


# The adoption of automated phenotyping by plant breeders

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**Abstract** Phenomics or automated phenotyping (AP) is an emerging approach, identified as a priority for future crop breeding research. This approach promises to provide accurate, precise, fast, large-scale, and accumulated phenotyping data which when integrated with corresponding genomic and environmental data is expected to trigger a great leap forward in plant breeding. However, despite promising applications, AP adoption in plant breeding is still in its infancy. It is unclear to many plant breeders how or if much of the enormous volume, diversity, and velocity of imaging and remote-sensing data generated by AP is going to be usefully integrated into breeding programs. This paper develops an economical model of heterogeneous breeders' decision-

making to examine adoption decisions regarding whether to adopt AP or continue using conventional phenotyping. The results of this model indicate that many interlocking factors, including genetic gain/expected return, variable and sunk costs, subsequent rate of technology improvement, and breeders' level of aversion to AP, are at work as breeders determine whether to adopt AP. This study also provides a numerical example to show the impact of breeders' aversion toward the adoption of a new technology (e.g., AP) on the expected return generated from breeding a new wheat variety.

**Keywords** Plant breeding · Phenomics · Economics of technology adoption · Decision-making · Genomics

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## Introduction

There is a widespread and long-standing agreement that global improvement in crop productivity has mainly been achieved through the development and adoption of new agricultural technologies (Hurley et al. 2016; Hurley et al. 2014; Alston et al. 2010; Alston et al. 2000). Greater crop production is forecast to be needed to ensure food security as competition for scarce land and water resources intensifies in the face of climate change, and population and income growth (Hunter et al. 2017). Most of the increase in this

production must come from lands already in cultivation—80% of the global growth in crop production must come from intensification in the form of yield gains, 10% from cropping intensities, and 10% from arable land expansion (FAO 2012). Plant genomics and phenomics represent the most promising tools for accelerating yield gains, and plant breeding is at heart of that mission. One place of particular focus for some is the selection process, whereby breeders select materials for further development based on phenomic expression. While many breeders have adopted genomics and various advanced genetic breeding or selection processes, for the most part, plant breeders have not exploited many of the opportunities for mechanisation or intensive analysis now available due to enhanced sensing, imaging and phenotype data collection.

A phenotype is the composite of an observable expression of a genome for traits in a given environment. Traits could be visible to the naked eye (conventional phenotype, CP), or visible by using technical procedures. Phenomics—the systematic genome-wide study of an organism's phenotype—is an emerging approach that aims to automate and standardize the phenotyping process to capture information about the minutiae of plant growth, composition and performance by using a wide array of non-invasive and non-destructive imaging and remote sensing techniques, including high-throughput methods of data acquisition and analysis. This approach promises to deliver accurate, precise, fast, large-scale, and accumulated data in controlled and varying environmental conditions and to provide the opportunity to 'datify' or turn into data phenotyping activities that were previously un-quantified (Kumar et al. 2015; Singh and Singh 2015, Newell and Marabelli 2015). Interdisciplinary collaboration of expertise including biologists, engineers, and computer scientists is crucial for the implementation of phenomics or automated phenotyping (AP) into practice (Cobb et al. 2013; Kumar et al. 2015).

In plant breeding, AP could be used to screen germplasm collections for desirable traits (forward phenomics) and to dissect traits shown to be of value to reveal their mechanistic basis, including various physiological, biochemical, and biophysical processes and genes controlling these traits (reverse phenomics) (Singh and Singh 2015; Kumar et al. 2015). The greatest benefit of AP would be achieved if this

technology allows breeders to select superior plants that would otherwise be rejected by using CP methods.

With the deluge of cheap high-throughput genotype data and the rapid developments in plant molecular-based breeding technologies, there is an increased interest in AP as an approach that will provide precise and correspondingly high-throughput phenotypic data to harness the potential of genomic investigations, including mapping initiatives and training genomic selection (GS) models. This is especially important when breeding for quantitative traits (QT), such as yield and drought tolerance, as these traits usually show continuous phenotype variation due to their polygenic inheritance and environmental influence and, thus, need to be repeatedly measured during the life cycle of a plant in multi-environmental conditions (Bassi et al. 2016; Desta and Rodomiro 2014; Cobb et al. 2013).<sup>1</sup>

Despite promising applications, the adoption of AP in plant breeding is still in its infancy (Australian Government, GRDC 2017; Kumar et al. 2015). It is still not clear to many plant breeders if or how much of the generated AP data could be usefully integrated into breeding programs. The enormous volume, diversity, and velocity of imaging and remote-sensing data generated by AP makes it a 'big data' problem. An essential factor for the application of AP will be the ability to present related information as tools that support decision-making in breeding programs. Much work is needed to address issues of ease of access, ease of use and data management before AP technologies are likely to see widespread uptake in plant breeding. The development of ontology-based big data

<sup>1</sup> Traits can be grouped into two genetic categories: (1) qualitative traits and (2) quantitative traits (QTs). Qualitative traits are generally governed by one or a few major genes, called oligogenes, where each of these genes produces a large effect on the trait phenotype. Qualitative traits have Mendelian inheritance (high heritability), provide discrete/discontinuous phenotypic variation, and the phenotypic expression of oligogenes is generally minimally affected by the environment. Therefore, as their phenotypes are good indicators of their concerned genotype loci, qualitative traits are easy to manipulate and evaluate in a breeding program (Singh and Singh 2015). QTs are governed by many genes, called polygenes. Each of these genes has a small effect on trait phenotype; the effect of each gene is too small to be individually identified; and the effects of all polygenes affecting a trait are cumulative. QTs show continuous phenotypic variation (non-discrete) because of the polygenic inheritance and environmental influences, and thus, cannot be grouped into distinct phenotyping classes.

management is needed to facilitate the integration of metadata to establish genotype, phenotype and environmental-data-point relationships that create meaningful insights and provide opportunities to enhance the breeding process (Kumar et al. 2015; International Plant Phenotyping Network 2016; Phenospex 2016).

This paper develops an economical model of adoption decision to assess breeders' attitude towards the adoption of the AP approach; the assumption of breeder homogeneity is relaxed. Breeders' preferences towards technology adoption are assumed linked to the characteristics of the technology. Breeders, according to their preferences, choose the technology for which they obtain the highest return or profit. Thus, heterogeneous breeders are assumed to differ in the relative gain or profit they generate from breeding a cultivar under AP and CP. The model focuses on the evolving nature of technologies, assuming that breeders may expect a future technology improvement in AP which could affect their decisions to adopt AP at the present time and in the future.

Among the parameters in the model, we analyze the importance of breeder's aversion toward the adoption of a new technology. For that, we provide a numerical example to describe how the rate of aversion may affect the expected return perceived by heterogeneous breeders from the adoption of a new technology, which in turn may affect their decision to adopt the technology.

### Automated plant phenotyping

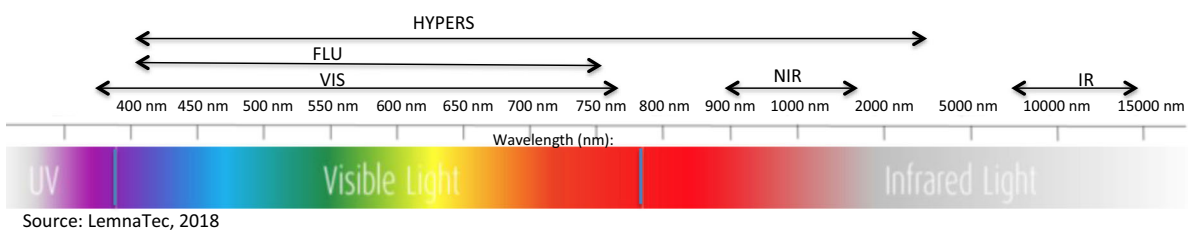
Several phenotyping facilities have been established and some are currently underway to develop controlled and field-based AP. A variety of wavelength-range cameras are available to capture signals from the visible and infrared spectrum of light (Fig. 1). The image technology includes: (1) visible (VIS) camera

RGB (red, green, and blue) to quantify the phenotype plant architecture, height, stem diameter, leaf number and area, color classification, and growth rate; (2) near infrared (NIR) imaging which provides detailed information on the watering status of plant leaves and their reaction to water availability (e.g., drought), and combined with specially-designed NIR unit for roots can monitor the relative water content of the soil surface; (3) infrared (IR) imaging measures above ground plant water content and sense levels of abiotic stress; (4) fluorescence (FLU) imaging for stress identification and quantification, photosynthesis and chlorophyll contents; (5) and hyperspectral (HYPERs) imaging for measuring abiotic and biotic stresses, pigment composition, nitrogen (N) use efficiency, and other biochemical features (Kumar et al. 2015; LemnaTec 2018).

Field-based phenotyping combines advances in sensing technologies, aeronautics, robotics, automatic image acquisition, and automated environmental data collection (Araus and Cairns 2014).

### Plant breeding and the need for automated phenotyping

The most common techniques used in plant breeding are presented in Table 1. These techniques may involve the introduction of new genetic variation and the identification and tracking of genes for key traits, in order to achieve greater genetic gain ( $\Delta G$ ) from selection and to accelerate the breeding cycle. Regardless of the technology used, the following general steps are associated with plant breeding: (1) defining the objective(s) of the breeding program, including such factors as improved farmer and/or processor productivity, new product attributes to satisfy consumer preferences, and improved environmental impacts; (2) developing population or germplasm



**Fig. 1** Imaging technologies

**Table 1** Techniques used in plant breeding. *Sources* Lusser et al. (2011), Acquaah (2012), Benkeblia (2014) and Mahesh (2016)*Traditional techniques*

Emasculation; hybridization; wide crossing; chromosome doubling; chromosome counting; male sterility; triploidy; linkage analysis; and statistical tools

*Random mutation techniques*

Mutagenesis; tissue culture; haploidy; isozyme; markers; in situ hybridization; Molecular markers; DNA sequencing; plant genomic analysis; bioinformatics; Microarray analysis; primer design; and plant transformation

*New biotechnological techniques*

Oligonucleotide-directed mutagenesis (ODM); Cisgenesis/intragenesis; genome editing (e.g., Zink finger nuclease (ZFN); TALENS & CRISPRs; GM rootstock grafting; RNA-dependent DNA methylation (RdDM); Reverse breeding; and agro-infiltration

**Table 2** Selection methods in plant breeding. *Sources*: Benkeblia (2014) and Singh and Singh (2015)

*Conventional selection methods/conventional phenotype (CP) selection* Pedigree selection; mass selection; pure line selection; bulk population selection; and single-seed descent selection

*Molecular selection methods/marker selection methods* marker-based selection (MBS); marker-assisted selection (MAS); marker-assisted backcrossing (MABC); marker-assisted recurrent selection (MARS); genomic selection (GS) or genome-wide selection (GWS)

collections that include the genetic variations of interest; and (3) identifying and selecting individuals with superior characteristics. If successful, selection produces a new population that is phenotypically and genetically different from the base population. The new population is then used to develop new varieties that eventually, after evaluation and certification, find their way to a farmer's field.

The most common selection methods used in plant breeding are presented in Table 2. Traditionally, selection of superior plants involves visual assessment for traits—otherwise known as conventional phenotype (CP) selection. In the field, breeders focus on a plant's appearance—they use the field to visually study plant phenotypic expression in different environmental conditions and to select the type of lines they will use to identify traits that have the potential to improve agronomic features, offer higher yields or produce specific qualities. However, CP methods are labour and time intensive, environmentally sensitive and costly. The data collected are frequently subjectively encoded and can vary significantly. In addition, CP has a limited capacity for measuring traits in very large genetic populations, particularly for low heritability and dynamic traits that have phenotypes that change with time and environment and, thus, require to be repeatedly measured during the life cycle of a plant in multi-environment trials.

Recently, advances in genomics technologies (i.e., next generation sequencing technologies) have provided a better understanding of the genetic basis of a trait and improved the efficiency of selection through the use of marker selection methods (Table 2). The integration of molecular-marker and conventional selection methods into the breeding programs can improve the precision and accelerate the breeding cycle, as markers can be screened before the plant is grown rather than measured in seeds or at the seedling stage. The ability of markers to predict the phenotype of a trait allows breeders to select for multiple generations each year in a greenhouse.<sup>2</sup>

The genomic selection (GS) or genome-wide selection (GWS) model is seen as a promising molecular-based selection approach. GS generates marker effects, called genomic estimated breeding values (GEBVs), across the whole genome of a breeding population (BP) based on a statistical model developed in a training

<sup>2</sup> Note that the new molecular methods supplement and extend, but do not replace, conventional breeding. The ultimate test of value of a genotype is its performance in the targeted environment. For instance, although molecular selection based on molecular markers can be used in early generations at F<sub>2</sub>, population size at F<sub>2</sub> is often very large, and thus, it is not efficient to perform molecular selection at this stage. Breeders usually use conventional breeding based on phenotypic selection up until generation F<sub>4</sub>, after which they use molecular selection in order to increase the frequency of desirable alleles (Bonnett et al. 2005; Richards et al. 2010).

population (TP). The training population includes related individuals that have been both genotyped and phenotyped, while the breeding population includes the descendants of a TP that are only genotyped but not phenotyped. GS has the ability to consider the effects of all markers spread across the genome, thus capturing more of the genetic variance of additive effects/breeding value. GS does not eliminate phenotypic selection but rather replaces many of the selections with whole-genome predictions. The greater the phenotypic similarity between the true breeding value in the TP and the expected GEBV in the BP, the greater the accuracy of the prediction model. Therefore, precision phenotyping is important for evaluating a training population because the resulting dataset serves as a foundation for GS to build the accuracy of the statistical models (Desta and Rodomiro 2014; Cobb et al. 2013).

However, like conventional selection methods, the application of molecular methods has not measurably improved the selection of QTs. As previously indicated, QTs show continuous phenotypic variation due to the low level of inheritance of polygenes and the influence of environmental factors. These characteristics usually result in a deviation from the genetic variance of additive effects (breeding value) ( $\sigma_A^2$ ).<sup>3</sup> This deviation could be due to the dominant effects ( $\sigma_D^2$ ), epistatic effects ( $\sigma_P^2$ ), and/or the variance ( $\sigma_{GE}^2$ ) arising from the interaction between the genotype and environment ( $G \times E$ ).

Previous studies of quantitative trait loci (QTL), e.g., Crossa et al. 2014; Nakaya and Isobe 2012; Singh and Singh 2015; and Thomas 2010, suggest that to overcome  $G \times E$  it is important to accumulate and evaluate field phenotypes of QT by planting the mapping populations in replicated trials conducted over different environments and years. For overcoming dominant and epistatic effects, Lu et al. (2011), Nakaya and Isobe (2012) and Singh and Singh (2015) and suggested the use of mapping causative loci such as interval mapping, association mapping/linkage disequilibrium (LD), and genome-wide association studies (GWAS). Mapping causative loci includes phenotypic, genotypic and pedigree data.

The discussion so far suggests that the application of genomic information may trigger a great leap forward

in plant breeding, but only if linked and integrated with corresponding phenomic and environmental information (Fig. 2). Figure 2 summarizes the processes that have to be taken before the application of automated phenotyping in plant breeding programs. In light of this challenge, several phenomic facilities [e.g., Julich Plant Phenotyping Centre, Australian Plant Phenomics, and Canada Plant Phenotyping and Imaging Research Centre (P2IRC)] and networks (e.g., International Plant Phenotyping Network, and European Plant Phenotyping Network) have been established and are operating at the national and global level. Looking forward, improvements in digital phenotyping technology, computing capacity, and statistical methodology should pave the way to efficiently archive, retrieve, analyze, integrate, and interpret phenomic data. The compelling social science research question is where will those innovations most likely be adopted and used.

## Breeders' decision to adopt automated plant phenotyping

### Model assumptions

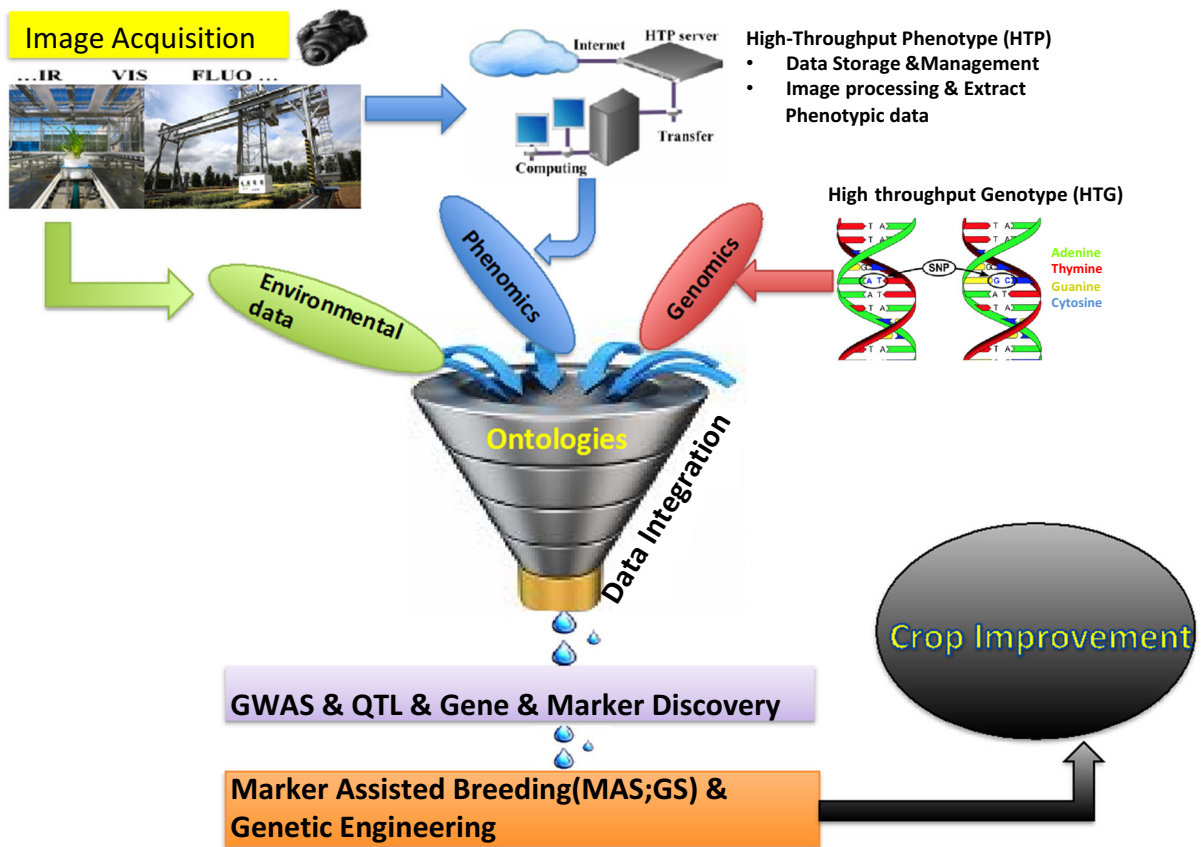
The model builds on previous work by Fulton and Giannakas (2004) and Awada and Yiannka (2012) who study the decision-making and welfare of heterogeneous consumers and producers in differentiated markets. In this model, we assume a group of heterogeneous breeders, each of whom is trying to optimize their relative profit function and needs to decide whether to adopt AP or to keep using CP. At time  $t$ , a breeder with attribute  $A$  has the following profit function:

$$\pi_t^{AP} = R^{AP} - (C^{AP} + \delta A) - K_t \quad \text{if a cultivar is produced using AP} \quad (1)$$

$$\pi_t^{CP} = R^{CP} - C^{CP} \quad \text{if a cultivar is produced using CP} \quad (2)$$

where  $\pi_t^{AP}$  and  $\pi_t^{CP}$  are the per unit profits associated with breeding a cultivar using AP and CP, respectively. The  $R^{AP}$  and  $R^{CP}$  are the economic revenue, and  $C^{AP}$  and  $C^{CP}$  are the costs of breeding a cultivar under AP and CP, respectively.  $C^{AP}$  and  $C^{CP}$  include the cost of breeder's activities, input costs, cost of information/data, and costs of quality testing, variety registration and release under each approach. Parameter  $A$

<sup>3</sup> Additive effects are also known as the breeding values as they are predictably transmitted to progeny.



**Fig. 2** Integration of genomic, phenomic and environmental data

captures heterogeneous breeders’ preferences and, thus, differences in their willingness to adopt AP. The sources of heterogeneity can reside in breeders’ experience, education, management skills, management of large/small scale breeding program, and information sources, among other attributes.  $A$  is assumed to be uniformly distributed with a unit density  $f(A) = 1$  in an interval  $A \in [0, 1]$ , such that the greater is the differentiating  $A$  (i.e.,  $A$  value is closer to 1), the lower is the breeder preference for AP. The parameter  $\delta$  is the cost enhancement factor that captures the degree of aversion to AP and is assumed to be a non-negative constant across all breeders. Thus,  $\delta A$  denotes the additional cost that a breeder with attribute  $A$  incurs when adopting AP.<sup>4</sup> The term

$K_t$  is the sunk cost at time  $t$ —an expense that typically incurred at the time of adoption and cannot be recovered once spent (e.g., training to operate the new technology, R&D, and specialized asset costs). Since AP is an emerging technology and many breeders are still uncertain about its integration into breeding programs, there is an option value to waiting before expending (‘sinking’) the costs of adoption. Thus,  $K_t$  can be seen as the loss that a breeder sustains by not waiting until the next period to adopt the technology and the delayed benefits from the subsequent higher rate of improvement.

In this study, the genetic gain ( $\Delta G$ ) is used to determine the revenue,  $R$ , from breeding a cultivar. Following Brennan (1989), the economic revenue from breeding a new cultivar of crop  $i$  is given by:

$$R_i = YES \left[ \Delta G_{iy} W_{iy} + \left( 1 + \frac{\Delta G_{iy}}{100} \right) (\Delta G_{iq} W_{iq}) \right] \quad (3)$$

<sup>4</sup> Due to the economies of scale and affordability, breeders who are managing larger programs are more likely to adopt AP. In this case, the value of the parameter  $A$  is closer to 0, indicating a stronger preference for the adoption of AP, the additional cost  $\delta A$  is lower, and thus, the adoption of AP is larger.

where  $Y$  is the mean yield (tonne/ha) before the introduction of the new cultivar,  $E$  is the crop  $i$  total growing area (ha); and  $S$  is the share of area  $E$  sown to the new cultivar (the adoption rate of the new cultivar);  $\Delta G_{iy}$  is the percentage genetic gain in trait affecting yield;  $W_{iy}$  is the unit value of  $\Delta G_{iy}$ ;  $\Delta G_{iq}$  is the percentage genetic gain in traits affecting quality; and  $W_{iq}$  is the unit value of  $\Delta G_{iq}$ .

Regardless of the technique or selection method employed, the genetic gain ( $\Delta G$ ) from selection serves as a universal concept for quantifying improvements in a cultivar. Hence, it is called the breeders' equation.  $\Delta G$  is the predicted change in the mean value of a trait within a population that happens by selection, and results in the introduction of a new cultivar in characters affecting yield and/or quality. The genetic gain is given by:

$$\Delta G = h^2 \sigma_p i / L \tag{4}$$

where  $h^2$  is the heritability parameter and represents the probability that a trait will be transmitted from parents to offspring.  $h^2$  in Eq. (4) is used in its narrow sense representing the proportion of phenotypic variation due to additive genetic effects ( $h^2 = \sigma_A^2 / \sigma_P^2$ ). The additive effect/breeding value is important in plant breeding as it represents what is transferred to offspring and can be changed by selection. As previously indicated QTs are more difficult to breed because of the large impact of dominance and epistatic effects, which reduce heritability. The term  $\sigma_p$  is the phenotypic variability in the original source population (parental population), which is positively associated with genetic diversity, and affected by the environment and the interactions between genotype and the environment ( $G \times E$ ). The term  $i$  is the selection intensity, expressed in units of standard deviation from mean, and represents the fraction of the current population retained and used as parents to produce the next generation (i.e., if the whole population is retained,  $i$  is zero). Finally, the term  $L$  is the length of cycle interval, which is usually one generation (i.e., how quickly a generation can be completed and the number of possible generations per year) (Acquaah 2012; Moose and Mumm 2008).

Automated phenotyping enables breeders to improve  $\Delta G$  by: (1) estimating  $h^2$  through the use of large-scale selection of (phenotype  $\times$  genotype) association data (GWAS) and large training population in GS that is

phenotyped and genotyped to estimate breeding value (GEBV). In addition, automated phenotype can improve  $h^2$  by determining the environmental effects on traits at multiple field environmental conditions ( $G \times E$ ); (2) increasing  $\sigma_p$  by introducing new genes, a large phenotypic variance would provide the breeder with a wide range of variability from which to select, and thus resulting in a higher  $\Delta G$ ; (3) increasing selection intensity,  $i$ , by helping breeders to choose a lower proportion of individuals having a mean superior to the population mean; and (4) shortening cycles ( $L$ ), as individuals can be chosen in early growing stage.

### Breeder's decision-making

A breeder's adoption decision is determined by comparing the profit derived from producing a cultivar under CP and AP so the breeder with a differentiating attribute  $\hat{A}_t = \frac{(R^{AP} - R^{CP}) - [(C^{AP} + K_t) - C^{CP}]}{\delta}$  (found by equating  $\pi_t^{AP} = \pi_t^{CP}$ ) is indifferent between breeding a cultivar under AP and CP (Fig. 3). Breeders with attributes  $A \in [0, \hat{A}_t)$  find it optimal to breed under AP, while breeders with attributes  $A \in (\hat{A}_t, 1]$  breed using CP. Given that breeders are uniformly distributed in the interval  $[0, 1]$ , the indifferent breeder  $\hat{A}_t$ , determines the share of AP and CT at time  $t$ , given by Eqs. (5) and (6), respectively.

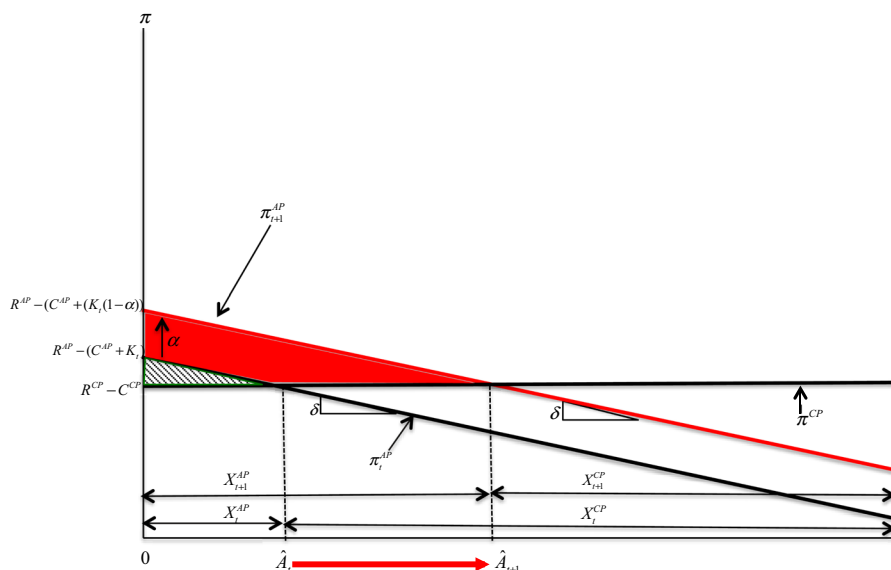
$$x_t^{AP} = \hat{A}_t = \frac{(R^{AP} - R^{CP}) - [(C^{AP} + K_t) - C^{CP}]}{\delta} \tag{5}$$

$$x_t^{CP} = 1 - \hat{A}_t = \frac{\delta - (R^{AP} - R^{CP}) - [(C^{AP} + K_t) - C^{CP}]}{\delta} \tag{6}$$

Equation (5) shows that for the AP to have a positive adoption the following conditions must hold:  $R^{AP} > ((R^{CP} - C^{CP}) + (C^{AP} + K_t))$  and/or  $(C^{AP} + K_t) < ((R^{AP} - R^{CP}) - C^{CP})$ . Otherwise, the profit curve of the AP,  $\pi_t^{AP}$ , will lie below the profit curve of the CP,  $\pi_t^{CP}$ , for all  $A$  values, and all breeders will not adopt AP and continue using CP (Fig. 3).

Figure 3 depicts the profit curves, the adoption shares, and aggregate breeder welfare when the revenue, cost, and breeder preference parameters are such that both AP and CP enjoy a positive share. At

**Fig. 3** Breeder’s decisions to adopt AP or keep using CP



time  $t$ , breeder welfare is given by the area below the  $\pi_t^{CP}$  curve plus the green dashed area in Fig. 3.

The above results are based on the assumption that a plant breeder is trying to make a decision whether to adopt AP or to keep using CP by optimizing their relative profit function. However, if AP is a complementary technology that is used, alongside, with the exciting CP technology, or a technology that offers a new information that is not provided by CP, the decision to adopt AP doesn’t affect the use of CP. In this case, the profit function of CP (i.e.,  $\pi_t^{CP}$ , Eq. 2) does not enter into the breeders’ analysis process to adopt AP, and thus, a breeder decision is determined by only examining the profitability of AP (i.e.,  $\pi_t^{AP}$ , Eq. 1). That is, for AP to have a positive adoption/market share the following condition must hold:  $R^{AP} > (C^{AP} + \delta A + K_t)$ , for all values of  $A \in [0, 1]$ .

At time  $t + 1$ , if AP improves, the sunk cost,  $K_t$ , decreases. Assuming that the technology improvement decreases  $K_t$  by a constant rate  $\alpha \in (0, 1)$  ( $\alpha$  could address aspects such as improvement in robotics and automation, big data management, training and education needed and collaborations) the profit function, *ceteris paribus*, of the breeder with attribute  $A$  from the adoption of AP at time  $t + 1$  is given by:

$$\pi_{t+1}^{AP} = R^{AP} - (C^{AP} + \delta A) - K_t(1 - \alpha) \tag{7}$$

if a cultivar is produced using AP

At time  $t + 1$ , the indifferent breeder with attribute  $\hat{A}_{t+1}$  is given by equating Eqs. (2) and (7):  $\hat{A}_{t+1} = \frac{(R^{AP} - R^{CP}) - [(C^{AP} + K_t(1 - \alpha)) - C^{CP}]}{\delta}$ . In Fig. 3, breeders with  $A \in [0, \hat{A}_{t+1})$  find it optimal to adopt AP, while breeders with  $A \in (\hat{A}_{t+1}, 1]$  keep breeding by using CP. The breeder with  $\hat{A}_{t+1}$  determines the adoption/share of AP and CP at time  $t + 1$ , given by Eqs. (8) and (9), respectively.

$$x_{t+1}^{AP} = \hat{A}_{t+1} = \frac{(R^{AP} - R^{CP}) - [(C^{AP} + K_t(1 - \alpha)) - C^{CP}]}{\delta} \tag{8}$$

$$x_{t+1}^{CP} = 1 - \hat{A}_{t+1} = \frac{\delta - (R^{AP} - R^{CP}) - [(C^{AP} + K_t(1 - \alpha)) - C^{CP}]}{\delta} \tag{9}$$

Equation (9) shows that the greater the rate of technology improvement ( $\alpha$ ) the lower the sunk cost,  $K_t$ , and thus the higher the proportion of breeders who use AP at time  $t + 1$ . This is shown graphically in Fig. 3 by shifting the profit curve of AP upward from  $\pi_t^{AP}$  to  $\pi_{t+1}^{AP}$  indicating an increase in the return to breeders from using AP by  $K_t(\alpha)$ , and, thus, an increase in the proportion of breeders who adopted AP by the interval  $[\hat{A}_t, \hat{A}_{t+1}]$ . Breeders who were using CP at time  $t$  decided to start using AP at time  $t + 1$  as a



result of the improvement in AP technology. At time  $t + 1$ , breeder welfare is given by the area below the  $\pi_t^{CP}$  curve plus the green and red dashed areas in Fig. 3, indicating an increase in breeder welfare by the dashed red area as a result of technology improvement ( $\alpha$ ).

In addition to decreasing any sunk cost, technology improvement,  $\alpha$ , may increase the genetic gain ( $\Delta G$ ) from selection, which in turn improves the return,  $R^{AP}$ , from the adoption of AP. The result is an upward parallel shift in the profit curve of AP in Fig. 3, and in an increase in the adoption of AP.

It is clear that the subsequent rate of improvement is an important determinant in advancing the adoption of AP by plant breeders. Progress in developing interdisciplinary technologies that empowers AP is moving forward rapidly. Tremendous investments in phenomic projects—Awada et al. (2017) reported that more than 33 plant phenotyping facilities were developed and seven networks were established around the world—are underway to develop standards and ontologies for trait measurement and to facilitate the integration of the large volume of phenotypic data with other big data relevant to plant breeding.

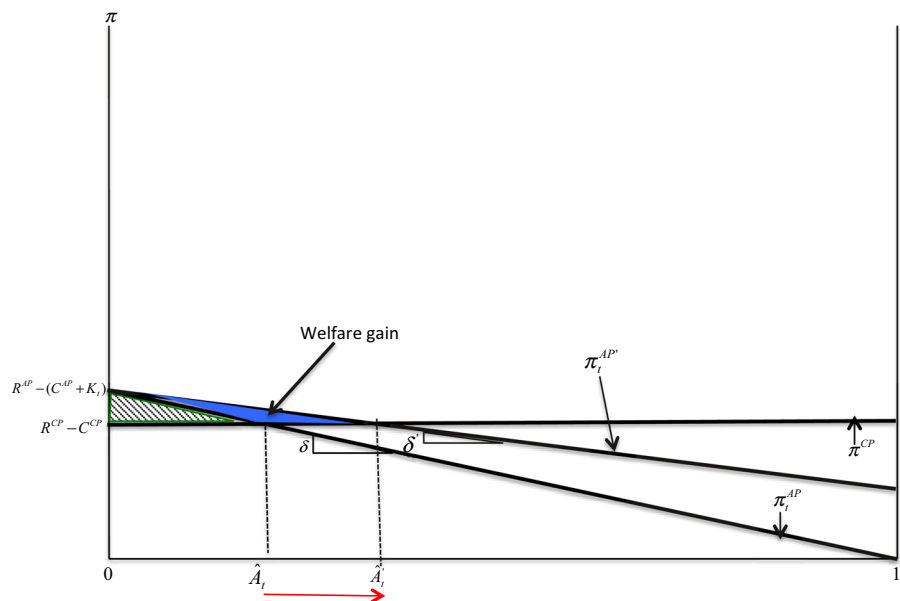
An important parameter in the model is breeder aversion,  $\delta$ , to AP. Notice that, the parameter  $\delta$  is the slope of the AP profit function, and represents the rate of AP adoption associated with the differentiating attribute A. For simplicity and without loss of

generality, we initially assumed that  $\delta$  is constant across all breeders over time. However, as a result of technological change and increase in the information available on AP,  $\delta$  may have variable values over time, which in turn may result in a non-linear adoption of AP. Figure 4 shows the impact of a change in the value of the parameter  $\delta$ . Lower  $\delta$ , *ceteris paribus*, leads to a decrease in the cost,  $\delta A$ , for all breeders (see Eq. 1) and, thus, higher AP adoption,  $x_t^{AP}$ , (see Eq. 5). In Fig. 4, the decrease in  $\delta$  causes the AP profit curve to rotate counter-clockwise from  $\pi_t^{AP}$  to  $\pi_t^{AP'}$ , resulting in an increase in the adoption of AP by the segment  $[\hat{A}_t, \hat{A}'_t]$ . Breeders' welfare increases by the blue dotted area in Fig. 4.

### The impact of different levels of breeder aversion on the expected return and the adoption of a technology

This section provides a numerical example to describe how the rate of aversion,  $\delta$ , may affect breeder's decision-making to adopt a new technology. We focus on the sensitivity of the expected return perceived by heterogeneous breeders having different levels of aversion toward the adoption of a technology (e.g., AP technology). Breeders characterized with high rate of aversion  $\delta$  seems to perceive the value of future returns less valuable than the return perceived by breeders

**Fig. 4** Impact of a decrease in breeder aversion on the adoption of AP



with low  $\delta$ . Basically, breeders adjust the discount rate on the future returns by  $\delta$  to reflect the risk they perceive by adoption the new technology. The higher the risk they perceive, the higher is  $\delta$ , and thus, the lower is the future return from the adoption of a technology.

In this example, we use wheat crop data in Saskatchewan, Canada. Because wheat is a self-pollinating non-hybrid crop, farmers can save harvested seeds without significant yield deterioration. This reduces the ability to repeatedly capture a return of the value created with the release of a new variety and discourages private investments in wheat breeding, the result is a high concentration of Canada's wheat breeding in public-funded programs, and an economic return that is mostly captured by farmers.

As previously indicated in Eq. (5), for the AP to have a positive adoption the following conditions must hold:  $R^{AP} > ((R^{CP} - C^{CP}) + (C^{AP} + K_t))$ . In this example,  $R^{AP}$  is assumed to be equal to the return from the introduction of a new wheat variety when the percentage of genetic gain,  $\Delta G$ , in trait is affecting yield (i.e.,  $R^{AP} = YES[\Delta G_{iy} W_{iy}]$  and  $(1 + \frac{\Delta G_{iy}}{100})(\Delta G_{iq} W_{iq}) = 0$  (see Eq. (3)).

Taking into account the rate of aversion,  $\delta$ , the present value of the social returns (PVR) from the release of a new cultivar can be estimated as:

$$\begin{aligned}
 PVR &= \sum \frac{R_t(1+g)}{[1+(r+\delta)]^t} \\
 &= \sum \frac{YES[\Delta G_{iy} W_{iy}](1+g)}{[1+(r+\delta)]^t} \quad (10) \\
 &\text{for } t = 1 \dots n
 \end{aligned}$$

where  $R_t = YES[\Delta G_{iy} W_{iy}]$  is the annual social return from releasing a new wheat variety, calculated based on an average target growing area sowing to wheat in Saskatchewan,  $E$ , of 5.3 million ha with mean yields,  $Y$ , of 2.34 t/ha in the years 2001–2017; a new variety is assumed to have a genetic gain in yield/yield advantage,  $\Delta G$ , of 2%; and wheat price,  $W$ , is \$226/t (Statistics Canada, CANSIM Tables: 001-0010; 002-0043). The rate of adoption of a new wheat variety,  $S$ , is derived from Covey (2012). In Covey (2012), a prediction model was built to derive the adoption pattern of wheat varieties in Western Canada, which depends on the yield advantage, available varieties, maturity, resistance to sawfly, rust, lodging, clearfield,

midge and loose smut, and the number of years since release. Based on this study, a wheat variety reaches its maximum adoption of 10.57% of wheat area in Western Canada in the thirteenth year after its release.

The term  $g$  in Eq. (10) is the expected growth rate, a normal random variable with mean 2 and 1% standard deviation ( $g = \mu + \sigma z$ ). The growth rate reflects the expected fluctuation in the price over the covered period. The term  $r$  is the real discount rate and is equal to 5%;  $\delta$  is the rate of breeder aversion;  $(r + \delta)$  represents the risk-adjusted discount rate which reflects the relationship between risk and return; and  $t$  is the adoption period, representing the total life of the new variety after its release, assumed to be equal to forty-five years.

### Estimation of total return

Using Eq. (10), the estimated annual returns for the base run ( $\delta \approx 0$ ) from the release of a new wheat variety are presented in Table 4 in Appendix 1. Table 4 shows that the return rises to a maximum of \$5.9 million in year thirteen before declining as the variety is overtaken by newer and more competitive varieties and gradually replaced. Total returns are equal to \$161.2 million, and total present value of the returns (PVR) is \$78.2 million at 5% discount rate.

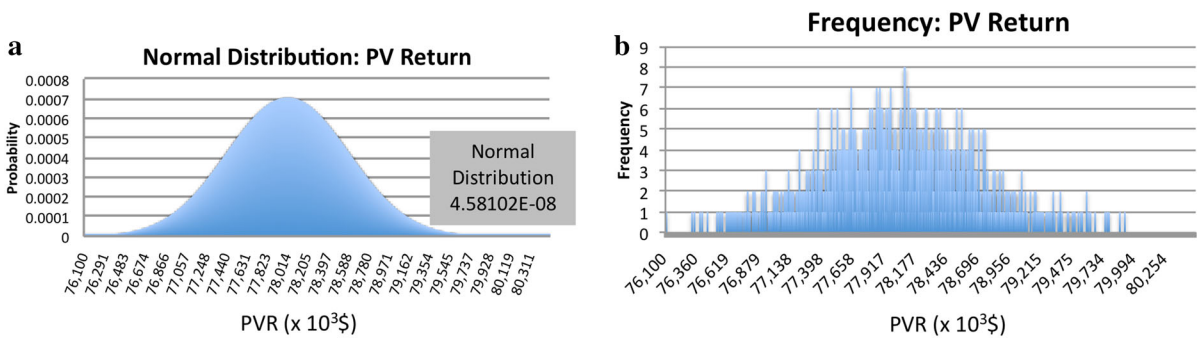
Since plant-breeding programs are highly characterized with uncertainty, a Monte Carlo simulation (MCS) analysis is used to account for the variability in the related variables, and to produce a distribution of possible return values. Using MCS with 2000 runs, the key statistics on the estimated returns based upon the probability distributions of the related variables, are summarized in Table 3. Results of the base run are presented in Table 3, column 1, and the distribution and frequency of the base run PVR are graphed in Fig. 5a, b, respectively. The mean of PVR for the base run is found equal to \$78 million with a standard deviation of \$0.57 million. The mean of the Monte Carlo simulations is found close to the analytical result.

Columns 2–6 in Table 3 present the sensitivity of the expected PVR results to different values of the breeders' aversion rates. Compared to the base run, when breeders' aversion,  $\delta$ , is equal to 2%, the mean of the PVR decreases by 21%, and when  $\delta = 50\%$ , the return decreases by 69%, indicating the high sensitivity of the results to the rate of aversion.

**Table 3** Sensitivity analysis a Monte Carlo simulation: the impact of different values of breeders’ aversion rate ( $\delta$ ) on the present value of the returns (PVR)

|                                                         | Rate of breeder aversion (%) |              |              |               |               |               |
|---------------------------------------------------------|------------------------------|--------------|--------------|---------------|---------------|---------------|
|                                                         | Base run                     |              |              |               |               |               |
|                                                         | $\delta \approx 0$           | $\delta = 2$ | $\delta = 5$ | $\delta = 10$ | $\delta = 15$ | $\delta = 50$ |
| Mean PVR ( $\times 10^6$ \$)                            | 78.01                        | 61.51        | 45.65        | 30.23         | 22.10         | 6.77          |
| Standard deviation ( $\times 10^6$ \$)                  | .57                          | .68          | .77          | .81           | .81           | .52           |
| Minimum ( $\times 10^6$ \$)                             | 76.00                        | 59.16        | 42.16        | 27.29         | 19.50         | 4.57          |
| Maximum ( $\times 10^6$ \$)                             | 79.90                        | 64.04        | 48.20        | 33.13         | 24.60         | 8.51          |
| Upper limit at 95% confidence level ( $\times 10^6$ \$) | 78.04                        | 61.54        | 45.68        | 30.27         | 22.13         | 6.80          |
| Lower limit at 95% confidence level ( $\times 10^6$ \$) | 77.98                        | 61.48        | 45.61        | 30.19         | 22.06         | 6.75          |

Monte Carlo Simulation is based on 2000 runs. Returns calculation is based an average target growing area,  $E$ , of 5.3 million ha with mean yields,  $Y$ , of 2.34 t/ha (2001-17); new variety has a genetic gain in yield/yield advantage,  $\Delta G$ , of 2%; wheat price,  $W$ , is \$226/t (Statistics Canada, CANSIM Tables: 001-0010; 002-0043); discount rate is equal to  $r = 5\%$  per annum; expected growth rate,  $g$ , has mean 2% and 1% standard deviation (*i.e.*,  $g = \mu + \sigma z$ ); and rates of adoption of new wheat variety in Western Canada are obtained from Covey (2012)



**Fig. 5** Base run result of the present value of the returns (PVR)

Table 3 shows that the expected return from the adoption of a new technology to improve wheat varieties decreases when  $\delta$  increases, indicating that breeders with higher  $\delta$ , tend to discount the return at higher rate, and thus, to perceive lower return, which in turn may negatively influence their adoption of the technology.

The above framework can be applied to analyze the impact of breeders’ aversion on the expected return generated from the introduction of any new crop variety. However, in the case of genetically modified and hybridized crops, which are heavily concentrated in the private sector, the emphasis would be mostly on the economic returns to the seed breeding companies. In this case, the return would be determined based on the market size and structure and on the

public sector policies within the geography area under study.<sup>5</sup>

**Future research**

Clearly the next step is to operationalize the theoretical model by collecting specific data on each of the

<sup>5</sup> Hybridized crops are characterized by their ability to exhibit heterosis – the ability of offspring to outperform their parents with respect to different characteristics and agronomical important traits. Heterosis effects disappear after the cultivation of the first generation (F1), which compels farmers to purchase new seeds every year, and makes it profitable for private seed company to invest in breeding hybrid crops. In the case of genetically modified crops patents prevent farmers from saving their seed and secure monopoly profits to the seed companies.

model parameters to examine the adoption of AP technology by plant breeders. Data collection and subsequent profitability framework analyses (i.e., benefit–cost ratio and internal rate of return) will also allow the calculation of the return to investment in AP technology by plant breeders. However, as AP technology is still in its developing stage, there is a paucity of accurate information about the costs (variable and fixed costs) of breeding a new variety using AP and on the contribution of this technology in achieving a greater genetic gain and thus a greater return from breeding. Moreover, collecting data on breeders' heterogeneity and their level of aversion to AP is a complex, largely empirical task. The nature and formation of a breeders' behaviour involves a psychological process that breeders go through, starting with recognizing the need for AP and then interpreting information, making an adoption decision, and implementing the technology in their programs. The process blends elements from four types of social sciences—psychology, sociology, anthropology, and economics. Typically, data collection implies the use of diverse research methods including survey research, interviews, statistical analysis, econometrics, social network analysis, case studies, behavioural experiments, and model building, among other approaches.

## Conclusion

Some researchers believe that the adoption of the latest high-throughput genomics and phenomics technologies by plant breeders can deliver better new cultivars and accelerate the process of breeding. While in the last two decades we have witnessed a large adoption of genomic technologies, the adoption of automated phenotyping/phenomics by plant breeders is still in its infancy. The question remains whether widespread adoption of phenomics can happen? And what will it take to be realized?

Adoption of new technology is always difficult to anticipate. While the literature is rife with examples of innovators capturing first-mover advantage, including lock-in and network effects (Shapiro and Varian 1999), there are many real impediments to realizing that vision. Just because a new method improves output does not assure uptake and use. Sunk costs, individual characteristics and preferences, and uncertainty about the evolution of the technology are all factors that

could limit adoption and use of a new technology. The emergence of AP approaches, the enormous volume, diversity, and velocity of imaging and remote-sensing data generated by AP, and the difficulty of linking this data to genotypic and environmental data looks exciting but could end up stranded. This paper has explored one way to model this decision space. A theoretical model of heterogeneous breeders is built to analyze breeders' decision-making as they ponder whether to adopt automated phenotyping or to keep using conventional phenotyping. The model focuses on the evolving nature of technologies, which assumes that future R&D will improve the technology and, thus, breeders may have an incentive to wait to adopt AP to mitigate the impacts of sunk cost. The result of this model indicates that many interlocking factors are at work as breeders determine whether to adopt AP. We found that factors, including the expected return, adoption costs, the rate of technology improvement, and breeders' preference and degree of aversion to AP can affect the present and future adoption of AP. A priori it is not possible to determine the adoption path for this technology—practical estimation of the model parameters and manipulation of the model is necessary to determine the likely path.

This paper does not address the impact of the institutional policy framework on the adoption of AP in plant breeding programs. Future research may focus on the role that might be played by regulatory and governance models in facilitating or delaying the adoption and application of the phenomics technology in plant breeding. Future research may address the mechanisms for the protection of Big Data process, such as access, sharing, and reuse of the data generated by the automated phenotyping technology.

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## Appendix 1

See Table 4.

**Table 4** Adoption rate and annual return from adoption: base run rate of aversion equal zero ( $\delta \approx 0$ )

| Years after the release, $t$ | Average rate of adoption, $S^a$ (%) | Revenue <sup>b</sup> ( $\times 10^6$ \$) = $YES[\Delta GW]$ | Present value revenue <sup>c</sup> ( $\times 10^6$ \$) |
|------------------------------|-------------------------------------|-------------------------------------------------------------|--------------------------------------------------------|
| 1                            | 5.20                                | 2.89                                                        | 2.83                                                   |
| 2                            | 6.00                                | 3.34                                                        | 3.05                                                   |
| 3                            | 7.00                                | 3.89                                                        | 3.42                                                   |
| 4                            | 7.80                                | 4.34                                                        | 3.60                                                   |
| 5                            | 8.30                                | 4.61                                                        | 3.73                                                   |
| 6                            | 9.00                                | 5.00                                                        | 3.86                                                   |
| 7                            | 9.20                                | 5.11                                                        | 3.72                                                   |
| 8                            | 9.80                                | 5.45                                                        | 3.75                                                   |
| 9                            | 10.00                               | 5.56                                                        | 3.65                                                   |
| 10                           | 10.20                               | 5.67                                                        | 3.51                                                   |
| 11                           | 10.40                               | 5.78                                                        | 3.41                                                   |
| 12                           | 10.45                               | 5.81                                                        | 3.29                                                   |
| 13                           | 10.57                               | 5.88                                                        | 3.23                                                   |
| 14                           | 10.45                               | 5.81                                                        | 3.00                                                   |
| 15                           | 10.40                               | 5.78                                                        | 2.83                                                   |
| 16                           | 10.20                               | 5.67                                                        | 2.62                                                   |
| 17                           | 10.00                               | 5.56                                                        | 2.44                                                   |
| 18                           | 9.90                                | 5.50                                                        | 2.33                                                   |
| 19                           | 9.50                                | 5.28                                                        | 2.16                                                   |
| 20                           | 9.30                                | 5.17                                                        | 2.02                                                   |
| 21                           | 9.00                                | 5.00                                                        | 1.82                                                   |
| 22                           | 8.90                                | 4.95                                                        | 1.75                                                   |
| 23                           | 8.50                                | 4.73                                                        | 1.60                                                   |
| 24                           | 8.00                                | 4.45                                                        | 1.40                                                   |
| 25                           | 7.70                                | 4.28                                                        | 1.30                                                   |
| 26                           | 7.00                                | 3.89                                                        | 1.12                                                   |
| 27                           | 6.50                                | 3.61                                                        | 1.01                                                   |
| 28                           | 6.00                                | 3.34                                                        | 0.87                                                   |
| 29                           | 5.50                                | 3.06                                                        | 0.76                                                   |
| 30                           | 5.00                                | 2.78                                                        | 0.65                                                   |
| 31                           | 4.80                                | 2.67                                                        | 0.60                                                   |
| 32                           | 4.30                                | 2.39                                                        | 0.51                                                   |
| 33                           | 4.00                                | 2.22                                                        | 0.45                                                   |
| 34                           | 3.80                                | 2.11                                                        | 0.41                                                   |
| 35                           | 3.50                                | 1.95                                                        | 0.36                                                   |
| 36                           | 2.80                                | 1.56                                                        | 0.27                                                   |
| 37                           | 2.20                                | 1.22                                                        | 0.21                                                   |
| 38                           | 2.00                                | 1.11                                                        | 0.17                                                   |
| 39                           | 1.80                                | 1.00                                                        | 0.15                                                   |
| 40                           | 1.20                                | 0.67                                                        | 0.10                                                   |

**Table 4** continued

| Years after the release, $t$ | Average rate of adoption, $S^a$ (%) | Revenue <sup>b</sup> ( $\times 10^6$ \$) = $YES[\Delta GW]$ | Present value revenue <sup>c</sup> ( $\times 10^6$ \$) |
|------------------------------|-------------------------------------|-------------------------------------------------------------|--------------------------------------------------------|
| 41                           | 1.00                                | 0.56                                                        | 0.08                                                   |
| 42                           | 0.80                                | 0.45                                                        | 0.06                                                   |
| 43                           | 0.70                                | 0.39                                                        | 0.05                                                   |
| 44                           | 0.65                                | 0.36                                                        | 0.04                                                   |
| 45                           | 0.60                                | 0.33                                                        | 0.04                                                   |
| Total ( $\times 10^6$ \$)    |                                     | 161.15                                                      | 78.22                                                  |

<sup>a</sup>Source: Covey (2012)

<sup>b</sup>Based on an average target growing area,  $E$ , of 5.3 million ha with mean yields,  $Y$ , of 2.34 t/ha (2001–2017); new variety has a genetic gain in yield/yield advantage,  $\Delta G$ , of 2%; wheat price,  $W$ , is \$226/t; value of 2% yield increase is \$4.5/t (Statistics Canada, CANSIM Tables: 001-0010; 002-0043)

<sup>c</sup>Based on discount rate,  $r = 5\%$  per annum;  $\delta = 0$ ; and expected growth rate,  $g$ , with mean 2 and 1% standard deviation (i.e.,  $g = \mu + \sigma z$ )

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