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Transgenic crops, production risk, and agrobiodiversity

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ZEF-Discussion Papers on Development Policy No. 186

Vijesh Krishna, Matin Qaim and David Zilberman

Transgenic Crops, Production Risk, and Agrobiodiversity

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Abstract

Do transgenic crops cause agrobiodiversity erosion? We hypothesize that they increase productivity and reduce production risk and may therefore reduce farmer demand for on-farm varietal diversity, especially when only a few transgenic varieties are available. We also hypothesize that varietal diversity can be preserved when more transgenic varieties are supplied. These hypotheses are tested and confirmed with panel data for the case of transgenic cotton in India. Cotton varietal diversity in India, with of over 90% adoption of transgenic technology, is now at the same level than it was before the introduction of this technology. Some policy implications are discussed.

Keywords: varietal diversity, biotechnology, smallholder farmers, production risk, India

JEL classification: D24, D81, O13, O44, Q12, Q16, Q57

1. Introduction

This study analyzes the impact of transgenic crop adoption on agricultural production risk and agrobiodiversity. The genetic erosion hypothesis suggests that global biodiversity is affected by various anthropogenic stresses (Van Straalen and Timmermans, 2002) that have caused serious biodiversity loss over the past few decades (Millennium Ecosystem Assessment, 2005). This also applies to agrobiodiversity, comprising the diversity of species used in agricultural production and varietal diversity within those species. One of the major factors that have influenced agrobiodiversity over the last 100 years is plant breeding, coupled with the intensification of agricultural systems. Farmer adoption of a few genetically uniform high-yielding varieties (HYVs) has the potential to erode landraces and reduce the diversity of indigenous crop varieties (Harlan, 1975; Brush, 2000). Modern high-yielding varieties may be attractive for farmers from a short-term profit maximizing perspective, but it is argued that a narrower genetic base may increase production risk and disrupt the stability and resilience of farming systems in the long run (Cooper, Engels and Frison, 1994; Tripp, 1996). Indeed, there is broad evidence that varietal diversity has a natural insurance function (Baumgärtner and Quaas, 2010; Di Falco and Chavas, 2009). Against this background, some argue that the Green Revolution (i.e., the introduction of HYVs of wheat and rice since the late 1960s in Asia and other parts of the developing world) has contributed to serious ecological and social problems in the small farm sector (Shiva 1991).¹ And there are widespread concerns that the loss of agrobiodiversity may be further exacerbated through the introduction of new breeding technologies, such as transgenic crops (Holt-Gimenez and Altieri, 2013).

Several recent studies have analyzed the impact of transgenic crops on agricultural productivity and income, concluding that farmers can benefit significantly from adopting these crops (Qaim, 2009; Carpenter, 2010). This also applies to smallholder farmers in developing countries (Croft et al., 2007; Huang et al., 2010; Subramanian and Qaim, 2010; Qaim and Kouser, 2013). There are also studies that have analyzed potential biodiversity impacts occurring through outcrossing of transgenes into wild relatives of domesticated

¹ Smale (1997) showed that the negative impacts of the Green Revolution on agrobiodiversity are actually smaller than often assumed.

crops (Bellon and Berthaud, 2004; Raven, 2010). While certain risks for biodiversity exist, Raven (2010) concludes that these do not differ between transgenic and conventionally bred crops. However, to the best of our knowledge, the impact of transgenic technology on the diversity of crop varieties grown by farmers has never been studied empirically in developing countries.²

There are at least three aspects that make transgenic crops different from HYVs of the Green Revolution, so previous results on the impact of breeding technologies on varietal diversity cannot simply be extrapolated. First, many transgenic technologies involve crop resistance to biotic and abiotic stress factors. Thus, transgenic crops may not only be higher yielding but also risk reducing (Crost and Shankar, 2008). Adoption of stress-resistant transgenic crops may reduce demand for the insurance function of agrobiodiversity, potentially resulting in accelerated loss of varietal diversity. Second, the product of transgenic breeding is not only one single new crop variety. Rather, transgenic technology allows the introduction of desirable genes and traits into many existing varieties. Thus, it may be easier to preserve varietal diversity (Zilberman, Ameden and Qaim, 2007). Third, transgenic crops are primarily commercialized by private companies, and they are also associated with new regulations, including intellectual property rights (IPRs) and complex biosafety approval procedures. Such institutional factors may also influence the technology's impacts on varietal diversity (Qaim, Yarkin, Zilberman, 2005).

Here, we use data from the Indian cotton sector to analyze linkages between transgenic technology, production risk, institutional factors, and varietal diversity. Transgenic cotton with inbuilt insect resistance was first commercialized in India in 2002. Since then, it has been adopted by several million smallholder farmers on over 90% of the national cotton area (James, 2012). We use four rounds of panel data that we collected between 2002 and 2008. Hence, we capture the early diffusion phase of transgenic cotton in India with relatively low adoption, as well as later diffusion phases with high adoption rates. The data also provide a quasi-experimental setting for the analysis of interesting institutional and policy aspects. In the first few years of technology diffusion, only a small number of transgenic cotton varieties had received approval by the national biosafety authorities.

² In an ex ante study, Kolady and Lesser (2012) have analyzed the possible effects of transgenic eggplant technology on varietal diversity in India, but this technology was not yet commercially released in the country, so that ex post data are not available.

Hence, only these few approved transgenic varieties were supplied in the seed market, alongside a much larger number of conventional cotton varieties (Qaim et al., 2006; Smale et al., 2009). In later years, additional transgenic varieties were approved and marketed by several seed companies. Since 2006, the number of transgenic varieties supplied in the market has increased manifold (Tripp, 2009; Choudhary and Gaur, 2010).

The remaining part of this paper is organized as follows. In the next section, we develop a conceptual framework and derive concrete research hypotheses. Details of the situation in India and the data collected from cotton farms are presented in section 3. In section 4, we describe the empirical methods, and in section 5 we present and discuss the estimation results. Section 6 concludes with some broader policy implications.

2. Conceptual Framework and Research Hypotheses

In traditional farming with little impact of modern technology, smallholders often grow several varieties of the same crop, that is, they have a relatively high level of on-farm varietal diversity. Such diversity is associated with societal benefits, because the option value of a broad base of plant genetic resources is preserved (Smale, 2006). But on-farm varietal diversity also has private benefit components. One can discern two possible functions that varietal diversity may offer to farmers, first, an insurance function, and second, a productivity enhancement function (Di Falco and Chavas, 2009).

The insurance function is related to production risks due to pests, diseases, and erratic weather conditions. Different varieties have different levels of susceptibility to such stresses; hence growing several varieties tends to reduce covariate risks. In this situation, when a new HYV is introduced it may be adopted only partially, especially in the absence of formal insurance markets (Baumgärtner and Quaas, 2010). Farmers who seek to avoid downside income risk may choose to include lower-productive but less-vulnerable traditional varieties in their varietal portfolio, even though full adoption of the HYV might be more profitable on average (Smale, Just and Leathers, 1994). The productivity enhancement function of varietal diversity implies that growing several varieties on the same farm may also increase mean yield levels, which may be due to complementarity or scale effects (Chavas and Di Falco, 2012; Boreux et al., 2013). Complementarity effects occur in a production system when

particular varieties perform better in the presence of others, for instance through lower infestation levels of certain pests or diseases. Scale effects arise when the functioning of the system is affected by its degree of fragmentation. Different plots on the same farm may differ in soil type, slope, and other characteristics, so that crop performance may be increased when varieties that are optimally suited for each plot are cultivated. Again, a new HYV that is not optimally suited for all plots may be adopted only partially, especially when plot heterogeneity is significant.

What will happen to on-farm varietal diversity when a new transgenic crop is introduced? The answer to this question will depend on the importance of the insurance and productivity enhancement functions of diversity in the initial situation, and on the concrete transgenic trait that is newly introduced. Most transgenic crop technologies available so far involve insect resistance, virus resistance, or herbicide tolerance (James, 2012). Other transgenic traits that are in the research pipeline include fungal and bacterial resistance, and tolerance to drought, heat, and other abiotic stresses (Qaim, 2009). Hence, the new transgenic crop is likely to reduce production risk. At the same time, it is likely to increase yield, not necessarily through higher yield potential but through more effective damage control (Qaim and Zilberman, 2003). We will start the analysis with the following general hypothesis:

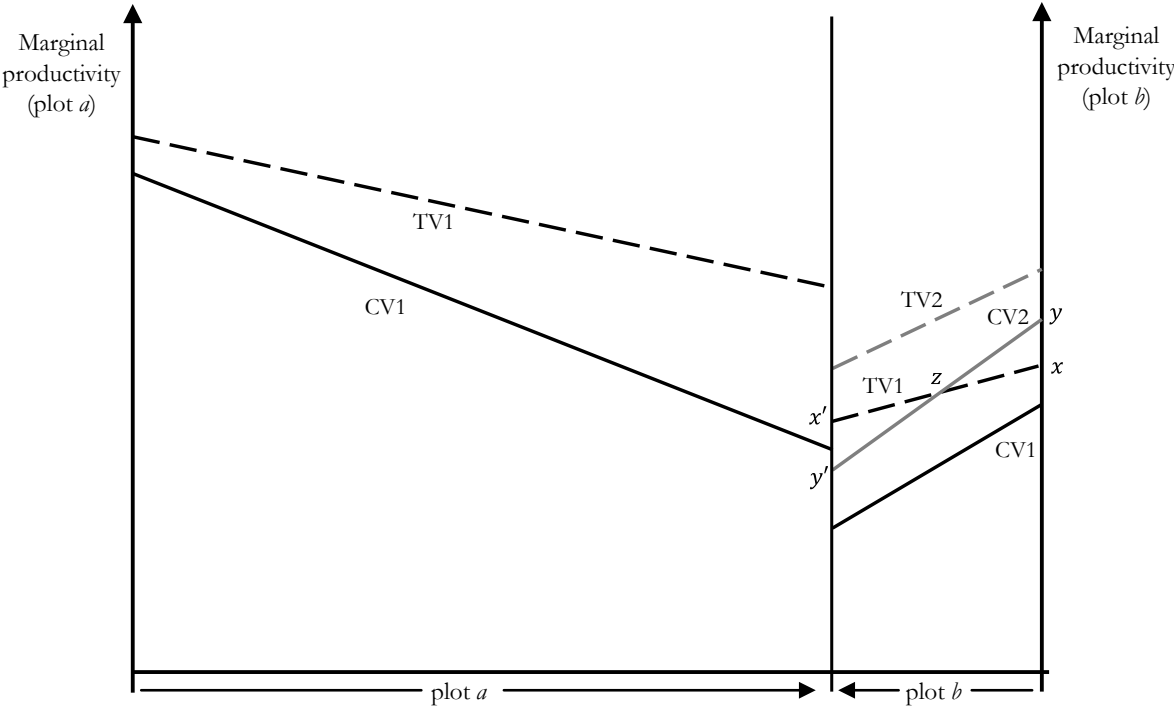
Hypothesis 1: Transgenic technology adoption increases yield and reduces production risk

If this hypothesis is true, the transgenic crop technology may potentially substitute for both the productivity enhancement function and the insurance function of varietal diversity. Most of the currently available transgenic crops address only single stress factors, so the degree of substitution will depend on the importance of the particular stress factor and of other stress factors in the local setting. Moreover, it will depend on the local suitability of crop varieties into which the transgenic trait is being introduced. For developing concrete hypotheses on the impacts of transgenic technology on varietal diversity, we use two stylized conceptual models – the first focusing on the productivity enhancement function and the second one addressing the insurance function of agrobiodiversity.

We consider the case of a farmer who operates on a given area of land and decides whether to adopt the transgenic technology and what level of varietal diversity to maintain across different plots in order to maximize farm income. This model builds on Smale, Just and

Leathers (1994), Van Dusen and Taylor (2005), and Krishna et al. (2013), who explored farmer adoption of different crop varieties with varying degrees of adaptability to different plots on a given farm, yet without considering transgenic technology. The model is graphically represented in Figure 1. For simplicity, we assume that the farm only has two plots (plots *a* and *b*) that differ in terms of soil type and other characteristics, although the scenario can be easily extended to a farm with multiple plots. The horizontal axis shows the land area of the two plots, and the vertical axes show marginal productivity of a single output produced. Different crop varieties will lead to different yields on the two plots. Other factors and inputs are used in the production process, but these are held fixed, so that marginal productivity is diminishing with increasing plot size. As a starting point, the farmer grows conventional variety 1 (CV1) on plot *a*. The same variety could also be grown on plot *b*, but its productivity would be significantly lower, because CV1 is not optimally adapted to the soil and other conditions of plot *b*. Conventional variety 2 (CV2) is better suited to these conditions and leads to higher productivity. Hence, total production is higher when the farmer cultivates two varieties instead of monoculture of CV1 on both plots.

Figure 1: Potential impact of transgenic technology on crop productivity and varietal diversity on a farm with heterogeneous plots



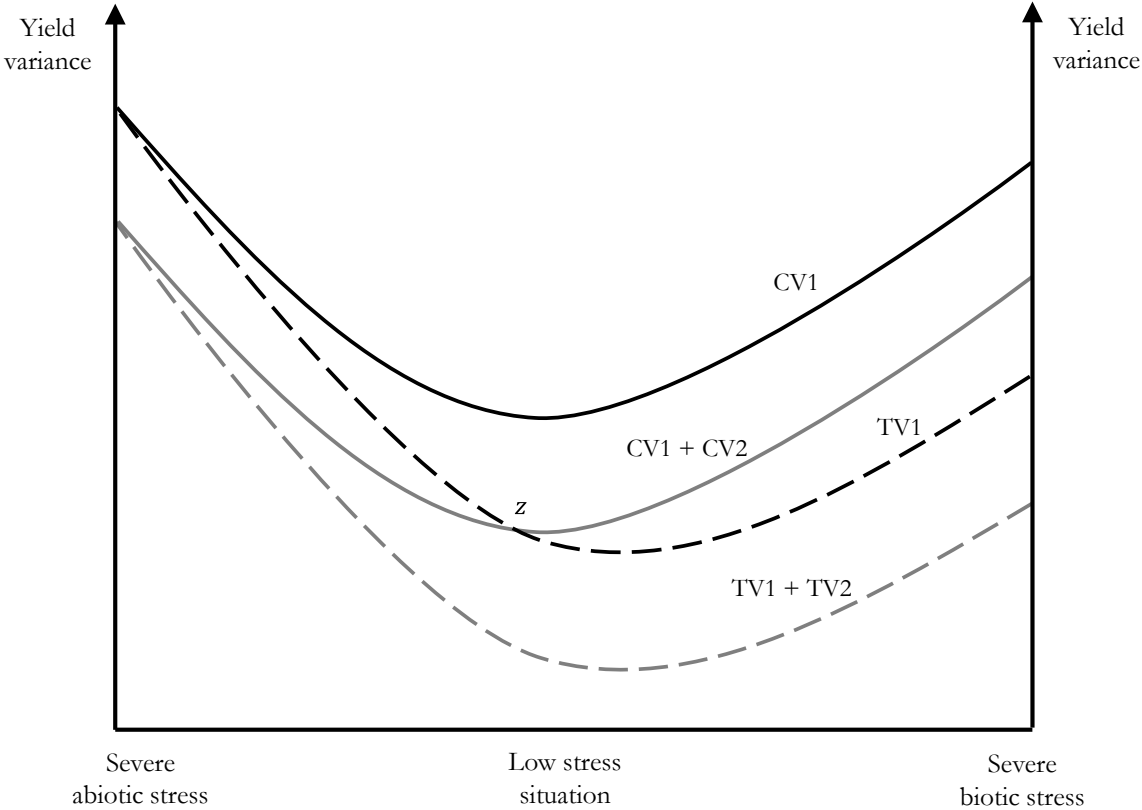
Now we consider that a new transgenic trait (e.g., insect resistance) becomes available and is introduced in variety 1; hence a transgenic version of variety 1 (TV1) is sold in the seed market. Figure 1 shows that TV1 will lead to a higher productivity than CV1, due to more effective pest control and thus lower crop damage. The farmer is likely to adopt TV1 on plot *a*. The farmer may also adopt TV1 on plot *b* and thus replace CV2, if the productivity gain from the transgenic trait is larger than the productivity loss from using a variety that is otherwise not optimally adapted to the conditions of plot *b*. In Figure 1, such replacement would occur if triangle area $x'y'z$ is larger than triangle area xyz . In that case, on-farm varietal diversity would be reduced. The probability of such diversity erosion would be much lower if the transgenic trait were also introduced in variety 2, so that transgenic versions of both varieties (TV1 and TV2) would be sold in the seed market. As mentioned above, such introduction of desirable traits into different varieties is possible and is one of the major differences between transgenic crops and HYVs of the Green Revolution. In summary, if varietal diversity has a productivity-enhancing function, the supply of various transgenic varieties that are well adapted to heterogeneous local conditions would not only increase farm production and income but would also help to avoid agrobiodiversity erosion.

Next, we examine the insurance function of varietal diversity. Again, we consider the production of one single crop. The crop is affected by two stress factors, one abiotic stress (e.g., drought) and one biotic stress (e.g., insect pest), which are shown on the horizontal axis of Figure 2. Both stress factors affect the crop's yield variance, which is measured on the vertical axes. Yield variance follows a U-shaped curve: in a low stress situation, yield variance is also low, whereas it increases with higher severity of either abiotic or biotic stress.³ When the farmer only grows one conventional variety (CV1), yield variance is higher than when two different varieties (CV1 + CV2) are grown. This is because different varieties have different levels of susceptibility to individual stress factors. Now we consider that a transgenic version of variety 1 (TV1) becomes available, which reduces yield variability due to biotic stress but not abiotic stress. The adoption outcome will depend on the relative importance of biotic and abiotic stress on the farm. With significant abiotic stress (to the left of point *z* in Figure 2), the farmer – wishing to reduce yield variance – would adopt TV1 only

³ The stylized graphical presentation in Figure 2 does not reflect that there may be complex interactions between abiotic and biotic stress factors (Rosenzweig et al., 2001). However, the results of this analysis would not change through possible stress interactions.

on part of the area and continue to grow CV2 on the other land. However, when biotic stress is more important, TV1 would be adopted on the total land, entailing loss in on-farm varietal diversity. This situation would change if the transgenic technology were introduced also in variety 2. Adoption of TV1 and TV2 would not only reduce yield variability further, but would also preserve agrobiodiversity.

Figure 2: Potential impact of transgenic technology on production risk and varietal diversity



Based on these models in Figures 1 and 2, we derive the following additional hypotheses:

Hypothesis II: Transgenic crop technology has a negative impact on varietal diversity when the number of different transgenic varieties supplied is small

Hypothesis III: With more transgenic varieties supplied, varietal diversity can be preserved

These three hypotheses are tested empirically in the following sections, using the example of cotton farmers in India.

3. Background and Data

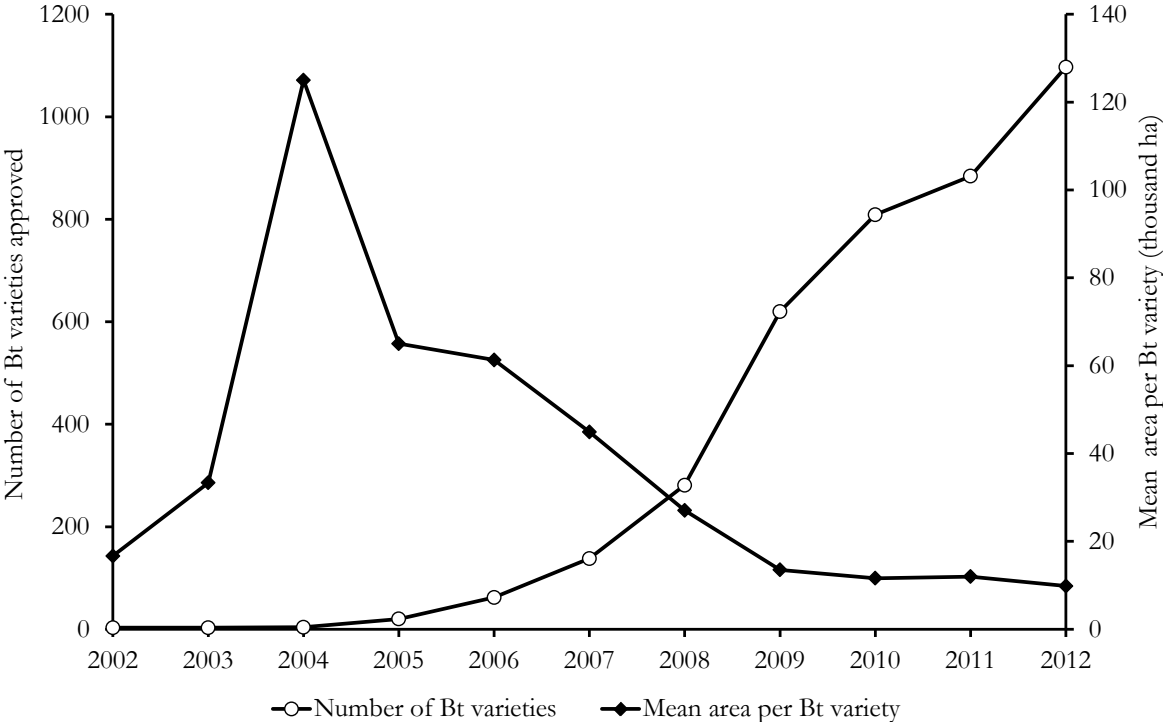
In India, cotton is primarily a smallholder crop, cultivated by farms with less than 5 ha of land and cotton holdings of 1.0-1.5 ha on average (Kathage and Qaim, 2012). Due to strong insect pest pressure, especially through bollworms (mainly *Helicoverpa armigera*), cotton is heavily sprayed with chemical pesticides. In the 1990s, cotton accounted for 45% of all chemical pesticide use in India (Krishna, Byju and Tamizheniyan, 2003). In spite of frequent pesticide applications, cotton bollworms were estimated to cause crop losses worth 20 billion Indian rupees per annum before the introduction of transgenic cotton technology (Birthal et al., 2000). The transgenic technology provides resistance to cotton bollworms through inbuilt genes from *Bacillus thuringiensis* (Bt). This so-called Bt cotton technology was developed by Monsanto and introgressed into a few locally developed cotton hybrids together with the Maharashtra Hybrid Seed Company (MAHYCO). Bt cotton was commercially approved in India for the first time in 2002. By 2012, this technology was grown on 10.8 million ha, equivalent to 93% of the total Indian cotton area (James, 2012). Today, India is the country with the largest area under Bt cotton worldwide.

When Bt technology was officially introduced in India in 2002, there were only three Bt cotton varieties approved.⁴ All three of them contained the *cry1Ac* Bt gene and were commercialized by the Monsanto-MAHYCO joint venture, marketed under the trade name Bollgard™. In 2004, one additional Bt variety, released by the company Rasi Seeds, was approved. The slow increase in the number of transgenic varieties in these early years was due to the fact that every single Bt variety had to undergo a regulatory procedure to be approved by the Genetic Engineering Approval Committee (GEAC), the responsible Government authority. Due to uncertainty and a politicized public debate about the technology's risks and benefits, GEAC was relatively slow to sanction additional Bt varieties that were waiting for approval. However, several additional Bt varieties were approved in 2005, and in 2006, more than 60 Bt cotton varieties developed by 13 different seed companies were available in the market. Most of these Bt varieties carried the Bollgard™ event with the *cry1Ac* gene under sub-licensing agreements with Monsanto-MAHYCO (Choudhary and Gaur, 2010). Also in 2006, Monsanto-MAHYCO commercialized the Bollgard II™ event, containing two Bt genes (*cry1Ac* and *cry2Ab*) that together provide resistance to a

⁴ In India, most cotton varieties are hybrids. We use the term variety here to also cover hybrids.

broader spectrum of insect pests.⁵ In the following years, the number of Bt cotton varieties available in the seed market further increased substantially.⁶ By 2012, close to 1100 different Bt cotton varieties were planted in India, meaning that each variety covered about 10 thousand ha on average (Figure 3). In terms of varietal diversity, this is a significant improvement over the initial phase of transgenic technology diffusion; in 2004, for instance, 125 thousand ha were planted with each Bt variety on average.

Figure 3: Diffusion of Bt cotton varieties in India



Sources: Choudhary and Gaur (2011); James (2012).

In this study, we use survey data from Indian cotton farmers, collected in four rounds between 2002 and 2008. In a multistage sampling framework, four states in central and southern India were purposively selected, namely Maharashtra, Karnataka, Andhra Pradesh,

⁵ Including two or more Bt genes can also reduce the probability of insect populations developing resistance to the transgenic technology (Tabashnik, Brévault, and Carrière, 2013).

⁶ The regulatory procedure in India was also changed from a variety-based to an event-based approval mechanism. This means that now not every single new Bt variety has to be approved by GEAC, as long as it involves a Bt event that was comprehensively tested and deregulated before (Karihaloo and Kumar, 2009).

and Tamil Nadu. In these states, we randomly selected 10 cotton-growing districts and 58 villages, using a combination of census data and agricultural production statistics. Within each village, farm households were randomly chosen from complete lists of cotton producers provided by the village heads. In total, 341 farmers were sampled in 2002. In 2004, a second round of the survey was carried out with the same farmers, whereby the overall sample size was slightly increased. A third and a fourth round of data collection with these farmers took place in 2006 and 2008, respectively. Further details of the survey are provided by Kathage and Qaim (2012) and Krishna and Qaim (2012). In total, we have 1431 household observations over the four survey rounds; a few of these observations could not be used for this analysis due to missing variables. The sample is representative for cotton growers in central and southern India. The panel data provide an interesting empirical base to analyze the effects of transgenic technology on on-farm varietal diversity and possible dynamics with changes in the supply of transgenic varieties.

4. Empirical Framework

Testing hypothesis I

To test the first research hypothesis, we analyze impacts of transgenic technology on crop yield and production risk. We expect that Bt technology increases yield (through reducing insect pest damage) and reduces production risk (through reducing yield variability caused by insect pests). Productivity-enhancing and risk-reducing effects are also expected through maintaining on-farm varietal diversity. For the analysis, we use the framework proposed by Just and Pope (1979) in a heteroscedastic regression model of the cotton production function. The Just and Pope (1979) framework has been used previously to analyze effects of Bt cotton (Crost and Shankar, 2008; Shankar, Bennett and Morse, 2008) and of varietal diversity (Smale et al., 1998; Di Falco and Chavas, 2009), but not jointly in one study. Here, we use cotton production per farm as dependent variable and regress this on a vector of inputs and production factors. In addition, we include Bt technology adoption and varietal diversity as explanatory variables. Bt adoption is represented as the area share of Bt cotton in the total cotton area of the respective farm; this share ranges from 0 when Bt is not

adopted to 1 when the technology is adopted on the whole cotton area. Varietal diversity is measured in terms of the number of cotton varieties cultivated on the farm in a given season, regardless of whether these varieties are transgenic or conventional. The production framework consists of a deterministic component to explain mean level of production, and a risk function to explain production variance, as follows:

$$y_{it} = \underbrace{f(x_{itl}, \sigma)}_{\text{deterministic}} + \underbrace{g(x_{itm}, \theta)u_{it}}_{\text{risk}} \quad \dots (1)$$

The deterministic component is elaborated in a generalized Cobb-Douglas function as,

$$E(y_{it}) = f(.) = \underbrace{\exp\left(\sigma_0 + \sigma_1 D_{it} + \sum_{l_1=1}^{l_1} \sigma_{l_1} x_{itl_1} + \sum_{l_2=1}^{l_2} \sigma_{l_2} \bar{x}_{il_2}\right)}_{\text{linear}} \underbrace{\prod_{l_3=1}^{l_3} x_{itl_3}^{\sigma_{l_3}} \prod_{l_4=1}^{l_4} \bar{x}_{il_4}^{\sigma_{l_4}}}_{\text{logarithmic}} \quad \dots (2)$$

and the risk function as,

$$V(y_{it}) = g^2(.) = \theta_0 + \sum_{m_1=1}^{m_1} \theta_{m_1} x_{itm_1} + \sum_{m_2=1}^{m_2} \theta_{m_2} \bar{x}_{im_2} + v_{it} + \bar{v}_i \quad \dots (3)$$

where y_{it} is cotton production per farm in logarithmic form, x_{itl_1} is the matrix of time-variant explanatory variables in linear form (including share of Bt area and number of cotton varieties), \bar{x}_{il_2} is the matrix of time-invariant explanatory variables in linear form, x_{itl_3} is the matrix of time-variant explanatory variables in logarithmic form, and \bar{x}_{il_4} is the matrix of time-invariant explanatory variables in logarithmic form. Parameter vectors to be estimated are σ and θ , and v_{it} and \bar{v}_i are individual and time-specific stochastic disturbance terms. The variance function $g^2(.)$ is commonly specified as a linear function of production inputs, human capital, and location-specific factors.

The production mean and variance functions are estimated using a three-step process, as suggested by Just and Pope (1979). First, an ordinary least squares (OLS) regression on production is estimated, accounting for heteroscedasticity. Second, the error terms are derived from this model and used for estimation of the variance function $g^2(.)$. Finally, a generalized least squares (GLS) production model is estimated with the inverse of the variance of predicted error terms from $g^2(.)$ as analytical weights. The hypothesis that

transgenic technology increases yield and reduces production risk assumes that the coefficient for Bt adoption has a positive sign in the GLS production model and a negative sign in the variance model.

Random and fixed effects panel specifications are tested to address possible issues of unobserved heterogeneity. The fixed effects model assumes that unobserved heterogeneity is correlated with the regressors, while the random effects specification assumes that there is no such correlation. If unobserved heterogeneity is correlated with any of the regressors and also with the dependent variable, the random effects estimates will be biased. In our case, Bt cotton adoption and on-farm varietal diversity are both possibly endogenous regressors, so that a random effects model might suffer from systematic selection bias. A Hausman specification test is performed to compare between the two specifications. When there is a systematic difference, the fixed effects specification is preferred, as it controls for the bias (Baltagi, 2005). However, when there is no systematic difference, the random effects alternative is a more efficient estimator.

Testing hypotheses II and III

The second and third hypotheses are more specifically concerned with the impact of transgenic technology on varietal diversity. Determinants of on-farm varietal diversity were analyzed in a number of studies (e.g., Benin et. al., 2004; Nagarajan, Smale and Giewwe, 2007), but none of these studies addressed the impact of transgenic technology adoption. We will start the analysis with some descriptive statistics, comparing levels of on-farm varietal diversity between full Bt adopters, partial adopters, and non-adopters over the survey years. Hypothesis II implies that on-farm diversity is lower among Bt adopters than among non-adopters in the early years of diffusion, whereas hypothesis III would imply that diversity increases in later years (especially in 2006 and 2008) with a larger number of Bt varieties becoming available in the seed market.

However, comparison of descriptive statistics can only be a first indicator, because there may be factors other than the increasing supply of Bt varieties that affect varietal diversity over time. We control for such other factors in regression models, using measures of varietal diversity as dependent and a set of possible determinants as independent variables. In a first model (*model 1*), we express varietal diversity as explained above, namely in terms of the

total number of cotton varieties grown on a farm. Yet there are also more specific indices that can be used to express varietal diversity, such as the Margalef index of varietal richness or Simpson's evenness index that both account for the size of the farm (Di Falco and Perrings, 2003; Benin et al., 2004; Nagarajan, Smale, and Glewwe, 2007; Di Falco and Chavas, 2009).⁷ To test whether the way of measurement influences the results we use a second model with the number of cotton varieties per ha of cotton (*model 2*) and a third model with Simpson's evenness index (*model 3*) as dependent variable. When only one single cotton variety is grown on a farm, Simpson's evenness index has a value of zero. *Model 1* with a count variable on the left-hand side is estimated with a Poisson specification, for *model 2* we use OLS, and model 3 with left-censoring of the dependent variable at zero is estimated with a Tobit specification. Again, random and fixed effects models are estimated and compared with a Hausman test.

In the set of explanatory variables, we include the farm area under cotton to control for possible scale effects. As time-variant variable, we include Bt adoption in terms of the share of the cotton area under this transgenic technology. Furthermore, we include a quadratic Bt adoption term to test for possible non-linearity. The square term is of particular relevance, because we expect that full adoption of transgenic technology will have a stronger effect on diversity than partial adoption. Hypothesis II implies that the overall Bt effect is negative. To test hypothesis III, we include the number of approved Bt varieties as an additional time-variant explanatory variable. This is measured at the state level, because Bt varieties are approved for specific states in India, depending on their suitability to local soil and climate conditions (Karihaloo and Kumar, 2009; James, 2012). We expect that the number of Bt varieties locally available in the seed market will affect the diversity on Bt adopting farms, so we use an interaction term between the number of approved Bt varieties and Bt adoption. Hypothesis III would imply that this interaction term has a positive and significant coefficient. Other time-variant variables that represent the level of abiotic risk are irrigation at the farm level and average rainfall measured at the district level over the last five cotton growing seasons. We also include a number of time-invariant variables, such as household

⁷ The Margalef index of varietal richness is calculated as $\frac{N-1}{\ln(A)}$, where N is the total number of varieties grown on a farm of size A measured in square meters. Simpson's evenness index is calculated as $1 - \sum_{n=1}^n \left(\frac{A_n}{A}\right)^2$, where A_n is area under variety n .

characteristics (household size, age and education of household head) and state dummies, which may also influence on-farm varietal diversity.

5. Results and Discussion

5.1. Impact of Bt adoption on cotton yield and production risk

In this section, we analyze the impact of Bt adoption on cotton yield and production risk with descriptive statistics and a production function model, as outlined above. Table 1 shows mean yield levels per ha of cotton for Bt adopters and non-adopters. These yield levels do not refer to a specific plot on the farm, but are calculated as total cotton production on the farm divided by cotton area. We differentiate between non-adopters of Bt, partial adopters, and full adopters with 100% Bt adoption. The Table also differentiates between different categories of varietal richness. Using the Margalef index, farms are divided into three categories: (i) zero diversity (only one cotton variety per farm), (ii) low diversity ($0 < \text{richness index} \leq 0.11$), and (iii) high diversity ($\text{richness index} > 0.11$). We use 0.11 as the boundary between low and high diversity, as this is the median of the Margalef index among the sample farmers. The results in Table 1 show that mean cotton yield increases consistently when the Bt area share increases. This holds true across all categories of varietal richness and suggests that Bt technology is indeed yield increasing. The yield difference between full adoption and non-adoption of Bt is 49% at zero varietal diversity, 62% when diversity is low, and 55% when diversity is high. When looking at the overall sample (last column in Table 1), a positive yield effect is also observed for increasing varietal diversity, although this is much smaller than for Bt and not consistent with varying levels of Bt adoption.

To assess impacts on production risk with descriptive statistics, we use the coefficient of variation (CoV) of yield as a normalized measure of dispersion. These values are also shown in Table 1. As expected, Bt technology and varietal diversity both seem to be risk-reducing. The CoV is 32% lower for full Bt adopters than for non-adopters, and it is 26% lower for farms with high varietal diversity than for farms with zero diversity. This suggests that adopting Bt may substitute for the insurance function of agrobiodiversity when only a small number of Bt varieties is available in the seed market. However, production risk can be

further reduced when full Bt adopters maintain varietal diversity, which is possible only with a larger number of Bt varieties available in the market.

Table 1. Mean yield and yield variability of Bt cotton adopters and non-adopters by varietal diversity category

Varietal diversity category	Bt adoption status			
	Non-adoption	Partial adoption	Full adoption	Overall
Zero diversity	1.29 [0.68]	1.78 [#] [0.28]	1.91 [0.48]	1.65 ^{***a} [0.57] ^{*a}
Low diversity	1.31 [0.59]	1.47 [0.57]	2.14 [0.39]	1.72 ^{***a} [0.89]
High diversity	1.31 [0.44]	1.61 [0.47]	2.03 [0.34]	1.78 ^{***a} [0.42]
Overall	1.30 [0.62] ^{**b}	1.55 ^{**b} [0.51]	2.00 ^{**b} [0.42] ^{***b}	1.71 ^{***a, ***b} [0.52] ^{*a, ***b}

Notes: N = 1417. Mean yield is measured in tons per hectare; coefficients of variation (CoV) are shown in square brackets. Varietal diversity categories are based on the Margalef index of varietal richness (see text). *, ** and *** imply that inter-group differences are statistically significant at the 0.10, 0.05 and 0.01 level, respectively. Mean yield differences are tested with the nonparametric k-sample mean comparison test; CoV differences are tested with Levene's F test. ^a and ^b show whether the level of significance is calculated between different Bt adoption groups or between varietal diversity categories, respectively. [#] Partial adoption with zero diversity indicates that Bt and non-Bt versions of the same variety were adopted.

We now turn to the production function analysis, using the Just and Pope (1979) framework. Summary statistics of the explanatory variables are shown in Table A1 in the Appendix.⁸ For both the mean production and production variance functions, the Hausman test suggests that the fixed and random effects estimates are systematically different at a 0.01 level of significance. Hence, fixed effects specifications are preferred. Estimation results are shown in Table 2. Bt adoption has a positive and significant coefficient on mean production levels.

⁸ In Table A1, we divide the observations into an early Bt diffusion phase (phase I, comprising 2002 and 2004) and a later diffusion phase (phase II, comprising 2006 and 2008). This distinction is of interest, because Bt adoption increased over time, and also the number of Bt varieties available in the market increased significantly in the later phase.

Controlling for other factors and estimating at the sample mean of varietal diversity, Bt adoption increased cotton yield by 28% in 2002. The interaction terms between Bt adoption and the year dummies have insignificant coefficients, indicating that the Bt yield effect remained stable over time. The year dummies themselves have positive and significant coefficients in the mean production function, implying that cotton yields increased over time also among the non-adopters of Bt technology. This may be due to general progress in breeding and agronomy. In addition, widespread adoption of Bt may have contributed to area-wide suppression of pest populations (Krishna and Qaim, 2012). Such positive spillovers of widespread Bt cotton adoption were also observed in China (Wu et al., 2008).

The number of cotton varieties grown has a positive impact on mean production levels, too, confirming the productivity-enhancing function of varietal diversity. This effect has also been shown in other contexts by Di Falco and Chavas (2009), Di Falco, Bezabih and Yesuf (2010), and Bangwayo-Skeete, Bezabih, and Zikhali (2012), among others. One additional variety grown on the farm increases cotton yield by about 5%. The interaction between Bt adoption and varietal diversity is insignificant, indicating that Bt adoption does not affect the productivity-enhancing function of varietal diversity. However, when we compare effect sizes, the yield impact of varietal diversity is lower than that of Bt adoption. For instance, an average farmer with five conventional cotton varieties could switch to one single Bt variety, without suffering a decline in yield. This suggests that – from a mere mean yield perspective – there may be incentives to reduce on-farm varietal diversity when only a small number of Bt varieties is available in the market.⁹

Crop duration, irrigation, rainfall, and off-farm income of households are also found to have positive impact on mean cotton production (Table 2). The magnitude of the cotton area coefficient indicates a negative scale effect: a 1% increase in area is associated with only a 0.84% increase in production. Together with the positive coefficient of varietal diversity, this result suggests that the functioning of the system is positively affected by the degree of fragmentation.

⁹ Kathage and Qaim (2012) showed that Bt adoption does not only increase mean yield, but also mean profit for cotton farmers in India.

Table 2. Cotton production and risk function estimates

	Cobb-Douglas mean production function (fixed effects GLS)	Production variance function (fixed effects)
Bt adoption [0-1 area share]	0.332 ^{***} (0.110)	-0.413 ^a (0.349)
Bt adoption * Year 2004 [interaction]	-0.113 (0.129)	0.482 (0.407)
Bt adoption * Year 2006 [interaction]	-0.072 (0.146)	0.444 (0.463)
Bt adoption * Year 2008 [interaction]	-0.245 (0.357)	0.253 (1.102)
Number of cotton varieties grown	0.049 [*] (0.026)	0.078 (0.075)
Bt adoption * Number of cotton varieties grown [interaction]	-0.030 (0.029)	-0.172 ^{**a} (0.086)
Date of sowing [number of days from May 1 st] [#]	0.029 (0.053)	0.189 (0.179)
Duration of crop [number of days] [#]	0.659 ^{***} (0.126)	-0.113 (0.396)
Cotton area [ha] [#]	0.839 ^{***} (0.039)	4.E-06 (0.118)
Chemical fertilizer [tons/ha] [#]	0.049 (0.031)	-0.067 (0.095)
Pesticide application [dummy]	0.027 (0.076)	0.617 ^{**} (0.268)
Quantity of pesticide [kg/ha] ^{##}	0.006 (0.018)	-0.009 (0.058)
Other input application [dummy]	-0.011 ^{**} (0.043)	-0.114 (0.136)
Value of other inputs [thousand rupees/ha] ^{##}	-0.055 (0.026)	0.067 (0.084)
Weeding operations [number]	0.019 (0.016)	-0.032 (0.050)
Irrigation applications [number]	0.023 ^{***} (0.007)	0.012 (0.021)
Rainfall at district level [millimeters] [#]	0.152 ^{***} (0.054)	-0.166 (0.167)
Household size [number]	4.E-05 (0.007)	0.026 (0.021)
Off-farm income [thousand rupees/year]	0.001 ^{***} (0.000)	-3.E-04 (0.001)
Year 2004 [dummy]	0.379 ^{***} (0.061)	-0.362 ^{**} (0.170)
Year 2006 [dummy]	0.606 ^{***} (0.108)	-0.381 (0.331)
Year 2008 [dummy]	0.656 [*] (0.346)	-0.031 (1.061)
Model intercept	-4.915 ^{***} (0.848)	-2.851 (2.691)
Adjusted R ²	0.80 ^{***}	0.45 ^{***}
Hausman test statistic	83.51 ^{***}	226.03 ^{***}

Notes: N = 1417. Coefficients are shown with robust standard errors in parentheses. [#] Variables included in logarithmic form; ^{##} Logarithms are taken for strictly positive values; 0 otherwise. *, **, *** Statistically significant at the 0.1, 0.05 and 0.01 level, respectively. ^a Joint significance at 0.05 level.

In the production variance function, which is shown in the second column of Table 2, most of the variables are statistically insignificant. One exception is the interaction term between Bt adoption and varietal diversity, which has a negative and significant coefficient, suggesting that these two factors have synergistic effects. Moreover, Bt adoption and this interaction term are jointly significant: a one percentage point increase in Bt area reduced yield risk by 0.71% in 2002. Somewhat surprisingly, the varietal diversity variable itself is insignificant in this model. In this context, the insurance function of varietal diversity seems to be weaker than that of Bt adoption, as the descriptive statistics had already suggested. In summary, this analysis shows that transgenic technology adoption increases yield and reduces production risk, thus confirming our first research hypothesis.

5.2. Impact of Bt adoption on varietal diversity

With Bt technology increasing mean yield and reducing production risk, farmers may have an incentive to reduce on-farm varietal diversity when only a small number of Bt varieties is available. In other words, transgenic technology may contribute to agrobiodiversity erosion in such situations. We now investigate whether such erosion actually took place for the case of Bt cotton in India. We start by comparing different diversity indicators between the early Bt diffusion phase with a low number of approved Bt varieties (phase I, comprising 2002 and 2004) and the later diffusion phase with a much larger number of approved Bt varieties (phase II comprising 2006 and 2008). Bt technology adoption, measured as the share of Bt cotton in the total cotton area, had increased from 25% in phase I to 92% in phase II. The comparisons are summarized in Table 3 (further details are given in Table A2 in the Appendix). Looking at the sample as a whole on the left-hand side of Table 3, we find no significant difference between the two phases in any of the diversity measures. In phase I, many farmers adopted Bt only partially, so that the diversity status was maintained through growing conventional cotton varieties on the same farm. In phase II, the availability of more Bt varieties helped farmers to preserve diversity even with full Bt adoption.

Table 3: On-farm varietal diversity with and without Bt cotton

	Overall		Bt adoption status	
	Phase I	Phase II	Non-adopters in phase	Full-adopters in phase II
	[2002 & 2004]	[2006 & 2008]	I	
Number of cotton varieties grown	2.03 (0.05)	2.11 (0.05)	1.77 (0.06)	2.17 ^{***} (0.05)
Cotton area [ha]	2.13 (0.08)	2.30 (0.08)	1.85 (0.09)	2.32 ^{***} (0.09)
Number of cotton varieties per ha (weighted by area)	0.94 (0.02)	0.92 (0.02)	0.96 (0.03)	0.93 (0.02)
Margalef's varietal richness index	0.10 (<0.01)	0.11 (<0.01)	0.08 (0.01)	0.11 ^{***} (0.01)
Simpson's evenness index	0.31 (0.01)	0.33 (0.01)	0.25 (0.01)	0.34 ^{***} (0.01)
Number of observations	703	722	405	646

Note: Mean values are shown with standard errors in parenthesis. *** Difference between full adopters in phase II and non-adopters in phase I is statistically significant at the 0.01 level. No significant differences are observed between phase I and II for the overall sample.

The right-hand part of Table 3 looks at the diversity impacts of Bt technology more specifically, by comparing non-adopters of Bt in phase I with full adopters in phase II. Strikingly, varietal diversity was significantly higher for the full adopters in phase II, suggesting that the adoption of Bt technology did not lead to diversity erosion. Yet this comparison masks some interesting variation that occurred within each of the phases. Table A2 shows that full adoption of Bt in phase I was associated with lower varietal diversity. On the other hand, non-adoption of Bt was associated with lower diversity in phase II.

To analyze these effects further, we estimate different varietal diversity regression models, as explained above. Estimation results are shown in Table 4. In *model 1*, the Hausman test indicates no significant difference between the random and fixed effects results, so the random effect specification is preferred. In *model 2*, a significant difference is detected, so we use the fixed effects specification. For the Tobit model (*model 3*), we use the random effects specification. The results of all three models are similar. In all cases, Bt adoption as such has a positive and significant coefficient, which may be surprising at the first glance. However, this effect is primarily driven by partial adoption. With full adoption (Bt area share of 1), Bt decreases varietal diversity because the negative square term overcompensates the positive direct effect. This negative impact of Bt technology on varietal diversity holds when the supply of different Bt varieties is small, thus confirming hypothesis II. With more Bt varieties supplied, the loss of on-farm diversity is reduced, as can be seen from the positive and significant interaction term between Bt adoption and the number of approved Bt varieties.

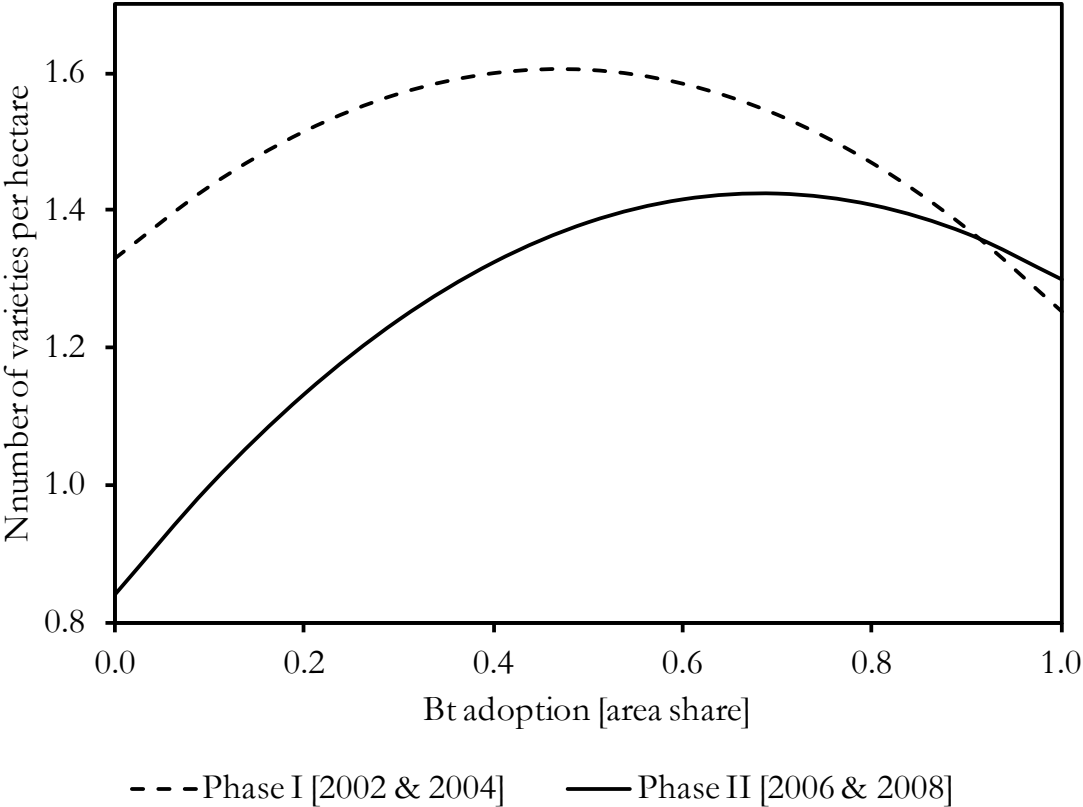
Table 4: Determinants of on-farm varietal diversity

	<i>Model 1:</i> Number of varieties per farm (Poisson, random effects)	<i>Model 2:</i> Number of varieties per ha (linear, fixed effects)	<i>Model 3:</i> Simpson's evenness index (Tobit, random effects)
Bt adoption [0-1 area share]	1.461*** (0.238)	1.152*** (0.289)	1.017*** (0.084)
Square of Bt adoption	-1.709*** (0.255)	-1.250*** (0.295)	-1.112*** (0.086)
Number of approved Bt varieties at state level	-0.034** (0.017)	-0.021 (0.016)	-0.019*** (0.005)
Bt adoption * Number of approved Bt varieties at state level [interaction]	0.012*** (0.004)	0.006** (0.003)	0.004*** (0.001)
Cotton area [ha]	0.085*** (0.007)	-0.167*** (0.016)	0.042*** (0.003)
Irrigation facility [dummy]	0.051*** (0.040)	0.064 (0.054)	0.024* (0.013)
Mean rainfall during last five years [millimeters]	0.055 (0.078)	-0.103 (0.099)	0.034 (0.023)
Age of household head [years]	-0.003** (0.002)		-0.002 (0.001)
Education of household head [years]	0.002 (0.004)		2.E-04 (1.E-03)
Household size [number]	-0.003 (0.005)	-2.E-04 (0.009)	-0.001 (0.002)
Off-farm income [thousand rupees/year]	-2.E-04 (2.E-04)	-3.E-04 (3.E-04)	-1.E-04* (7.E-05)
Andhra Pradesh [dummy]	-0.249*** (0.053)		-0.075*** (0.020)
Karnataka [dummy]	-0.570*** (0.054)		-0.246*** (0.019)
Tamil Nadu [dummy]	-0.553*** (0.118)		-0.245*** (0.035)
Year 2004 [dummy]	0.248*** (0.059)	0.049 (0.056)	0.106 (0.018)
Year 2006 [dummy]	1.041** (0.494)	0.464 (0.483)	0.591*** (0.160)
Year 2008 [dummy]	3.726 (2.378)	2.224 (2.359)	2.386*** (0.784)
Model intercept	0.440 (0.521)	2.410*** (0.681)	0.143 (0.154)
Adjusted R ²		0.64***	
Log-likelihood	-2056.06		82.87
Wald χ^2	522.55***		826.78***
Hausman test statistic	11.29	29.92***	NA

Notes: N = 1425. Coefficients are shown with robust standard errors in parentheses. . , ** , ***
Statistically significant at the 0.1, 0.05 and 0.01 level, respectively.

To analyze the relationship between Bt adoption, supply of Bt varieties, and on-farm varietal diversity further, we use the model estimates for some predictions, as shown in Figure 4. These predictions are based on *model 2*, where the dependent variable is the number of cotton varieties grown on a farm normalized by cotton area. The two curves shown represent the situation in technology diffusion phases I and II. In phase I, with only limited supply of transgenic varieties, full adoption of Bt had a negative impact on varietal diversity if compared to zero Bt adoption. However, partial Bt adopters were keeping higher levels of varietal diversity compared to both full adopters and zero adopters. In other words, in that early phase farmers had to relinquish diversity to accomplish higher level of Bt adoption. In phase II, the impact was different. The development and approval of many additional Bt varieties allowed Bt adopters to restore varietal diversity. The predictions suggest that on-farm varietal diversity in phase II with full Bt adoption was in the same magnitude as with zero Bt adoption in phase I. These results confirm research hypothesis III.

Figure 4: Impact of Bt adoption on-farm varietal diversity



Note: Predictions are based on model 2 of Table 4.

Another noteworthy result of this analysis is the negative direct effect of the number of approved Bt varieties on varietal diversity, which is significant in two of the models in Table 4. This implies that a larger supply of Bt varieties leads to lower on-farm varietal diversity among non-adopters of Bt. Indeed, Figure 4 shows a low level of diversity with zero Bt adoption in phase II. With over 90% adoption of Bt, seed companies now focus primarily on supplying transgenic seeds; it is not lucrative anymore to also supply non-Bt versions of all varieties. Given the high adoption of Bt, this is of little relevance for aggregate varietal diversity, but it may certainly affect varietal choices of individual farmers who prefer not to adopt Bt technology.

6. Conclusion and Policy Implications

During the Green Revolution it was observed that many local crop varieties were replaced with a few high-yielding ones in large parts of the developing world. There are widespread concerns that such agrobiodiversity erosion may continue and be accelerated through transgenic crop technologies. However, transgenic crops differ from high-yielding varieties of the Green Revolution and so warrant a closer look. In this study, we have analyzed the impact of transgenic crops on varietal diversity, first conceptually and then using the concrete example of Bt cotton in India.

From the private perspective of farmers, varietal diversity can have productivity-enhancing and risk-reducing effects. We have hypothesized that transgenic crops can also increase productivity and reduce production risk and may therefore substitute for on-farm varietal diversity. Yet, a transgenic technology is not only one new variety; the same genes coding for desirable traits can be introgressed into many varieties that are well adapted to various soil and climate conditions. If many transgenic varieties with the same traits are developed and adopted, agrobiodiversity can be preserved.

These hypotheses were confirmed in the empirical analysis. Insect-resistant Bt cotton has significantly increased productivity and reduced production risk for smallholder farmers in India. The panel data also allowed us to study developments over time. The observed dynamics are very interesting because seed market conditions changed considerably,

providing a quasi-experimental setting to analyze the diversity consequences of differing numbers of Bt cotton varieties. In the early phase of Bt technology diffusion, the Indian regulatory authorities had only approved a very small number of Bt varieties, while in later years many more Bt varieties became available in the seed market. Indeed, farmers that fully adopted Bt cotton in the early years, reduced their varietal diversity. In later years, with more Bt varieties available, these same technology adopters restored varietal diversity. These results underline that a combination of transgenic technology and high levels of varietal diversity is possible, and is even further increasing productivity and reducing production risk.

Overall, cotton varietal diversity in India with a Bt adoption rate of over 90% is now at the same level or even higher than it was before the introduction of this transgenic technology. Interestingly, even in the early phase of technology diffusion, with only a few Bt varieties available in the market, average diversity did not decline significantly, because many farmers adopted Bt only partially and maintained varietal diversity through growing conventional varieties on the same farm. This may be related to a general farmer preference for on-farm varietal diversity. Yet we have shown that full adoption would have been economically advantageous for many even with only a few Bt varieties available. Hence, we suppose that the observed partial adoption in the early phase was also a reflection of typical smallholder cautiousness. Smallholder farmers often adopt new technologies partially in the beginning, and increase adoption intensity when they are more certain that the technology is really beneficial for them. This implies that cotton varietal diversity would likely have been reduced if more Bt varieties had not become available in later years.

The empirical results from India do not necessarily hold for other situations, but one general conclusion can be drawn nevertheless: transgenic technology can help to preserve crop varietal diversity, but the concrete outcome depends on various institutional factors that determine how many transgenic varieties are available in the market. We now discuss a few of these institutional factors and also derive some policy implications. First, the biosafety regulatory framework matters. In India, the regulatory authorities were slow in the beginning to approve additional transgenic varieties, mainly due to the public debate about possible risks associated with transgenic technology. However, once a transgenic event has been tested and deregulated, introgressing that same event into other varieties cannot

reasonably be expected to lead to new risks (Bradford et al., 2005). Hence, a complex regulatory process for each new transgenic variety jeopardizes agrobiodiversity without increasing safety levels. Second, local breeding capacities in a country play an important role. India has a strong public and private breeding sector for cotton. Hence, many companies were technically able to introgress a transgenic trait into their varieties and breeding lines. Such introgression of an available transgenic trait is less complicated than identifying the trait and developing the transformation event, but it still requires some capacity that may not be available in many poorer countries in Africa. Public support through development organizations or international agricultural research centers may be required to ensure that transgenic traits of interest are introgressed into multiple local varieties. Innovative models of public-private partnership may also be an interesting approach in some situations (Krishna and Qaim, 2007). Third, IPRs may play an important role. Many of the transgenic technologies available so far are not patented in developing countries, so that local organizations can use these technologies for free or with relatively simple licensing agreements for introgression into their own varieties and breeding lines. Stronger IPRs may involve more complex licensing agreements. If many local organizations can obtain a license from the IPR holder, agrobiodiversity could be preserved. Restricted licenses to only one or a few organizations, however, could contribute to agrobiodiversity erosion. Such institutional aspects should be considered when designing national policies and regulatory frameworks for transgenic technologies.

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Appendix

Table A1: Summary statistics of explanatory variables used in regression models

	Unit of measurement	Phase I [2002 & 2004]		Phase II [2006 & 2008]	
		Mean	(Std. dev.)	Mean	(Std. dev.)
<i>Variables used in production function analysis [N = 1417]</i>					
Bt adoption, area share relative to total cotton area	0-1	0.25	(0.01)	0.92 ^{***}	(0.01)
Date of sowing	number of days from May 1 st	56.76	(0.75)	55.10 [*]	(0.66)
Duration of the crop	number of days	218.27	(1.16)	218.92	(1.42)
Cotton area	ha	2.13	(0.08)	2.30	(0.08)
Chemical fertilizer	tons/ha	0.59	(0.01)	0.61	(0.01)
Pesticide application	dummy	0.96		0.93 ^{***}	
Quantity of pesticides, if applied	kg/ha	8.26	(0.27)	2.82 ^{***}	(0.12)
Other input application (other than fertilizer, pesticide, and labor)	dummy	0.21		0.36 ^{***}	
Value of other inputs, if applied	thousand rupees/ha	1.21	(0.43)	1.14	(0.16)
Weeding operations	number	3.07	(0.05)	2.86 [*]	(0.05)
Irrigation applications	number	2.26	(0.15)	2.18	(0.11)
Rainfall at district level (current cotton season)	millimeters	648.60	(10.23)	724.14 ^{***}	(9.30)
Household size	number of members	6.45	(0.13)	6.29	(0.15)
Off-farm income	thousand rupees/year	28.37	(4.19)	27.79	(2.55)
<i>Variables used in varietal diversity analysis [N = 1425]</i>					
Approved Bt varieties at state level	number	3.51	(0.02)	93.69 ^{***}	(2.16)
Irrigation facility	dummy	0.50		0.58 ^{***}	
Mean rainfall during last five years	millimeters	914.75	(16.66)	747.08 ^{***}	(5.71)
Age of household head	years	44.60	(0.47)	45.40	(0.47)
Education of household head	years of schooling	7.34	(0.19)	7.14	(0.19)
Andhra Pradesh	dummy	0.30		0.32	
Karnataka	dummy	0.30		0.30	
Tamil Nadu	dummy	0.09		0.04 ^{***}	

^{*}, ^{***} Difference between phase I and II is statistically significant at the 0.1 and 0.01 level, respectively.

Table A2: Bt adoption and on-farm varietal diversity

	Mean (std. error)				Significance of difference between adoption categories		
	Non-adopters	Partial adopters	Full-adopters	Overall	Non vs. full	Non vs. partial	Full vs. partial
Phase I [2002 & 2004]							
<i>Number of observations</i>	405	201	97	703			
Number of cotton varieties	1.77 (0.06)	3.00 (0.10)	1.08 (0.03)	2.03 (0.05)	***	***	***
Cotton area [ha]	1.85 (0.09)	3.06 (0.20)	1.41 (0.18)	2.13 (0.08)	**	***	***
Number of cotton varieties per ha (weighted by area)	0.96 (0.03)	0.98 (0.04)	0.77 (0.07)	0.94 (0.02)	***		***
Margalef's varietal richness index	0.08 (0.01)	0.19 (0.01)	0.01 (0.00)	0.10 (0.00)	***	***	***
Simpson's evenness index	0.25 (0.01)	0.55 (0.01)	0.04 (0.01)	0.31 (0.01)	***	***	***
Phase II [2006 & 2008]							
<i>Number of observations</i>	47	29	646	722			
Number of cotton varieties	1.30 ^{###} (0.09)	2.14 ^{###} (0.18)	2.17 ^{###} (0.05)	2.11 (0.05)	***	***	
Cotton area [ha]	2.09 (0.39)	2.23 (0.39)	2.32 ^{###} (0.09)	2.30 (0.08)			
Number of cotton varieties per ha (weighted by area)	0.62 ^{###} (0.09)	0.96 (0.11)	0.93 ^{##} (0.02)	0.92 (0.02)	***	**	
Margalef's varietal richness index	0.03 ^{###} (0.01)	0.11 ^{###} (0.02)	0.11 ^{###} (0.01)	0.11 (0.00)	***	***	
Simpson's evenness index	0.11 ^{###} (0.03)	0.40 ^{###} (0.05)	0.34 ^{###} (0.01)	0.33 (0.01)	***	***	

, *: Difference is significant at the 0.05 and 0.01 level, respectively, across adoption categories during the same time period. ^{##}, ^{###} Difference is significant at the 0.05 and 0.01 level, respectively, across time periods within the same adoption category.