predicts a higher rate of yield gain than the main model, especially in the last two years. A linear trend through the amended VFE model would predict an average gain of 42 kg/ha each year or 35 kg/ha when the last two years are excluded. Thus, the main model gives a more conservative estimate of yield gain from genetics in this sample and the rate of gain in MG II could be somewhere between 25 and 35 kg/ha per year. In MG III, adding the yield of Williams 82 as a control variable brings the impacts even closer to the main model. In all years, the year-of-release fixed effects in the main model are statistically indistinguishable from the VFE model with the control variable. In contrast, the VFE model without the control variable predicts lower yield growth between 2005 and 2010 and higher yield growth between 2010 and 2020.

In Online Appendix S3, we conduct robustness checks on our results. First, one shortcoming of these data is that participation in the Illinois yield trials is inconsistent over time. Our estimates may be impacted by company attrition if certain companies drop out of the trials (e.g., ones that produce mainly GE varieties). We examine the influence of company attrition by analyzing a subset of the data with a balanced panel of companies. In this subset of the data, we find that GE varieties'

contribution to yield growth is much lower and even insignificant. We also test the robustness of the results by limiting the sample to regions 2 and 3 where our check varieties were planted in every year. Our results in this case are fundamentally unchanged. Finally, we examine the impacts of using the year of the trial instead of the first year the variety is tested. Using this year measure, the trends appear a littler larger but more unstable.

5 | CONCLUSION

The purpose of our study is to estimate yield gain from genetic change using multiple years of university yield trial data. Using these yield trial data, we preserve the advantages of an experimental design while allowing a much broader examination of genetic improvement than many heritage studies in the crop sciences literature. However, our approach differs from previous studies using these data by using a check variety's yield as a control variable to better align estimation with the design of the experimental plots. Looking at soybean trials in Illinois, our estimates of genetic improvement are a growth rate of about 25–26 kg/ha (0.37–0.4 bu/acre) or 0.7% per year. Our results suggest that GE varieties did positively contribute to genetic improvement, though in many years, conventional varieties contribute just as much as GE varieties do. Comparing other methods from the economics literature, we find that estimating variety fixed effects without our controls leads to much more nonlinear estimates of genetic improvement that may result from weather interacting with genetics, especially after 2010. However, by adding the check variety's yield as a control variable, we find less difference between our main model and what the variety fixed effect approach predicts. This suggests that the check variety's yield is an important control variable in future studies of yield trial data that aim to understand how genetics contribute to yield gain.

These findings are highly relevant to the debate surrounding biofuels and climate change. Increasing demand for renewable bio-based diesel (especially renewable diesel) is likely to increase demand for soybeans, which can ignite another "food versus fuel" debate if supply does not increase to meet demand (Tenenbaum 2008). Understanding the role of genetic change in yield growth is essential for understanding to what extent company innovation in genetics is helping to keep prices stable. Yield growth is also a meaningful way to reduce the contribution of agriculture to climate change since a large portion of its role in climate change is due to extensive land use (Ortiz-Bobea and Tack 2018). However, recent increases in yield growth in Illinois are not fully explained by genetic improvement and may have been strongly influenced by favorable weather (Butler et al. 2018). Nevertheless, our results here suggest an important role for genetic improvement in yield trends, complementing recent work like Taylor and Schlenker (2023), which emphasizes the role of environmental factors like CO_2 fertilization in yield trends.

The role of GE in yield improvement is less clear. While Xu et al. (2013) finds evidence of a limited role for GE in soybean yields, we find that GE varieties either outperformed or performed the same as conventional varieties. The challenge of understanding the exact contribution of GE to yield growth continues to be the fewer conventional varieties entering the market. This is the benefit and cost of using Illinois yield trial data. On one hand, these data have a larger number of conventional varieties, which provides more variation to estimate the true effect of GE varieties on yield growth. On the other hand, these data may have more conventional varieties because fewer companies are participating in university yield trials. To increase the usefulness of yield trial data, more research is also needed to understand why participation in university yield trials by private companies is declining. By understanding how firms participate in these trials, we can enhance the usefulness of these data for future economic analyses.

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