

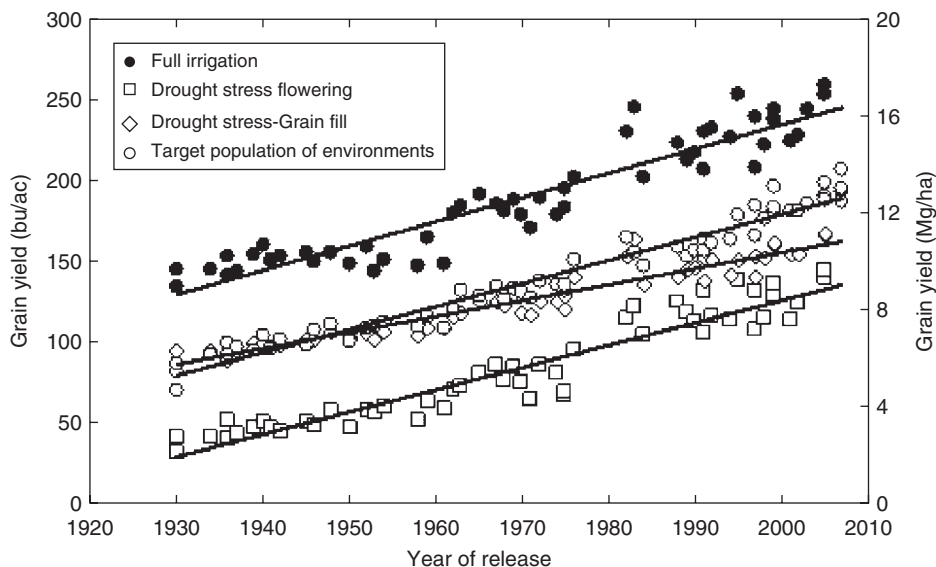
Modelling Crop Improvement in a $G \times E \times M$ Framework via Gene–Trait–Phenotype Relationships

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1. INTRODUCTION

Crop performance is determined by the combined effects of the genotype of the crop and the environmental conditions of the production system. Improving crop performance to satisfy an increasing demand for plant products is a constant challenge to plant scientists. Plant breeders approach this challenge by searching the genetic space for superior genotypes that have improved performance across the environments of the production system (Figure 1), while agronomists pursue the same goal by optimising management for the cohort of elite genotypes developed by plant breeding. Historically, plant breeding and agronomy have co-evolved, and both have contributed to improved crop performance. This iterative process has been extremely successful in creating superior crops as demonstrated by the steady increase in maize yields in the USA (Duvick et al., 2004; Duvick and Cassman, 1999; Castleberry et al., 1984), and the consistent but discontinuous progress in wheat yield in Australia (Chapter 2). Crop physiology and modelling, although useful to interpret and describe the physiological process underpinning such yield improvements (i.e. Gifford et al., 1984; Duncan et al., 1978; Duvick et al., 2004; Slafer, 1994; Otegui and Slafer, 2000), have provided little guidance for how to apply these concepts to improve the efficiency of the breeding process (Campos et al., 2004; Evans, 1976; Sinclair et al., 2004; Lee, 1995).

The current paradigm of creating improved crops by breeding new genotypes and then optimising their management at a later stage of the crop improvement process constrains breeders and agronomists to exploring a reduced set of the vast space defined by the full set of possible genotype (G) and management (M) combinations. In addition, variable environmental (E) conditions interacting with G and M ($G \times E \times M$) complicates the definition of the possible paths towards realised genetic gain in production environments and limits our ability to make inferences on the effects of alternative management practices. The size and complexity of the $G \times E \times M$ system, and the difficulty of dealing with many interactions simultaneously, has traditionally been tackled by crop scientists through a discipline-centred approach that deals with components of the $G \times E \times M$ interactions separately, most frequently as $G \times E$ by plant breeders and $M \times E$ by agronomists (Cooper and Hammer, 1996; Boote et al., 1996; Loomis and Connor, 1992). An open question is whether enhanced rates of crop improvement can be realised by a more integrated approach. The quantification of these interactions relies on the use of statistical methods (i.e. Cooper and Hammer, 1996), yet interpretation of these $G \times E \times M$ interactions could be improved by means of crop modelling and simulation applied to understand their causes and their relevance to the target production system (Cooper and Hammer, 1996; Löffler et al., 2005).

**FIGURE 1**

Maize yield improvement for a set of Pioneer hybrids released between 1920 and 2007 grown in the target population of environments ($y = 1.43x + 78.95$; $r^2 = 0.96$), full irrigation ($y = 1.51x + 129.4$; $r^2 = 0.88$) and drought stress imposed at flowering ($y = 1.39x + 28.6$; $r^2 = 0.90$), or grain filling ($y = 0.99x + 86$; $r^2 = 0.90$). Linear regressions estimate using 1930 as base year. Conversion factor between bu/a and Mg/ha is 0.06271.

The vast size and complexity of the $G \times E \times M$ space that confronts breeders and agronomists present many challenges to the definition of practical approaches for developing improved crops and management practices as integrated and coordinated products since most of this space remains unobserved. The exhaustive empirical exploration of this space is not feasible. This led to the proposition that development of superior cultivars is limited by the ability to simultaneously identify favourable combinations of genomic regions and sustainable management systems that optimise resource capture in cropping systems operating in a target population of environment (TPE), given the resources available to plant breeders and agronomists to search among possible $G \times M$ combinations (Cooper and Hammer, 1996; Hammer and Jordan, 2007). In a context of rapid technological innovation in agronomy (Chapters 2 and 3), environmental change (Karl and Trenberth, 2003; Chapter 20) and increasing costs per unit yield gain (Duvick and Cassman, 1999), it is opportune to contemplate the following questions:

- Can we explore the $G \times E \times M$ space more effectively?
- Can we leverage advances in knowledge of $G \times E \times M$ interactions, and associated physiological concepts, to tackle this complexity in an integrated approach to develop improved crops?

It can be anticipated that positive answers to these two questions would lead to crop improvement methods that enable breeders and agronomists to project trajectories in the $G \times E \times M$ space into the future and gain insights into the consequences of manipulating genomes to create improved crops for targeted management and environments. Central to these methods are the quantification of gene-to-phenotype (GP) relationships for key traits in the reference population of a breeding program and the capacity of the framework to identify genetic hypotheses that could be tested and utilised in the breeding program.

Significant efforts have been made to tackle the GP problem by seeking approaches that link information at the level of gene or genomic region to the expressed phenotype in a manner that is useful for selection

(Cooper et al., 2002, 2005; Hammer et al., 2006; Tardieu, 2003). An emergent synthesis of the promising approaches to the GP problem involves advancing mathematical models of crop growth and development to link genetic variation in adaptive traits to physiological determinants, developing advanced statistical methods that help relate genomic regions to parameters in the model control equations (van Eeuwijk et al., 2005) and modelling of the $G \times E \times M$ systems as an extension of Kauffman's NK model (Box 1). The integration of these tools and their application in breeding has proven to be non-trivial. There is still debate about the level of details needed for crop growth models to be able to integrate processes across levels of organisation while predicting emergent functional consequences for the organism that arise from the interplay among gene networks, cell metabolism, plant organs, individuals in the crop and the environment (Hammer et al., 2006).

BOX 1 The $E(NK)$ Model

The $E(NK)$ model, and an informal extension to accommodate M , provides a framework to consider adaptation and fitness landscape. In this model N represent the number of genes involved in determining the performance of the genotype, K the average level of epistasis (interactions between a gene and any of the other $N - 1$ genes for a given E) and E the number of environment types in the TPE (Cooper and Podlich, 2002). The parenthesis notation indicates that the number of genes and the level of epistasis can change with E , and by extension with M . The simplest form of the model assumes one environment and management to generate a fixed structure or potential surface, on which peaks are positions sought through

breeding. The two-allele diploid $NK = N:0$ family of models, which corresponds to the additive finite locus genetic model used in quantitative genetics, has a landscape characterised by a single peak and a smooth surface, that is, the trait performance of genetically similar individuals are highly correlated. Landscapes become more rugged as K (level of epistasis) increases. In the limit where $K = N - 1$ ($N:N - 1$ family of models), the landscape is fully random (Kauffman, 1993). For a given family of NK models, changes in environment types and their frequencies induce deformations to the adaptation landscapes; the magnitude of the deformation depends on the underlying trait physiology (Cooper and Podlich, 2002).

The aim of this chapter is to introduce fundamental concepts of modelling natural systems using a $G \times E \times M$ framework and discuss prospects for an integrated approach for improving crop performance that tackles the $G \times E \times M$ interactions holistically. First, we outline general principles of modelling biophysical systems, including a description of fundamental components of crop models. Second, we describe $G \times E \times M$ systems and introduce GP models, the $E(NK)$ framework and concepts of adaptation landscapes as applied to plant breeding. Finally, we demonstrate and discuss the application of the framework by studying genetic improvement of maize in the US Corn Belt.

2. MODELLING BIOPHYSICAL SYSTEMS

Crop models are implementations of theoretical frameworks in the form of a series of quantitative expressions. As such, crop models formalise and integrate concepts from disciplines such as physiology, micrometeorology, soil science and biophysics into an interrelated system of mathematical equations that describes the dynamic growth and development of a crop (de Wit, 1982; Thornley and Johnson, 2000). Crop models represent a simplified view of all or part of the natural system. The motivation for seeking a simplified quantitative representation of the target system is to help scientists approach complex problems by focusing on the important components and achieve their research objectives. The structure and complexity of a crop model (e.g. time step for integration) thus depends on the research or technology objective. In this context, crop modelling should be viewed as an iterative process in which model predictions become testable hypotheses, and the results of testing these hypotheses generate feedback to the model-building process

to improve the representation of the biological and physical processes and the model structure whenever necessary. Simulation, which involves exercising the model in order to study system dynamics and properties, is a critical activity in this iterative model-building approach, as it provides a method to study the natural system through the properties captured in the quantitative model. With an acceptable model, such research can help understand emergent behaviour of the system and conceive new concepts that translate into new knowledge, sometimes expressed in the form of new equations and algorithms. The result of the systems modelling and simulation process is the assimilation of knowledge into an integrated theoretical framework from which quantitative predictions and testable hypotheses are proposed for experimental investigation (Hammer and Jordan, 2007; Thornley and Johnson, 2000).

The crop models in use today integrate physiological knowledge developed through more than 30 years of empirical research (Sinclair and Seligman, 1996). Since the first developments by de Wit in the 1960s (van Ittersum et al., 2003), many crop models have been built with different scope and objectives in mind. A recent symposium on Farming Systems Design listed more than 70 models (<http://www.iemss.org/farmsys07/index.php>). The review of all these models and their component processes is beyond the scope of this chapter. A description of the most common modelling platforms used in agricultural sciences and their 'pedigree' can be found elsewhere (Jones et al., 2003; Keating et al., 2003; van Ittersum et al., 2003; Stöckle et al., 2003). Reference publications provide detailed treatments and models for simulating energy balance and transpiration (Jones, 1992; Nobel, 2005), photosynthesis (Nobel, 2005; Boote and Loomis, 1991), different aspects of soil water and nutrient balance (Hanks and Ritchie, 1991; Ritchie, 1998; Loomis and Connor, 1992) and soil carbon dynamics (Parton et al., 1988, 1994). Chapter 20 (Section 4) outlines modelling approaches with emphasis on grain yield and climate change. With a narrower, more specific focus, other chapters discuss modelling approaches for capture and efficiency in the use of radiation (Chapter 7) and aspects of grain quality (Chapter 16). Here we outline common modelling approaches and fundamental components of crop models with emphasis on genetic, environmental, management and $G \times E \times M$ drivers of grain yield.

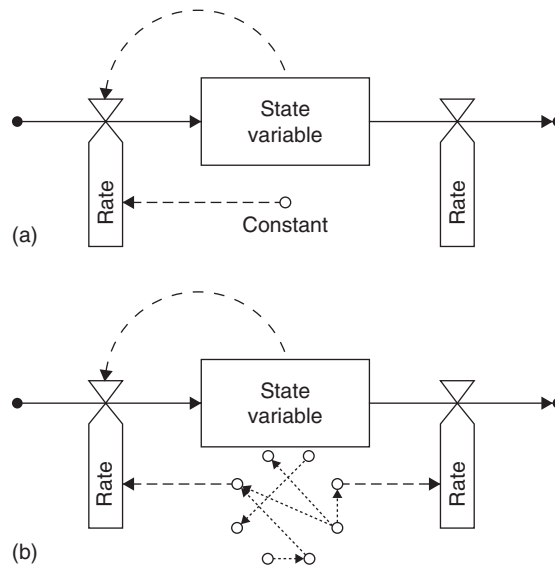
Crop models of interest in crop physiology, and in particular those suitable to modelling $G \times E \times M$ interactions, are continuous, dynamic (include a time dimension) and foremost explanatory (Thornley and Johnson, 2000; Hammer et al., 2006). This type of model can be viewed as a bridge across levels of biological organisation enabling the researcher to understand the behaviour of a system based on the knowledge gained by experimentation on its key component systems (de Wit, 1982). Experience has indicated that stable and credible models usually do not include components that simulate physiological determinants occurring at more than two levels of organisation away from the target level (Hammer et al., 2004; Sinclair and Seligman, 1996). Explanatory models thus focus on modelling processes that are formalised as rate variables (Figure 2; de Wit, 1982; Loomis et al., 1979). The separation of states of the system from underpinning determinant processes enables the identification of useful links among the environment, physiological processes and genetic determinants, and to formalise these links as metaproceses that provide the backbone for GP modelling (Figure 2b; Tardieu, 2003; Hammer et al., 2006).

2.1. Anatomy of a crop model

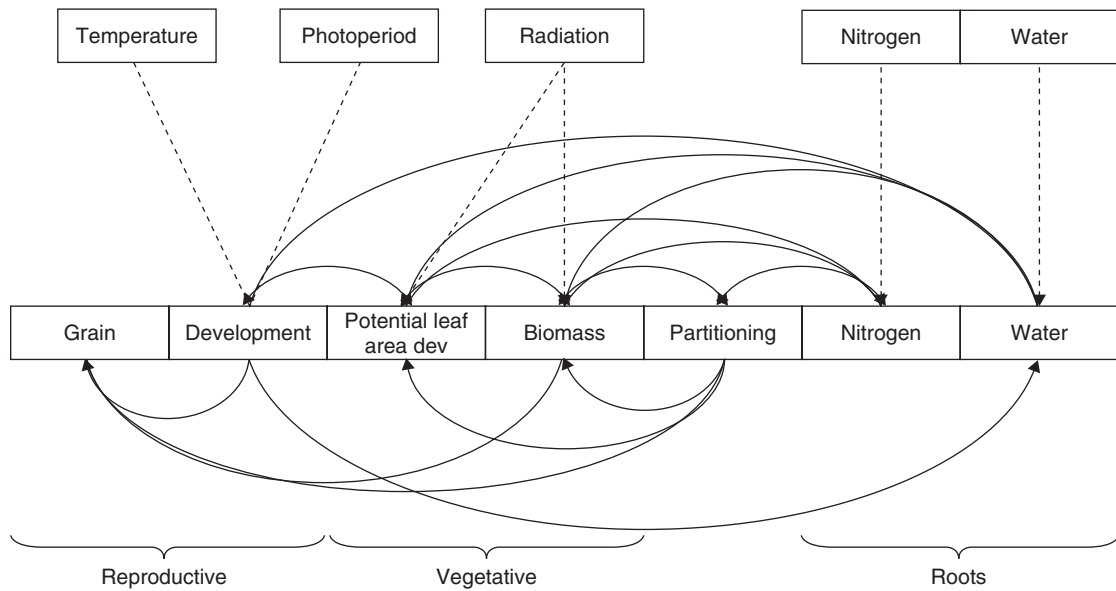
Figure 3 highlights interactions between crop processes, and between crop processes and the environment, as captured in a generic simulation model. Algorithms associated with key aspects of plant growth and development are critical features of crop models. Plant development sets out the master control of the timing of events in the plant life cycle (i.e. transition between vegetative and reproductive growth; duration of reproductive growth). Plant growth is driven by organ development (e.g. canopy, roots), and the ability of the crop to capture resources (light, water and nitrogen) and convert them into vegetative and reproductive biomass.

2.1.1. Development

The prediction of the duration of the crop life cycle, and the timing of milestones that affect resource capture and partitioning, is the central component of any crop model; Chapter 12 summarises the environmental

**FIGURE 2**

(a) Representation of a system model using a state-variable approach and drawn according to the convention of Forrester (1961).
 (b) Integration of the NK model to predict systems state based on any genetic architecture via its effects on process rates.

**FIGURE 3**

Schematic of major components of a crop model, their interactions among components and with the environment.

and genetic controls of crop development. There are many models of crop development through the various phases of the crop life cycle (Hammer et al., 1989; McMaster and Wilhelm, 1997; Ritchie and NeSmith, 1991; Grimm et al., 1994; Erskine et al., 1990; Sinclair, 1996). Because the genetic architecture of plant development is only incipient (Simpson et al., 1999; Koornneef et al., 1998; Corbesier et al., 2007; Tamaki et al., 2007), models of crop development remain empirical descriptions of the relationship between development rates and temperature and photoperiod. The metaphor of physiological day is an appealing and intuitive approach to model crop development. The concept proposes that under optimal temperature and photoperiod, the development rate is at its maximum and that the rate decreases as these conditions deviate from the optimum (Hammer et al., 1989). Then a development milestone (e.g. transition of a meristem from vegetative to reproductive) is reached after n physiological days, which is the inverse of the maximum development rate. The algorithm that implements this concept is represented by the following set of equations (Grimm et al., 1994; Soltani et al., 2006):

$$R(t) = F(N) \times F(T) \quad (1)$$

where $R(t)$ is the development rate (derivative of development with respect to time) on day t ; $F(N)$ is the night length (or photoperiod) function; and $F(T)$ is the temperature function. $F(N)$ and $F(T)$ are computed each day and assume values between zero and one. A value of one represents the greatest development rate and occurs when one 'physiological day' is achieved in one calendar day. The generalised representation of these multiple linear response functions is illustrated for $F(T)$ as:

$$\begin{aligned} F(T) &= 0 & \text{if } T < T_b \\ F(T) &= \frac{T - T_b}{T_{opt1} - T_b} & \text{if } T_b < T < T_{opt1} \\ F(T) &= 1 & \text{if } T_{opt1} < T < T_{opt2} \\ F(T) &= \frac{T_{opt2} - T}{T_u - T_{opt2}} & \text{if } T_{opt2} < T < T_u \\ F(T) &= 0 & \text{if } T > T_u \end{aligned} \quad (2)$$

where T_b is the base temperature below which no development occurs; T_{opt1} and T_{opt2} are the lower and upper bounds of the optimal temperature range for development; and T_u is the upper temperature limit for development. Similar equations could be used to model effects of abiotic stresses on development (Boote et al., 1998).

2.1.2. Capture of resources and crop growth

Crop growth depends on the ability of the crop to capture resources and convert them to biomass. Assuming no nutrients or pest limitations, radiation and water are the key drivers of growth, and crop biomass increments can be calculated by identifying whether the crop is primarily limited by radiation or water (Monteith, 1988; Chapman et al., 1993). Elsewhere, the book presents detailed accounts of capture and efficiency in the use of water (Chapter 6), radiation (Chapter 7) and nitrogen (Chapter 8). Here we deal briefly with radiation and water, from a modelling perspective.

2.1.2.1. Radiation-limited growth

In light-limited situations, above-ground crop growth rate depends on the radiation intercepted and radiation use efficiency (RUE). RUE has been studied widely and considered relatively stable for many given species (Sinclair and Muchow, 1999). However, recent studies have identified increases in RUE in modern elite maize hybrids (Lindquist et al., 2005). Although the cause of this increase remains unknown, other studies

in wheat (Miralles and Slafer, 1997) have linked differences in RUE with root–shoot partitioning for lines varying in height. RUE can be derived from the photosynthetic response to light of leaf elements in the canopy and is dependent on the leaf nitrogen status of those leaf elements, via effects on maximum photosynthetic rate (Sinclair and Horie, 1989), and the amount and nature of the incident radiation (Hammer and Wright, 1994). Hence, RUE is a canopy-level measure of photosynthetic performance that sets limits on productivity under potential growth conditions.

The extent of radiation intercepted depends on the canopy leaf area and architecture. Light interception is commonly modelled via the Beer–Lambert Law of light extinction in a canopy (Monsi and Saeki, 2005), which quantifies the exponential decay of light with increasing leaf area. The extinction coefficient (k) is dependent on leaf angle (LA) in the canopy. Lower k is associated with more erect leaves (Monsi and Saeki, 2005), which can increase crop growth rate and RUE in canopies with high leaf area index by distributing light more effectively over the layers of leaf area within the canopy (Duncan et al., 1967). Hence, the development of the canopy leaf area is critical to the dynamics of radiation-limited crop growth through the crop cycle.

2.1.2.2. Water-limited growth

The demand for water in transpiration can be determined from the ratio of crop growth and transpiration efficiency (TE), with the latter adjusted for the effect of daytime vapour pressure deficit (Tanner and Sinclair, 1983; Sinclair et al., 1984). While this biophysical approach is robust for estimating transpiration demand, recent studies (Kemanian et al., 2005) have indicated it needs some adjustments under low-vapour-pressure-deficit conditions (Section 6.4 in Chapter 7).

Water-limited situations occur when the potential supply of water from root uptake cannot meet transpiration demand. In that situation, crop growth can be calculated as the product of the transpiration supply and TE (Monteith, 1988; Chapman et al., 1993). The supply of water from the soil can be modelled via predicting the depth of the root system and the amount of water that can be extracted from each occupied layer. The extraction potential follows an exponential decay equation (Passioura, 1983) that depends on the moisture content of the layer and a coefficient (kl) that quantifies the relevant soil–root system attributes that influence water extraction patterns. This approach, first outlined by Monteith (1986), has been applied successfully in a number of species (Meinke et al., 1993; Robertson et al., 1993; Thomas et al., 1995; Dardanelli et al., 1997, 2004).

In water-limited situations, given any specific soil condition, crop water uptake depends on the nature of the plant root system and its spatial arrangement. The extraction front velocity of sorghum and maize roots is about 3 cm day^{-1} up to flowering (Robertson et al., 1993; Dardanelli et al., 1997). In both crops, a rooting depth of around 2 m has been observed by early grain filling. The lateral spread of root systems is usually not incorporated in crop models, but it can also influence their occupancy of the soil and uptake capacity. Studies on root architecture in wheat (Manschadi et al., 2006) have noted a relationship among encompassing seminal root angle (RA), root system architecture and consequent water extraction from the soil. The variety with the narrower RA occupied a smaller soil volume but was able to extract more water, especially at depth. In maize, Campos et al. (2004) observed differences in water extraction between old and modern maize hybrids. During a period of water limitation, the old hybrid extracted more water from shallow soil depth, whereas the new hybrid appeared to be more effective at depth. A simulation study that included a two-dimensional root development model showed that such differences in rooting behaviour provide a plausible explanation for genetic improvement of drought tolerance as a component of the historical maize yield trends in the US Corn Belt (Hammer et al., 2008; Figure 1).

2.1.3. Canopy development

The potential for both light capture and water use are dependent on the canopy leaf area and the nature of its display. In cereal crops, potential leaf appearance and expansion are controlled by temperature and modelled

as functions of thermal time that define the temperature-driven rates of leaf initiation, appearance and expansion rate (Tardieu et al., 1999; Hammer et al., 1993; Carberry et al., 1993; Birch et al., 1998b; Chenu et al., 2008; Ritchie and NeSmith, 1991). Potential rates of area growth are then reduced by water status, nitrogen or carbohydrate availability if any of these factors become limiting.

Approaches to predicting canopy leaf area growth have been developed at whole-plant and individual leaf levels. At the whole-plant level, functions describing the progression of potential leaf area with thermal time have been used to estimate potential leaf area growth (Amir and Sinclair, 1991; Hammer and Muchow, 1994; Sadras and Hall, 1988). At the individual leaf level, functions quantifying the potential size of individual leaves have been used in conjunction with estimates of leaf appearance rate (Birch et al., 1998a; Dwyer and Stewart, 1986; Jones and Kiniry, 1986). A number of studies (e.g. Birch et al., 1998b; Clerget et al., 2008) have shown that leaf initiation and appearance rates are stable when expressed in thermal time units.

Perhaps the least understood yet complex determinant of canopy development is the process of canopy senescence. Senescence is an emergent behaviour of the canopy that results from the dynamic interplay among resource capture, reproductive growth, the very own structure of the canopy and internal and external signals. Approaches to predicting canopy senescence have been developed for whole plants and canopies. In the absence of water and nitrogen stress, senescence is often modelled as a function of thermal time (Jones and Kiniry, 1986; Muchow and Carberry, 1989; Sadras and Hall, 1988), potential plant leaf area (Birch et al., 1998a) and the rate of green leaf area increase (Villalobos et al., 1996). Models that simulate water and nitrogen balances simulate leaf area senescence as a proportion of green leaf area and the severity of the abiotic stress (Jones and Kiniry, 1986) or as the result of the balance between nitrogen supply and demand. The latter suite of models enables nitrogen remobilisation and sink strength to drive leaf senescence (Sinclair, 1986; Villalobos et al., 1996; Boote et al., 1998; Borrell et al., 2001).

2.1.4. Reproductive growth

There are a number of approaches to simulating the growth of reproductive organs. The simplest models do not distinguish among yield components, fertile plants and tillers, fruit and seed number and weight; all components are lumped together in a coefficient (harvest index) that describes the fraction of total growth that corresponds to reproductive structures (Figure 4a; Sinclair, 1986; Muchow et al., 1990; Hammer et al., 1995). This approach is robust for the simulation of variation in yield across a range of environments but lacks sufficient detail to describe genotypic effects such as differences in maturity in sorghum (Hammer and Broad, 2003), as well as other genotypic effects underpinning yield improvement and tolerance to stresses.

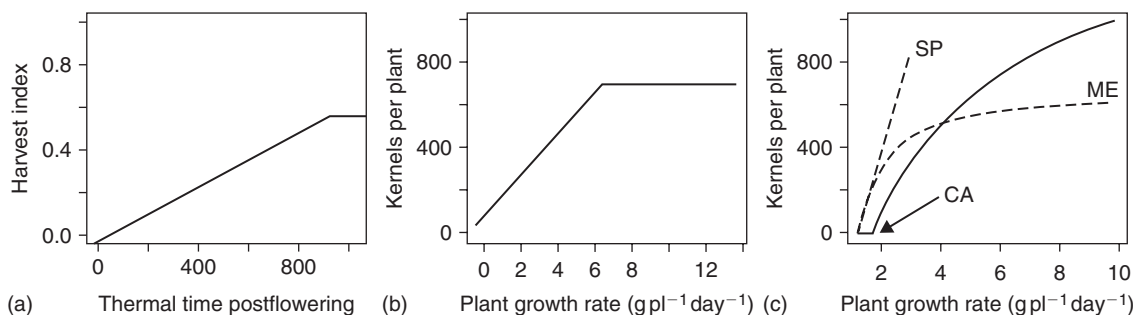


FIGURE 4

Models to simulate reproductive growth: (a) harvest index approach, and approach based on kernel number as a function of plant growth rate around flowering using (b) bilinear or (c) negative exponential or hyperbolic function. ME: maximum ear size representing kernel number at high plant growth rates; SP: initial slope and curvature integrate processes of silk exertion, synchronism in pollination, within-ear carbon allocation and kernel abortion; CA: carbon allocation to the ear and barrenness threshold.

More detailed models simulate barrenness, grain set and growth as separate processes. Grain growth is often simulated using a linear approximation of the commonly observed sigmoid growth pattern. The maximum grain growth rate is assumed characteristic of the genotype and independent of the kernel number (e.g. Duncan et al., 1978; Jones et al., 2003). Recent findings in maize questioned this assumption and suggested the need to model potential kernel growth rate as a function of plant growth per kernel around flowering time (Gambín et al., 2006). Once the potential is established, realised grain growth rate is determined by daily plant growth and the extent of carbon and nitrogen remobilisation (e.g. Jones et al., 2003; Keating et al., 2003; Boote et al., 1998).

Grain set is often modelled as a function of cumulative intercepted radiation (Ritchie and Alagarswamy, 2003; Andrade et al., 1993), crop growth rate (e.g. Andrade et al., 1999; Jones et al., 2003; Jiang and Egli, 1995; Vega et al., 2001; Tollenaar et al., 1992) or ear (panicle) growth rate (van Oosterom and Hammer, 2008) during a critical developmental period around flowering. The onset and duration of the critical window for grain set determination varies among crops (e.g. Otegui and Bonhomme, 1998; Fischer, 1985; Jiang and Egli, 1995). Critical windows for grain set are discussed in Chapters 12 (Section 5) and 15 (Section 3.2.2) from a breeding perspective and in Chapter 3 (Figure 4) from the viewpoint of integrating crops in cropping systems.

Figure 4b and 4c illustrate approaches to modelling kernel set in maize. Figure 4b is the function implemented in CERES-Maize (Jones and Kiniry, 1986) and could be considered the simplest approximation of the non-linear model in Figure 4c (Andrade et al., 1999; Tollenaar et al., 1992). Regardless of the mathematical formulation of the non-linear model, this form implicitly incorporates concepts of sink limitation due to maximum ear size (ME) and prolificacy (asymptote, ME; Figure 4c), silk exertion dynamics, synchronism in pollination, within-ear carbon allocation (CA) and kernel abortion (initial slope and curvature, SP; Figure 4c) and CA to the ear and barrenness (threshold, CA; Figure 4c). Ritchie and Alagarswamy (2003) extended the non-linear model shown in Figure 4c to simulate barrenness by modelling the fraction of ear-bearing plants as a function of cumulative intercepted radiation. An immediate advance on the framework, as proposed by Vega et al. (2001), is to explicitly simulate carbon partitioning to the ear and how this mass is converted into viable kernels. More mechanistic approaches to simulate fruit set, often applied to simulate pod number in legume crops, consider these fruits as populations of competing and interacting sinks for carbon and nitrogen. In this framework, fruit number at any time during the reproductive stage of the crop results from the balance between the addition of fruits as determined by crop development and the removal of fruits resulting from abortion due to insufficient resources (Wardlaw, 1990; Boote et al., 1998).

3. MODELLING GENOTYPE–ENVIRONMENT–MANAGEMENT SYSTEMS

A fundamental step in modelling is to define the purpose of the model or framework to be developed, the type of problems that the model should help investigate and solve and a concept map that relates the target natural system and the corresponding abstractions that become components of the framework (Peart and Curry, 1998; Thornley and Johnson, 2000). These principles were followed to design applications of crop growth models, and associated physiological concepts, to enhance plant breeding (Cooper et al., 2002; Chapman et al., 2003). More often, these applications have focused on valuing traits and attempts to design universal ideotypes (e.g. Boote and Tollenaar, 1994; Boote et al., 2001; Aggarwal et al., 1997; Yin et al., 2003; Sinclair and Muchow, 2001), and to understand genotype by environment interactions (Chapman et al., 2000, 2002a, b; Löffler et al., 2005). The development of these latter methods was dominated by typological thinking (e.g. Donald, 1968; Long et al., 2006; Century et al., 2008; Lee and Tollenaar, 2007) rather than population genetics concepts (e.g. frequency of favourable alleles, traits and phenotypes changing in a breeding population) as proposed in evolutionary (Nowak, 2006) and breeding studies (Cooper and Podlich, 2002). Approaches that sought to find universal ideotypes have imposed limitations on the successful

integration of physiological knowledge into breeding programs by largely ignoring breeding objectives, germplasm context dependencies and genetic sources of unexplained phenotypic variation, and by often placing undue reliance on the ability of models to connect genetics and physiology to credibly predict subtle interactions and feedbacks associated with genetic variation for traits within the reference germplasm of a breeding program (Hammer et al., 2002).

3.1. Breeding objectives and purpose of framework

To define a relevant context for modelling the $G \times E \times M$ system, it is convenient to distinguish between breeding objectives where:

- (i) a genetic answer to the problem is known; for example, a target genotype has been identified, and the objective is to close the genetic gap between the current germplasm and the defined target to test the hypothesis, for example, to increase resistance to a biotic factor by introgressing alleles from exotic germplasm;
- (ii) plausible genetic answers to the problem are currently unknown; for example, to increase grain yield or drought tolerance beyond those of the elite commercial products.

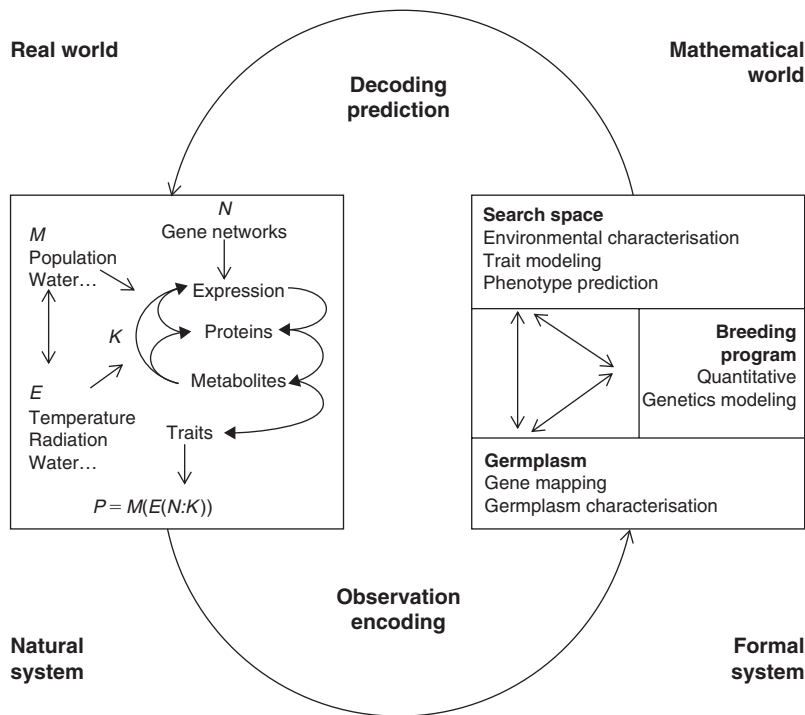
It is clear that the opportunity for modelling and physiology to contribute to plant breeding is closely tied to the second class of breeding objective, and that these should be components of a suite of methods to help breeders address questions about trade-offs between traits, the structure of adaptation landscapes, plausible selection trajectories towards interesting trait phenotypes and genotypes, the likelihood of finding improved genotypes in the adjacent possible genetic space and outcomes of competing selection and breeding strategies (Hammer et al., 2006).

3.2. Concept map

Figure 5 shows a simplified yet extended concept map to build a $G \times E \times M$ system (Cooper and Hammer, 1996). Cooper et al. (2002) formalised the concept that was later demonstrated in a theoretical study for sorghum by Chapman et al. (2003). The testing of the hypotheses proposed in the theoretical study is currently underway (Hammer et al., 2005). In this dynamic and iterative framework, empirical data are continually analysed and used to encode knowledge for model building and enhancement (Podlich et al., 2004). Model-based predictions and concepts become genetic, physiological and agronomic hypotheses to test through experimentation in the real world of the target $G \times E \times M$ system. A central concept to the quantitative framework is that of adaptation landscapes to represent the complexity of the $G \times E \times M$ system to be explored, equivalent to the concept of fitness landscapes discussed in evolutionary studies (Wright, 1932; Kauffman, 1993; Fontana et al., 1989). Applying this framework, plant breeding can be viewed as a set of search strategies applied to that landscape or search space and constrained by the germplasm available to the breeder, the prescribed agronomic management and the environments sampled in the field trials. In this framework, a breeding population can be thought of as a cluster of individuals located at neighbouring positions that flow through regions of the adaptation landscape in response to selection (Kauffman, 1993; Cooper et al., 2002).

3.3. Definition and consideration of the search space and adaptation landscapes

The search space could be defined by the outcome of all possible combinations of genomic regions, environments and management practices. A narrow-sense definition of this space, perhaps a practical one, assumes limits imposed by the germplasm available to the breeder, the target agronomic management and the composition of the TPE. A broad-sense definition can extend the search space to include novel cropping systems (Section 5 in Chapter 3), alternative environment scenarios (Chapter 20; Ainsworth et al., 2008; Karl and

**FIGURE 5**

Concept map, main system components and model-building framework for modelling genotype–environment–management systems in the context of plant breeding. G: genotype; M: management; N: number of genes involved; E: environment; K: average level of epistatic interactions; P: phenotype.

Trenberth, 2003) and novel sources of germplasm and engineered genetic elements (e.g. Century et al., 2008). The $G \times E \times M$ search space has an associated adaptation landscape. The $E(NK)$ model (Box 1), and an informal extension to accommodate M, provides a framework to consider this landscape.

A number of approaches were proposed to parameterise the $E(NK)$ model and assign a fitness value to a given genotype:

1. constructing Boolean networks and assigning fitness contributions to each gene from a statistical distribution (Kauffman et al., 2004; Kauffman, 1993);
2. defining inheritance models using empirical evidence from quantitative genetics parameters (Wang et al., 2003; Cooper et al., 2005);
3. specifying gene networks to represent attributes of known genetic networks and biochemical pathways (e.g. Ravasz et al., 2002; Bhalla and Iyengar, 1999; Peccoud et al., 2004);
4. directly parameterising, using results from mapping studies (Cooper et al., 2005);
5. considering the $E(NK)$ model as the consequence of N genes that control variation for physiological traits, the number of E identified for the TPE and the physiological relations encoded in a crop model that determine the patterns of crop growth and development (Cooper et al., 2002; Chapman et al., 2003; Hammer et al., 2005).

Approach 5 can be considered as partitioning the predictable component of the GP relationship continuum into gene-to-trait (physiological process) and trait-to-phenotype relationships; crop models predict crop performance phenotypes associated with trait performance (e.g. yield), based on the interplay among traits, environment cues and resources and management (Figure 5).

3.4. Crop modelling as a component in gene-to-phenotype mapping

The links between genes and phenotypes can be approached using top-down or bottom-up methods. Top-down methods use physiological dissection and integration via crop modelling to work from whole-plant phenotypes to the molecular genomic level (Hammer et al., 2004). This is also the classical forward genetics approach used to study the genetic architecture of traits; observe phenotypic variation and attempt to determine an appropriate genetic model to explain the phenotypic variation. When applying crop models to enhance genetic discovery, the central paradigm of this method is the focus on understanding and modelling processes at or around the level of organisation at which phenotypic predictions are being targeted and use a level of abstraction necessary to model processes and functional controls following the philosophy pioneered by de Wit and Penning de Vries (1983) of 'modelling plant hormone action without modelling the hormones'. The bottom-up approach integrates knowledge at the molecular level, across levels of organisation, to explain trait phenotypic variation (Minorsky, 2003; Yuan et al., 2008). This method is aligned with the reverse genetics approach to gene discovery (Section 2 in Chapter 14). It has been argued that the application of such bottom-up approaches to understand the genetic architecture of complex traits would face several challenges common to the study of other complex systems and in particular the challenge of integration of genetic information to capture emergent behaviour at the whole-plant level, with limited scientific understanding (Hammer et al., 2004). Simulation and propagation of errors across spatial and temporal scales that could vary by orders of magnitude would complicate making accurate predictions (Thornley and Johnson, 2000).

3.4.1. From the top-down

Top-down approaches have been tried with variable success. Yin et al. (2003) described the use of a crop model for barley based on the SUCROS crop model (Goudriaan and Van Laar, 1994) with quantitative trait loci (QTL) mapping to predict yields from QTL allele information. The model used as inputs the specific leaf area, the leaf N concentration, the fraction of biomass partitioned to leaves and to spikes and the separation of the life cycle into vegetative and reproductive stages. Using 94 recombinant inbred lines, these parameters were mapped, allele values for each QTL and trait calculated and yield predictions made using the ecophysiological model. Predictions for yield were clustered in two meaningful groups, based on two- and six-row types of virtually constant yield within each group. A similar study that used a crop model to link information for known loci and model parameters led to the Genegro model (White and Hoogenboom, 1996). This model incorporated effects of seven genes affecting phenology, growth habit and seed size of common bean (*Phaseolus vulgaris* L.). The parameters in the Genegro model were derived from the states of alleles at each of the seven loci, using a set of linear functions. These linear functions were estimated by regressing allele values (alleles were coded as either 1 or 0) against model parameters calibrated ('reverse engineered') using a set of field trials. Genegro accurately predicted dry bean phenological development but poorly explained yield variations between sites (Hoogenboom et al., 1997). These two examples demonstrate the limitations of using reverse engineering approaches to GP modelling and the importance of understanding the genetic architecture that controls the trait of interest. The ability of Genegro to predict bean phenology is due to a fundamental understanding of the genetic controls and genotypic variability on the response of beans to temperature and photoperiod (Coyne, 1970; Kornegay et al., 1993; White and Laing, 1989).

GP models developed for individual physiological components showed promising results for both plant development (Messina et al., 2006; Yin et al., 2005) and leaf growth (Reymond et al., 2003). Yin et al. (2005) combined ecophysiological modelling for phenology (of the form presented in Eq. 1) and QTL

composite mapping to predict barley response to temperature and photoperiod. Parameters for the eco-physiological model were first estimated for genotypes, and QTL mapping was conducted on the population variation for these parameters. Using the allele values for each QTL and consequent model parameters, predictions were made for a set of recombinant inbred line genotypes in eight environments. The QTL-based model accounted for 72% of the observed variation among the recombinant inbred lines. Messina et al. (2006) used a photothermal model (Eq. 1) to determine allele values at six QTL loci for soybean model parameters. The model accounted for 75% of the time-to-maturity variance when tested in multi-environment trials (MET). Reymond et al. (2003) mapped QTL for the parameters of an ecophysiological model of leaf elongation rate (LER) for maize (Ben Haj Salah and Tardieu, 1997),

$$LER = (T - T_0) (a + bVPD + c\psi) \quad (3)$$

where T is meristem temperature, VPD vapour pressure deficit and ψ soil water potential; b and c are constants coding for the response of LER to VPD and soil water potential after correction for T effects; a and T_0 are the slope and x -intercept of the LER response to meristem temperature. Under optimal soil water and VPD conditions, LER becomes a function of temperature alone and the model becomes equivalent to Eq. 1. Upon parameterisation of 11 recombinant inbred lines at marker loci, the model accounted for 74% of the variability of LER. Further evaluation demonstrated the model useful for describing genetic variation in LER for a large number of recombinant inbred lines (Sadok et al., 2007).

3.4.2. Genes, traits, phenotypes and adaptation

The LER model is a useful example to illustrate the concept of partitioning the GP continuum into gene-to-trait and trait-to-phenotype relationships and to connect the biophysical and the NK models. The state model in Eq. 3 can be reformulated to formally incorporate QTL effects as

$$\frac{dL}{dt} = (T - \sum w_{ij}QTL_i)(\sum w_{ij}QTL_i + \sum w_{ij}QTL_iVPD + \sum w_{ij}QTL_i\psi) \quad (4)$$

where w_{ij} are allele values of each QTL_i for the parameter j . Further generalisation suggests specifying Eq. 4 in terms of the NK model as

$$\frac{dL}{dt} = (T - NK_j)(NK_j + NK_jVPD + NK_j\psi) \quad (5)$$

where the NK model is allowed to vary among parameters j . That is, the genetic networks associated with each of the model parameters could have common components; pleiotropic effects are formally incorporated via shared nodes among networks; epistasis is implemented as described earlier (Box 1). This formulation based on the NK model can be extended to the $E(NK)$ model where network topology is allowed to vary in response to environment cues. Error terms could be included in the model to account for components of the unexplained variation in the GP relation continuum (Cooper et al., 2005).

The model in Eq. 5 fully describes the gene-to-trait relation. However, Eq. 5 applies only to single leaf and scaling of some sort from the organ to the whole plant is necessary to map the $G \times E \times M$ space into the phenotype space (e.g. plant leaf area). Chenu et al. (2008) developed a model that coordinates the growth of all leaves of a plant and uses the single-leaf LER model to drive growth. The framework was implemented as a component of APSIM (Keating et al., 2003), which provided the dynamic feedback effects on leaf growth via transpiration and soil water uptake. Because the LER model is integrated within a crop growth-modelling framework, the likely impact of genetic variation for QTL affecting LER on adaptation (e.g. grain yield) could be assessed as demonstrated in previous studies for sorghum (Chapman et al., 2003) and soybeans

(Messina et al., 2006). In summary, crop models have the potential to map the $G \times E \times M$ space into phenotype and adaptation landscapes. To enable these connections, however, thorough basic physiological and genetic studies are necessary to support the model architecture and provide validated evidence for the physiological determinants of genetic variation in adaptive traits.

3.5. Breeding programs as search strategies in genetic space

Plant breeders create new genotypes with improved crop performance and adaptation to a TPE by observing, understanding, predicting and creating new trajectories in genotype and phenotype space. Three fundamental processes under the breeders' control support the creation of these trajectories: (i) development of genotypic novelty through strategic sampling of germplasm, recombination and segregation; (ii) design of testing systems that adequately sample the TPE for evaluation of cultivars and expose genetic variation for traits of interest; and (iii) selection as a means to change gene frequencies in the germplasm to improve adaptation relative to the current set of cultivars. Breeders' decisions on these three components define the breeding strategy, and therefore the regions of the adaptation landscape that the breeding program would explore in search of peaks of adaptation and crop performance.

Breeding simulation provides a means to predict trajectories in GP space. QU-GENE (Podlich and Cooper, 1998) is a computer simulation platform to specify genetic models in the context of the $E(NK)$ framework and $G \times E \times M$ systems in order to evaluate alternative breeding strategies. The stochastic components in QU-GENE implement the simulation of genetic recombination and segregation, within the search for genotypes with higher fitness in the adaptation landscape; note the analogy between this component in QU-GENE and global optimisation algorithms (Mitchell, 1996). Specific modules in QU-GENE simulate the processes involved in the creation, evaluation and selection of genotypes within the breeding program and implement the simulation of breeding strategies such as mass selection, pedigree and single-seed descent, double haploid, S1 recurrent selection and half-sib reciprocal recurrent selection.

4. CASE STUDY: MAIZE BREEDING IN THE USA

Despite the complexity of the mechanisms underpinning yield determination, conventional breeding has effectively increased maize yield in well-watered and water-limited environments of the US Corn Belt (Figure 1; Duvick and Cassman, 1999; Duvick et al., 2004; Campos et al., 2006). Trajectories from over 50 years of maize breeding in the US Corn Belt show that many traits have changed markedly, even when there was no direct selection for these traits. These include decreases in tassel size, protein concentration in kernels, rate of leaf senescence during grain filling, root and stalk lodging, rows of kernels per ear, and anthesis-silking interval, and increases in LA (more erect leaves), ears per plant, kernel weight and harvest index (Duvick and Cassman, 1999; Duvick et al., 2004; Lee and Tollenaar, 2007). The future direction of these trajectories is a subject of debate (Lee and Tollenaar, 2007; Century et al., 2008; Tuberosa et al., 2007; Pennisi, 2008) and opens the opportunity to apply the framework described in the previous section to address questions of relevance to breeding. This section illustrates the use of a coupled crop system – breeding model to study past trajectories in GP space and outline plausible future trajectories in maize breeding.

4.1. Genotype–environment–management system

This study used the GP framework described in Section 3 to build a $G \times E \times M$ system representative of past and present maize production in the US Corn Belt. The breeding objective is to improve yield in the TPE beyond that of current germplasm. The purpose of the framework is to study past trajectories in maize breeding and to provide insights on future trait trajectories, given representative environment types and plausible changes in management. Components of this framework were constructed by modelling adaptive traits of interest to breeders based on their physiological determinants (Section 2); linking genetic variation to those determinants in the context of the NK model (Box 1); simulating maize phenotypes for relevant

genotypes, managements and environments; classifying production environments (Section 4.1.3); and simulating trait trajectories in genetic space for breeding programs conditioned to defined environments and management (Figure 5).

4.1.1. Trait modelling

A Pioneer proprietary module of APSIM-Maize was developed to incorporate adaptive traits of interest for trait variation relevant to Pioneer elite hybrids. The module includes algorithms that implement concepts that link RA with spatial and dynamics aspects of root exploration and occupancy of soil layers; thus RA controls time of access and intensity of resource capture (Hammer et al., 2008). LA and RUE are connected by implementing a series of equations to model canopy photosynthesis (Duncan et al., 1967; Hammer and Wright, 1994; Loomis and Connor, 1992). The module includes algorithms to model aspects of maize reproductive biology relevant to yield, including the connections between kernel set and CA to the ear and within the ear (Vega et al., 2001; Cárcova and Otegui, 2007), silking dynamics and synchronism in pollination (SP) (Cárcova et al., 2003; Borrás et al., 2007) and ME (Tollenaar et al., 1992). The model accounted for the connection between growth and development (Borrás et al., 2007), the co-regulation of kernel set and kernel size (Gambín et al., 2006) and their response to timing of drought stress during reproductive stages. Figure 6 compares simulated and observed yields for Pioneer hybrid P90-1 grown in a rain-free environment under six irrigation regimes. These regimes covered full irrigation control (FI) and five treatments where water was withdrawn for 500 °Cd for overlapping periods separated by 100–200 °Cd (S1–S5) at the commencement of the treatment.

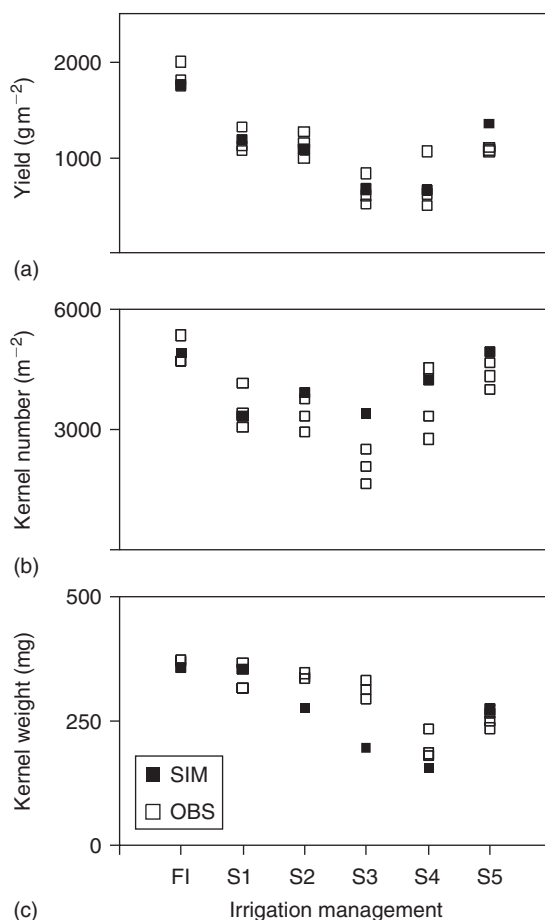
4.1.2. Linking genotypes and traits

To demonstrate an application of the framework, genetic variation for five adaptive traits was defined using an additive genetic model based on three genes (equal effects) and two alleles per locus ($NK = 3:0$). It was assumed that there were unique sets of genes for each trait and that genes were unlinked. Thus, for the purpose of demonstration here, the genetic model does not include epistasis and pleiotropic effects at the level of the genetic architecture of the five traits. For a single trait, this genetic model results in 27 unique genotypes but only 7 unique expression states, given the additive effects model. For each locus, one allele was considered to increase expression relative to the alternative allele. For example, at a given gene A, it is defined that allele A increases trait expression (+) relative to the allele a (–). Then the expression state for the genotype is defined by the sum across genes of the effects of the + alleles. For example, given the additive model, the genotypes *AAbbcc*, *aaBBcc*, *aabbCC* and *AaBbcc* all have the same expression state of two (e.g. two positive alleles each). For this simulation experiment, which was based on five adaptive traits, the genetic model defines 14×10^6 genotypes but only 1.6×10^4 expression states. This first approximation of the genetic architecture of the component traits is substantiated by multiple QTL mapping studies. It is the simplest representation suggested by the data that would enable the simulation and representation of the full adaptation landscape. Other genetic models could be considered and implemented in the framework, and would have generated different relations among genotypes, expression states and phenotypes.

This simulation experiment included genetic models for five adaptive traits: RA, LA, CA to reproductive growth, synchronous pollination (SP) and potential ear size (ME). Model parameters for the latter three traits could be interpreted as determinants of CA, SP and ME in the current models of kernel set outlined in Figure 4c. Herein, we refer to these traits and interpret the results in the context of the kernel set response to plant growth rates.

4.1.3. Environmental classification

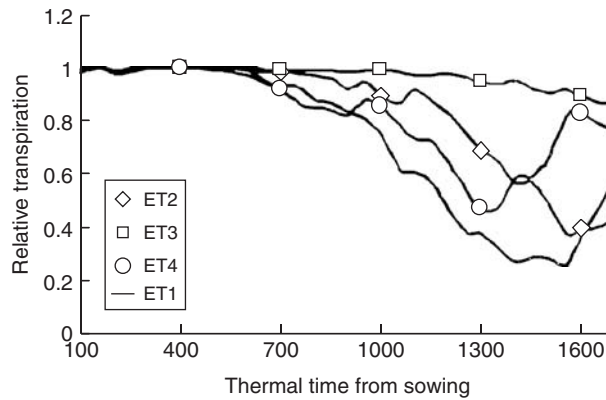
Maize phenotypes were simulated for a range of plant densities (8 and 12 pl m^{-2}), soil types (high and low soil water holding capacity; Löffler et al., 2005), 4 soil water contents at sowing and 50 years of weather in central Iowa, using APSIM-Maize (Keating et al., 2003) and Pioneer proprietary modules. Soil water content

**FIGURE 6**

Assessing model capacity to predict (a) yield and yield components, (b) kernel number and (c) kernel weight under six regimes of water supply. FI: full irrigation; S1–S5, water was withdrawn for 500°C d over overlapping periods of $100\text{--}200^{\circ}\text{C d}$. Experiment details are provided in Campos et al. (2006).

at sowing was estimated by simulating long-term soybean–maize rotations and clustering results to form groups of water content distribution in the soil profile at sowing. Each combination of plant density, soil type and soil water content at sowing defines a unique environment and could thus be considered as one of many possible outcomes in a multi-environment trial.

Each of the 800 ($2 \times 2 \times 4 \times 50$) simulated production environments was classified based on water supply and demand patterns (Hammer et al., 2005; Chapman et al., 2000) for a reference genotype. APSIM-Maize was parameterised and run for the Pioneer hybrid 3394 as the reference genotype; see Hammer et al. (2008) for model parameterisation. Daily outputs of the ratio of water supply to demand were averaged every 100°C d from emergence. Cluster analysis, using the *k*-means algorithm, revealed four major environment types depicted in Figure 7. The frequency of occurrence was 18% for severe terminal stress (ET1), 20% for early grain fill stress (ET4), 25% for moderate terminal stress (ET2) and 37% for no stress (ET3).

**FIGURE 7**

Drought stress patterns for environment types (ET) that define the Target Population of Environments. Relative transpiration simulated for a reference hybrid.

4.1.4. Adaptation landscape

The adaptation landscape was generated with yield as the measure of fitness. APSIM-Maize was run for each of the 16×10^4 expression states corresponding to unique combinations of adaptive traits, and each of the 1.6×10^3 environments and management combinations. Model parameters not determined by a genetic model, thus by any expression state, were set to the values determined for the hybrid 3394. This is a realistic representation of the execution of the framework in a real breeding program where genetic improvement is sought relative to a reference germplasm. For the purpose of this example, all conclusions about genetic improvement are drawn in reference to the hybrid 3394.

4.1.5. Breeding simulation

For each environment type and management, reciprocal recurrent selection with pedigree selection within two heterotic groups was simulated using QU-GENE (Podlich and Cooper, 1998; Podlich et al., 2004). The QU-GENE software managed the creation, evaluation and selection of genotypes within the breeding program. Reference breeding populations were created by specifying allele frequencies to 0.5 in two heterotic groups; any other starting point could have been considered. The evaluation system was set to a single breeding program and 10 testing sites. Each testing site sampled the TPE (Figure 7) in proportion to the frequency of occurrence of each environment type. Trait trajectories in G space conditioned to E and M emerge from breeding simulations that are similar to the trajectories reported for the sequence of hybrids in Figure 1. Selection experiments were conducted under a unique environment and management (e.g. ET1 and 8 pl m^{-2}), and for a sample of environments and plant populations.

4.2. Structure of simulated adaptation landscapes

Adaptation landscapes could be characterised by different metrics and graphical representations (Kauffman, 1993; Cooper and Podlich, 2002; Wright, 1932; Nowak, 2006; Fontana, 2002). In this example, the adaptation landscape was represented as a set of conditional cross sections for grain yield in the G and P dimensions (herein referred to as a GP plot). The grain yield distributions are conditional on the expression states for a defined trait. For example, for LA, there are seven expression states and therefore seven yield distributions. The yield distribution is generated by the yield variation created by all other traits conditional on the defined expression level for the selected trait of interest. The GP dimension views can be constructed for

specific environments or a combination of environments. Genotype relative frequencies at regular intervals for yield are shown as a heat map to visualise the distributions (Figure 8). This graphical representation of landscapes allows the identification of features such as position of global maxima, trends in central tendency and local optima for yield with respect to G and expression states, presence of saddles and plateau regions. The global maximum is identified as the maximum in the *y*-axis across all frequency distributions. In the example presented for drought stress environments, this maximum corresponds to genotype *AABBCC* for RA and *ddeeff* for LA (Figure 8). Local optima correspond to the maximum yield conditioned to G. Both global and local optima provide information about opportunities and paths to yield improvement in the adjacent genetic space, given the reference populations of the breeding program.

Trends could be identified in local optima and central tendencies. In environment ET3, trends in yield with respect to the expression state of LA are evident in both central tendency and local optima (Figure 8). In contrast, in ET1, the landscape is rather flat for genotype bins 1–4 (genotype *ddeeff* corresponds to bin 1), but there is a marked non-linear trend in the local optima. This trend reveals a point of instability due to the presence of a saddle and has implications for breeding. Yield increase is feasible by either increasing or decreasing LA. The resulting changes in allele frequencies, and LA phenotypes, in a breeding population selected for yield increase, will depend on the initial frequencies of alleles. At this point in G space, the behaviour of the breeding system and the potential for genetic improvement become dependent on initial conditions. The global maximum in ET1 can only be reached by increasing the frequency of + alleles. The alternative trajectory leads to a higher peak in the adaptation landscape but compromises the potential for continuous genetic gains due to variations in LA.

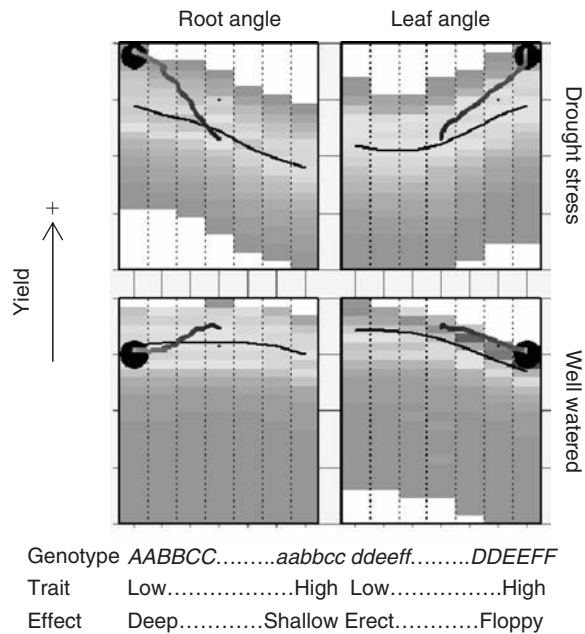


FIGURE 8
Breeding trajectories (thick lines) in a gene-to-phenotype adaptation landscape. Black dots represent individuals in the breeding population; dot size is proportional to the number of individuals. The thin line represents central tendency across genotypic bins. Landscapes correspond to environment type severe terminal stress (ET1) and no stress (ET3). Breeding simulation conducted for drought stress environments. Genotype frequency is colour coded in Plate 1.

Changes in environment types can induce deformations to the adaptation landscapes. The magnitude of any such deformation depends on the underlying trait physiology. Figure 8 illustrates this effect for RA and LA. Yield increased with increasing frequencies of + alleles conditioning the expression states for RA. Greater water capture associated with deeper root systems had a positive effect on simulated yields under ET1. In contrast, there were no marked effects on yield in ET3, which is manifested as a smooth and flat landscape (Figure 8). The comparison of landscapes for LA in ET1 and ET3 reveals a trade-off between light capture and RUE and water use. Yield increased with the increasing frequency of + alleles (erect-leaf-type phenotypes) under no-stress environments where light capture and its distribution within the canopy limits carbon assimilation and yield. The opposite pattern is evident in drought stress conditions where improved RUE generates higher water use, which intensifies the severity of stress during reproductive stages. Water conservation strategies that improve the partitioning of water use between vegetative and reproductive stages are discussed in Chapter 6 (Section 3).

The landscape structure generated for this small $G \times E \times M$ system has complex features as viewed through the GP plots. The complexity of the landscape is assessed by the analysis of all GP cross sections. The presence of weak trends in a given cross section indicates that a given trait is not a strong determinant of yield response in the context of all other traits (Figure 8). But the absence of any trends across all cross sections indicates a rugged landscape, where peaks in grain yield performance are dependent on the expression states for multiple traits. The example presented in Figure 8 illustrates this contrast. While the adaptation landscape view for ET3 is determined to a large extent by the frequency of + alleles for erect-leaf-type phenotypes, landscapes for ET1 are rather flat, with trends for both RA and LA and the presence of saddles. Adaptation landscapes under drought stress are more complex than in the absence of stress, and the GP plots indicate multiple paths are plausible for crops to cope with stress. The characterisation and understanding of adaptation landscapes and how these respond to E help to study, interpret and anticipate response to selection. The approach allows assessment of the relevance of traits in the context of all other traits under consideration in a specific environment, and aids in strategically selecting germplasm for breeding objectives that target specific sections of GP space.

4.3. Exploring trajectories in GP space: what traits can improve adaptation?

Breeding simulation is a step beyond the study of the structure of adaptation landscapes and has been used to assess breeding strategies (Podlich et al., 1999; Chapman et al., 2003; Wang et al., 2003; Cooper et al., 2005) and the integration of molecular technologies into breeding methods (Podlich et al., 2004; Cooper et al., 2005; Hammer et al., 2005). In the example presented here, breeding simulation was used to study plausible trait phenotype trajectories in GP space under contrasting management and drought stress environments (Figures 8 and 9). Each trajectory represents the average of an ensemble of 20 QU-GENE runs (i.e. 20 replications of the breeding program starting from the same reference breeding population). The common pattern across environment types and management in the allele frequency dynamics is the uniqueness in the relevance of traits and their interdependence. The relevance of a given trait could be judged by the onset and the rate of change in allele frequencies conditioning the expression states of the trait, and the effects of traits on yield at other loci. When the MET was simulated at commercial plant densities, LA was the first trait to change allele frequencies towards the + alleles, reaching fixation upon 20 cycles of selection. The direction of change, however, was opposite in the two environment types. LA decreased (shift towards erect leaf type) with increasing cycles of selection in ET3 (no stress) and increased (shift towards floppy leaf type) at about the same rate in ET1 (severe terminal stress). Similar patterns were simulated for high-density stands, but the rate of change was not as pronounced as under commercial density, and a delay in the onset of change was evident in ET3.

The frequency of the + alleles for RA increased in successive cycles of breeding when selecting for yield in drought environment type ET1. Conservative water use and enhanced water capture in deep soil layers dominated the trajectories, particularly during the first cycles (Figure 9). The value of this yield improvement

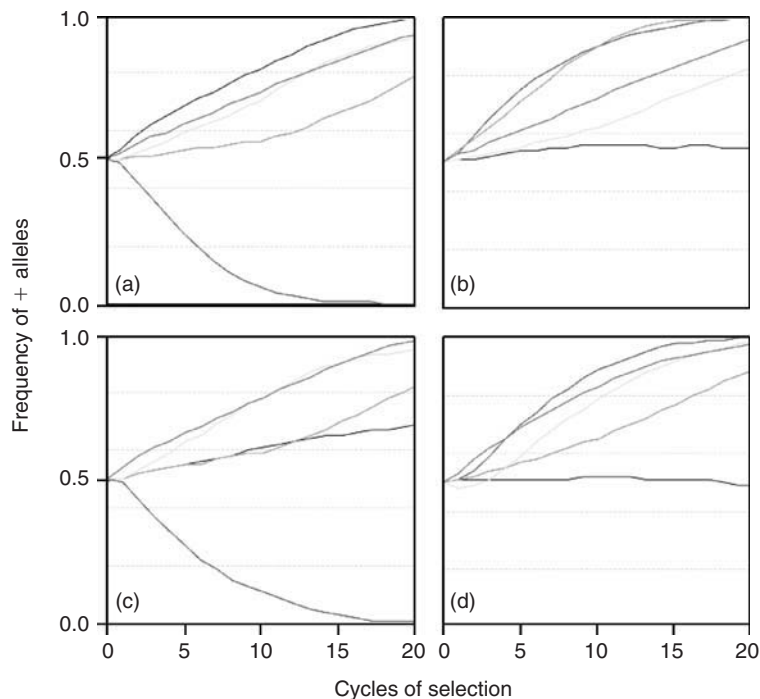


FIGURE 9

Mean changes in gene frequencies for alleles associated with root angle (RA), leaf angle (LA), potential ear size (ME), threshold carbon allocation to the ear and barrenness (CA) and synchronous pollination (SP) with cycle of selection. Selection simulated for specific management: 8 pl m^{-2} (a, b) and 12 pl m^{-2} (c, d); and two contrasting environment types: severe terminal drought stress (ET1) (a, c) and no stress (ET3) (b, d). Traits are colour coded in Plate 2.

strategy was demonstrated in maize populations selected for increased osmotic adjustment (Chimenti et al., 2006). Although this physiological mechanism underpinning the enhanced ability to access water stored in deep soil layers may not be valuable in some germplasm (Bolaños and Edmeades, 1991), the effectiveness of the strategy to improve the maintenance of leaf area, growth and yield in the simulation experiments provides the basis for a testable hypothesis. The reduction in RA, resulting in a deep root system, implies a redistribution of root mass among soil layers. The feasibility of this alternative path towards accessing additional water in deep soil layers is supported by evidence of genetic variation in root architecture (Tuberosa et al., 2002; Tuberosa and Salvi, 2006), variations in patterns of soil water uptake between modern and old hybrids (Campos et al., 2004) and root architecture response to selection (Edmeades et al., 2000). It is apparent from the breeding simulations that this strategy is not universal (Figure 9) and its contribution to yield improvement is constrained to defined domains in the $G \times E \times M$ space. Water use increased with increasing plant population, thus limiting some of the benefits of enhanced water capture as indicated by a lower rate of change in + alleles for RA. Chapter 13 discusses in detail root attributes for improved capture of resources.

In high-stress environments, ET1 and 12 pl m^{-2} , the breeding simulations showed that selection for yield favoured mechanisms to cope with stress. The frequency of + alleles for CA and SP rapidly increased in successive cycles of selection. The interpretation of these changes is that selection for yield results in lower thresholds to biomass allocation to the ear, to kernel set, and vigorous and synchronous silking (Figures 4c and 9). In contrast, when METs were simulated for low-stress environments and commercial plant populations,

selection favoured the main mechanism to realise the environmental potential by increasing + alleles' contribution to augment light interception and RUE (as discussed above) and to increase ME. There was a concurrent increase in + alleles for both traits ME and LA. Empirical evidence supporting this trait trajectory was documented for mid-maturity maize selected in Argentina (Luque et al., 2006). The frequency of + alleles for CA to the ear changed slowly from cycle 0 to 15. A break point becomes apparent following the realisation of improvements in resource capture and use efficiency, and alleles for LA are close to fixation in cycle 15 of the simulation; thus allocation to the ear becomes a limitation to yield improvement.

4.4. Breeding opportunities for broad and specific adaptation

Plant breeders often face the dilemma of designing breeding strategies with the right balance of efforts directed towards breeding for broad versus specific adaptation. Necessary conditions for breeding for specific adaptation are the occurrence of repeatable environment types, and the existence of genetic variation in traits that generate positive, sizable and repeatable $G \times E \times M$ interactions. Breeding simulations in Figure 9 could be studied as the outcome of a breeding strategy to evaluate opportunities for specific adaptation. Trait phenotype trajectories in Figure 9 suggest opportunities for improvements in both broad and specific adaptation to drought stress within the context of the simulated reference population of the breeding program. The increase in frequencies of + alleles contributing to higher CA and SP, regardless of the environment type and crop management, suggests a breeding strategy that favours selection for + alleles for these traits as a means to improve broad adaptation. Although change in root architecture contributed to yield improvement only in ET1 (Figure 9), the absence of crossover $G \times E \times M$ interactions (Figures 8 and 9) suggests that selection for + alleles for RA could be one component of a breeding strategy seeking improvement for broad adaptation. Successful improvement for this trait can create genotypes with enhanced yield stability (i.e. less susceptibility to drought stress) and thus extend their domain of adaptation in the $G \times E \times M$ space. It is also feasible to conceive selection for + alleles for RA as a component of a breeding strategy designed to improve specific adaptation to drought stress. Because changes in allele frequencies for LA generated crossover $G \times E$ interactions (Figure 8), this physiological trade-off forces plant breeders to accommodate selection for specific adaptation in the breeding program. To this end, it is necessary to formally define the TPE based on the classification of environments by type (Figure 7). The application of weights to the data from the multi-environment trials to match the environment-type expectations of the TPE, weighted selection strategy, was shown to increase response to selection (Podlich et al., 1999).

This study simulated genetic gains for yield when breeding for specific conditions (Figure 9) relative to those attained if selection samples the TPE. Simulated genetic gains differed little for selection performed in only ET3 environments, compared with the entire TPE. In contrast, genetic gains for selection in ET1, regardless of the management, were double those attained when selection was conducted in the entire TPE (data not shown). Management contributions to the rate of genetic gains were evident but of lower magnitude than those due to environment variation. These results lead to the proposition that incorporating knowledge on $G \times E \times M$ into breeding can increase genetic gain and hasten crop improvement.

4.5. Opportunities to enhance molecular breeding

Since the discovery of molecular markers and their application to the construction of molecular maps and to the mapping and dissection of quantitative traits (Lander and Botstein, 1989; Lander and Schork, 1994; Paterson et al., 1991), molecular marker technologies have been successfully integrated into many aspects of plant breeding. Opportunities for molecular breeding and use of marker-assisted selection were the motivations for *in silico* studies and reviews (Chapter 14; Cooper et al., 2005, 2006; Lee, 1995). But the realisation of the potential use of DNA markers to improve methods for predicting expected phenotypes of progeny from parental information as suggested by Paterson et al. (1991), and its utilisation in breeding programs, came about after significant developments in analyses and prediction methods, often based on a mixed-model framework (i.e. Malosetti et al., 2007; van Eeuwijk et al., 2005; Boer et al., 2007), and improvements in and the deployment of information management technologies (Cooper et al., 2006; Graham, 2008).

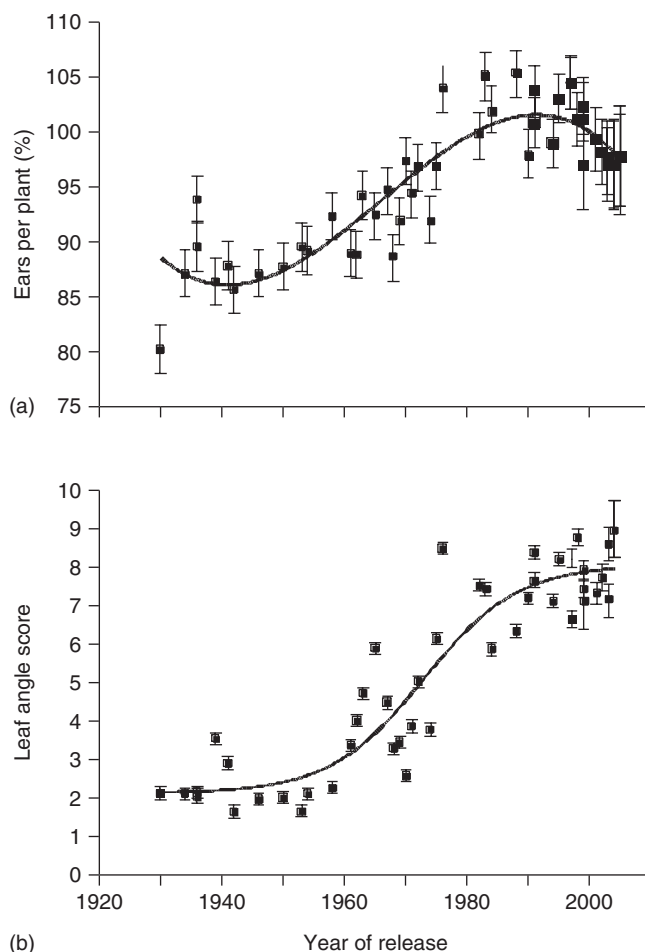
Many of the activities within molecular breeding rely on statistical models that summarise associations between genotypic and phenotypic variations. These statistical models often provide a static view of traits and their association with genomic regions (QTL). The treatment and analysis on a trait-by-trait basis limits these methods to effectively capture the dynamic relationships between traits, leaving to the breeder the subjective interpretation of the interplay and emerging trade-offs among traits. As evidence accumulates towards the need for considering epistasis and pleiotropy for the deployment of enhanced methods for molecular breeding, it is opportune to contemplate the utility of the $G \times E \times M$ modelling approach outlined in this chapter as a framework for considering the biological and physiological interplay of QTL, traits and environments in a way that adds value to the well-established and effective statistical framework for molecular breeding. In the $G \times E \times M$ framework, epistasis and pleiotropic effects are emergent properties of the physiological framework (Hammer et al., 2006). The trait trajectories depicted in Figure 9 illustrate the conditional dependencies among traits to contribute to yield improvement. While the genetic models defined for all traits in this study were additive at the individual trait level, the grain yield value of the different alleles for a given trait is conditional to the state of other loci as demonstrated by the non-linear structure of the trait trajectories in genotype space. These simulations suggest that physiological dissection and modelling can help assign biological function to QTLs, and explain and resolve $G \times E \times M$ interactions, thus providing a foundation to improve molecular breeding strategies in maize. This argument could be extended to the application of the framework to known genes for the assessment of their function at the whole-plant level, that is, to assess the extent to which the effects of gene expression at the molecular level propagate across levels of organisation. The framework could be used for designing *in silico* breeding strategies that make use of transgenics as a step prior to the initiation of experimentation that would require significant management and investment. Hammer et al. (2005) demonstrated in a theoretical study of sorghum that marker-assisted selection could be improved (enhanced rate of yield increase over cycles of selection) by considering knowledge from trait physiology and modelling.

4.6. How consistent are simulated trajectories with changes in traits due to genetic improvement for yield?

To interpret the results of the breeding simulation in the context of observed trait trajectories, we must define the environment types, changes in management and selection objectives that prevail during the selection process. Major breeding objectives are to increase yield and yield stability across years and geographies. Selection decisions in the past were mostly driven by data collected in the TPE; that is, a large fraction of the data driving selection decisions were obtained in environments that exposed maize crops to low drought stress (Löffler et al., 2005). However, as the TPE is by definition a mixture of environments, in certain years, drought stress could have contributed to the pool of data and germplasm improvement. Crop management also changed through time, with plant population, irrigation and N use increasing since 1960 (Cassman and Liska, 2007).

In the context outlined above for dominant environment types, management practices and breeding objectives, the expectation set by outcomes of breeding simulation (Figures 8 and 9) is to observe a rapid decrease in LA (towards hybrids with an erect leaf type) associated with improved RUE in high-density stands, to some degree deeper root systems selected in drought-prone environments and dry years and increased kernel set due to higher resource allocation to the ear. Observed trait trajectories for selection in the north-central USA compare well with the expectations from the breeding simulation (Duvick et al., 2004; Figure 10). After the onset of the era of intensive agriculture in the early 1960s, LA scores increased linearly, reaching a plateau denoted for hybrids released since the late 1980s. Breeding simulation indicated this trajectory in the absence of nitrogen limitations and in ET3 (Figures 7 and 9), which together with ET2 (low stress around flowering) accounts for 65% of environment types in the TPE. Both simulated and observed leaf scores (Figures 9 and 10) indicated that breeding for yield had moved the breeding populations towards a region in the G space that optimises light capture and use efficiency under $E \times M$ typical of intensive agriculture, with apparent little room for further contributions to yield improvement.

Changes in root architecture in response to selection have not been documented. However, there is evidence for a reduction in biomass allocation to roots in the topsoil (Bruce et al., 2002). This observation is

**FIGURE 10**

Observed trajectories in non-barren plants (a) leaf angle score (b) in a series of Pioneer hybrids released between 1930 and 2007. Leaf angle scores range from 0 to 10 assigned to floppy-type and erect-type hybrids.

consistent with a predicted trajectory towards deeper root systems and lower root density in upper soil layers (Figure 9). Lower RAs predict a more uniform water use pattern in depth and time as well as a more uniform biomass distribution in the profile. Campos et al. (2004) showed that older hybrids use more (less) water from the top (bottom) soil layers than modern hybrids. As suggested by breeding simulation, these observed patterns of increased water capture and conservative water use may have resulted as a consequence of selecting hybrids with yield stability across locations and years. Based on simulated trait trajectories for ET1 environments, it is suggested that there is unrealised potential to progress further yield stability in main production areas in the maize belt and yield under drought stress.

Reproductive traits ME, CA and SP increased in successive cycles of breeding (Figure 9), leading to the creation of hybrids with increased CA to the ear and increased kernel set for a given E and M (Figure 4c).

Empirical evidence and theoretical predictions agree well in that selection for yield increased the kernel number per plant, per ear and per unit area (Chapman and Edmeades, 1999; Echarte et al., 2004; Campos et al., 2006; Luque et al., 2006; Tollenaar et al., 1992; Duvick et al., 2004; Edmeades et al., 2000), and fertile ears per plant largely contributed to this increase (Duvick et al., 2004; Chapman and Edmeades, 1999; Tollenaar et al., 1992). Increased partitioning and reduced barrenness in the context of the modelling framework are related to the reduction in CA (Figures 4c and 9). Simulated trait trajectories are consistent with measurements by Echarte et al. (2004) but not by Luque et al. (2006) and Tollenaar et al. (1992). In the latter two studies, model parameters linked to ME and CA to the ear were correlated. Because of such correlation, it is difficult to contrast model predictions with empirical evidence. The framework used in this study captures some aspects of the underpinning mechanisms causal of barrenness but further advancement on the model, perhaps through incorporating theoretical aspects of interplant competition (Pagano et al., 2007; Pagano and Maddonni, 2007), will be necessary to better connect genetic variation and physiological determinants of barrenness. Luque et al. (2006) observed increases in ME only under high-yield environments, in agreement with predicted trait trajectories in this study (Figure 9, environment type ET3).

5. CONCLUDING REMARKS

This chapter reviewed and summarised theoretical developments towards a framework that integrates quantitative genetics, breeding simulation and modelling of physiological traits and dynamic GP relations. Such a framework is intended to enable breeders and agronomists to project trajectories in the $G \times E \times M$ space into the future and gain insights on the consequences of manipulating genomes to the creation of improved crops for target management and environments.

A central concept emphasised throughout this study and applied to the different aspects of modelling and simulation is the iterative nature of the process, and thus the need to integrate modelling and simulations as one component of the breeding program. The execution of this framework is feasible only through such integration that forces individuals to align breeding objectives, physiological questions and genetic hypotheses, which ultimately have to be tested in the breeding program.

This study demonstrated *in silico* the validity of a method to effectively explore the $G \times E \times M$ state space, to integrate and apply physiological concepts to plant breeding and the value of leveraging this knowledge to develop improved crops. Nevertheless, executing this framework poses a number of grand challenges, and a significant scientific and technological ground has yet to be covered. There is a clear need to advance the scientific debate about the detail and complexity needed for crop growth models to be able to integrate processes across levels of organisation while predicting emergent functional consequences for the organism. Related to this issue is the need for a considerable effort and investment in creating knowledge and developing robust links between genetic variation for adaptive traits relevant to breeders and the underlying physiological determinants. Despite the agreement between observed and simulated trait trajectories for the past 50 years of breeding in the US Corn Belt, there is a clear need for a theoretical and empirical demonstration that these technologies can be used to improve future rates of genetic gain in elite breeding populations.

We are optimistic that breeding simulation will help understand observed breeding trajectories for traits contributing to yield improvement; identify emergent, in some cases counterintuitive, behaviour of the breeding system; and quantify trait and environmental context dependencies. This understanding, along with quantitative knowledge of QTL function, via trait dissection and integration using physiological modelling and a $G \times E \times M$ framework, will enable predictions to be evaluated in the target breeding program. This emerging breeding technology can help manage and adapt germplasm to effectively navigate through the $G \times E \times M$ space, producing improved hybrids that meet the needs of changing farming systems and environments.

REFERENCES

- Aggarwal, P.K., Kropff, M.J., Cassman, K.G., ten Berge, H.F.M., 1997. Simulating genotypic strategies for increasing rice yield potential in irrigated, tropical environments. *Field Crops Res.* 51, 5–17.
- Ainsworth, E.A., Rogers, A., Leahey, A.D.B., 2008. Targets for crop biotechnology in a future high-CO₂ and high-O₃ world. *Plant Physiol.* 147, 13–19.
- Amir, J., Sinclair, T.R., 1991. A model of the temperature and solar radiation effects on spring wheat growth and yield. *Field Crops Res.* 28, 47–58.
- Andrade, F.H., Uhart, S.A., Frugone, M., 1993. Intercepted radiation at flowering and kernel number in maize: Shade versus plant density effects. *Crop Sci.* 33, 482–485.
- Andrade, F.H., Vega, C., Uehart, S., Cirilio, A., Cantarero, M., Valentinuz, O., 1999. Kernel number determination in maize. *Crop Sci.* 39, 453–459.
- Bhalla, U.S., Iyengar, R., 1999. Emergent properties of networks of biological signaling pathways. *Science* 283, 381–387.
- Ben Haj Salah, H., Tardieu, F., 1997. Control of leaf expansion rate of droughted maize plants under fluctuating evaporative demand: A superposition of hydraulic and chemical messages? *Plant Physiol.* 114, 893–900.
- Birch, C.J., Hammer, G.L., Rickert, K.G., 1998a. Improved methods for predicting individual leaf area and leaf senescence in maize (*Zea mays* L.). *Aust. J. Agric. Res.* 49, 249–262.
- Birch, C.J., Rickert, K.G., Hammer, G.L., 1998b. Modelling leaf production and crop development in maize (*Zea mays* L.) after tassel initiation under diverse conditions of temperature and photoperiod. *Field Crops Res.* 58, 81–95.
- Boer, M.P., Wright, D., Feng, L., Podlich, D.W., Luo, L., Cooper, M., van Eeuwijk, F.A., 2007. A mixed-model quantitative trait loci (QTL) analysis for multiple-environment trial data using environmental covariables for QTL-by-environment interactions, with an example in maize. *Genetics* 177, 1801–1813.
- Bolaños, J., Edmeades, G.O., 1991. Value of selection for osmotic potential in tropical maize. *Agron. J.* 83, 948–956.
- Boote, K.J., Jones, J.W., Hoogenboom, G.H., 1998. Simulation of crop growth: CROPGRO model. In: R.M. Peart and R.B. Curry (Eds.), *Agricultural Systems Modelling and Simulation*. Marcel Dekker, New York, pp. 651–693.
- Boote, K.J., Jones, J.W., Pickering, N.B., 1996. Potential uses and limitations of crop models. *Agron. J.* 88, 704–716.
- Boote, K.J., Kroft, M.J., Brindaban, P.S., 2001. Physiology and modelling of traits in crop plants: Implications for genetic improvement. *Agric. Syst.* 70, 395–420.
- Boote, K.J., Loomis, R.S., 1991. Modelling Crop Photosynthesis – From Biochemistry to Canopy. CSSA Special Publication Number 19. American Society of Agronomy, Crop Science Society of America, Madison, WI.
- Boote, K.J., Tollenaar, M., 1994. Modelling genetic yield potential. In: K.J. Boote, J.M. Bennett, T.R. Sinclair and G.M. Paulsen (Eds.), *Physiology and Determination of Crop Yield*. ASA-CSSA-SSSA, Madison, WI, pp. 533–561.
- Borrás, L., Westgate, M.E., Astini, J.P., Echarte, L., 2007. Coupling time to silking with plant growth rate in maize. *Field Crops Res.* 102, 73–85.
- Borrell, A.K., Hammer, G.L., and van Oosterom, E., 2001. Stay-green: A consequence of the balance between supply and demand for nitrogen during grain filling? *Ann. Appl. Biol.* 138, 91–95.
- Bruce, W.B., Edmeades, G.O., Barker, T.C., 2002. Molecular and physiological approaches to maize improvement for drought tolerance. *J. Exp. Bot.* 53, 13–25.
- Campos, H., Cooper, M., Edmeades, G.O., Löffler, C., Schussler, J.R., Ibañez, M., 2006. Changes in drought tolerance in maize associated with fifty years of breeding for yield in the US Corn Belt. *Maydica* 51, 369–381.
- Campos, H., Cooper, M., Habben, J.E., Edmeades, G.O., Schussler, J.R., 2004. Improving drought tolerance in maize: A view from industry. *Field Crops Res.* 90, 19–34.
- Carberry, P.S., Muchow, R.C., Hammer, G.L., 1993. Modelling genotypic and environmental control of leaf area dynamics in grain sorghum. II. Individual leaf level. *Field Crops Res.* 33, 311–328.
- Cárcova, J., Andrieu, B., Otegui, M.E., 2003. Silk elongation in maize: Relationship with flower development and pollination. *Crop Sci.* 43, 914–920.
- Cárcova, J., Otegui, M.E., 2007. Ovary growth and maize kernel set. *Crop Sci.* 47, 1104–1110.
- Cassman, K.G., Liska, A.J., 2007. Food and fuel for all: Realistic or foolish?. *Biofuels Bioprod. Bioref.* 1, 18–23.

- Castleberry, R.M., Crum, C.W., Krull, C.F., 1984. Genetic yield improvement of US maize cultivars under varying fertility and climatic environments. *Crop Sci.* 24, 33–36.
- Century, K., Reuber, T.L., Ratcliffe, O.J., 2008. Regulating the regulators: The future prospects for transcription-factor-based agricultural biotechnology products. *Plant Physiol.* 147, 20–29.
- Chapman, S., Cooper, M., Podlich, D., Hammer, G., 2003. Evaluating plant breeding strategies by simulating gene action in dryland environment effects. *Agron. J.* 95, 99–113.
- Chapman, S., Edmeades, G.O., 1999. Selection improves drought tolerance in tropical maize populations. II. Direct and correlated responses among secondary traits. *Crop Sci.* 39, 1315–1324.
- Chapman, S.C., Cooper, M., Hammer, G.L., 2002a. Using crop simulation to interpret broad adaptation and genotype by environment effects for sorghum in water-limited environments. *Aust. J. Agric. Res.* 53, 1–11.
- Chapman, S.C., Cooper, M., Hammer, G.L., 2002b. Using crop simulation to generate genotype by environment interaction effects for sorghum in water-limited environments. *Aust. J. Agric. Res.* 53, 379–389.
- Chapman, S.C., Cooper, M., Hammer, G.L., Butler, D., 2000. Genotype by environment interactions affecting grain sorghum. II. Frequencies of different seasonal patterns of drought stress are related to location effects on hybrid yields. *Aust. J. Agric. Res.* 50, 209–222.
- Chapman, S.C., Hammer, G.L., Meinke, H., 1993. A sunflower simulation model: I. Model development. *Agron. J.* 85, 725–735.
- Chenu, K., Chapman, S.C., Hammer, G.L., Mclean, G., Ben Haj Salah, H., Tardieu, F., 2008. Short-term responses of leaf growth rate to water deficit scale up to whole-plant and crop levels: An integrated modelling approach in maize. *Plant Cell Environ.* 31, 378–391.
- Chimenti, C.A., Marcantonio, M., Hall, A.J., 2006. Divergent selection for osmotic adjustment results in improved drought tolerance in maize (*Zea mays* L.) in both early growth and flowering phases. *Field Crops Res.* 95, 305–315.
- Clerget, B., Dingkuhn, M., Goze, E., Rattunde, H.F.W., Ney, B., 2008. Variability of phyllochron, plastochron and rate of increase in height in photoperiod-sensitive sorghum varieties. *Ann. Bot.* 101, 579–594.
- Cooper, M., Chapman, S.C., Podlich, D.W., Hammer, G.L., 2002. The GP problem: Quantifying gene-to-phenotype relationships. In *Silico Biol.* 2, 151–164 (Available on-line at <http://www.bioinfo.de/isb/2002/02/0013/>; verified 14 Aug. 2008).
- Cooper, M., Hammer, G.L., 1996. *Plant Adaptation and Crop Improvement*. CAB International, Wallingford, UK.
- Cooper, M., Podlich, D., 2002. The $E(NK)$ model: Extending the NK model to incorporate gene-by-environment interactions and epistasis for diploid genomes. *Complexity* 7, 31–47.
- Cooper, M., Podlich, D.W., Smith, O.S., 2005. Gene-to-phenotype models and complex trait genetics. *Aust. J. Agric. Res.* 56, 895–918.
- Cooper, M., Smith, O.S., Merrill, R.E., Arthur, L., Podlich, D.W., Loeffler, C.M., 2006. Integrating breeding tools to generate information for efficient breeding: Past, present, and future. In: K.R. Lamkey and M. Lee (Eds.), *Plant Breeding: The Arnel R. Hallauer International Symposium*. Blackwell Publishing, Oxford, UK, pp. 141–154.
- Corbesier, L., Vincent, C., Jang, S., Fornara, F., Fan, Q., Searle, I., Giakountis, A., Farrona, S., Gissot, L., Turnbull, C., Coupland, G., 2007. FT protein movement contributes to long-distance signalling in floral induction of *Arabidopsis*. *Science* 316, 1030–1033.
- Coyne, D.P., 1970. Genetic control of a photoperiodic-temperature response for flowering in beans (*Phaseolus vulgaris* L.). *Crop Sci.* 10, 246–248.
- Dardanelli, J.L., Bachmeier, O.A., Sereno, R., Gil, R., 1997. Rooting depth and soil water extraction patterns of different crops in a silty loam Haplustoll. *Field Crops Res.* 54, 29–38.
- Dardanelli, J.L., Ritchie, J.T., Calmon, M., Andriani, J.M., Collino, D.J., 2004. An empirical model of water uptake. *Field Crops Res.* 87, 59–71.
- de Wit, C.T., 1982. Simulation of living systems. In: F.W.T. Penning de Vries and H.H. van Laar (Eds.), *Simulation of Plant Growth and Crop Production*. Pudoc, Wageningen, The Netherlands, pp. 3–19.
- de Wit, C.T., Penning de Vries, F.W.T., 1983. Crop growth models without hormones. *Neth. J. Agric. Sci.* 31, 313–323.
- Donald, C.M., 1968. The breeding of crop ideotypes. *Euphytica* 17, 385–403.

- Duncan, W.G., Loomis, R.S., Williams, W.A., Hanau, R., 1967. A model for simulating photosynthesis in plant communities. *Hilgardia* 38, 181–205.
- Duncan, W.G., McCloud, D.E., McGraw, R.L., Boote, K.J., 1978. Physiological aspects of peanut yield improvement. *Crop Sci.* 18, 1015–1020.
- Duvick, D.N., Cassman, K.G., 1999. Post-Green Revolution trends in yield potential of temperate maize in the north-central United States. *Crop Sci.* 39, 1622–1630.
- Duvick, D.N., Smith, J.S.C., Cooper, M., 2004. Long-term selection in a commercial hybrid maize breeding program. *Plant Breed. Rev.* 24, 109–151.
- Dwyer, L.M., Stewart, D.W., 1986. Leaf area development in field-grown maize. *Agron. J.* 78, 334–343.
- Echarte, L., Andrade, F.H., Vega, C.R.C., Tollenaar, M., 2004. Kernel number determination in Argentinean maize hybrids released between 1965 and 1993. *Crop Sci.* 44, 1654–1661.
- Edmeades, G.O., Baezinger, M., Ribaut, J., 2000. Chapter 6. Maize improvement for drought-limited environments. In: M.E. Otegui and G.A. Slafer (Eds.), *Physiological Basis for Maize Improvement*. Food Products Press, New York, pp. 75–112.
- Erskine, W., Ellis, R.H., Summerfield, R.J., Roberts, E.H., Hussain, A., 1990. Characterization of responses to temperature and photoperiod for time to flowering in a world lentil collection. *Theor. Appl. Genet.* 80, 193–199.
- Evans, L.T., 1976. *Crop Physiology: Some Case Histories*. Cambridge University Press, Cambridge, UK.
- Fischer, R.A., 1985. Number of Kernels in wheat crops and the influence of solar radiation and temperature. *J. Agri. Sci. UK.* 105, 447–461.
- Fontana, W., 2002. Modelling ‘evo-devo’ with RNA. *Bioessays* 24, 1164–1177.
- Fontana, W., Schnabl, W., Schuster, P., 1989. Physical aspects of evolutionary optimization and adaptation. *Phys. Rev. A* 40, 3301–3321.
- Forrester, J.W., 1961. *Industrial Dynamics*. Wiley, New York.
- Gambín, B.L., Borrás, L., Otegui, M.E., 2006. Source-sink relations and kernel weight differences in maize temperate hybrids. *Field Crops Res.* 95, 316–326.
- Gifford, R.M., Thorne, J.H., Hitz, W.D., Giaquinta, R.T., 1984. Crop productivity and photoassimilate partitioning. *Science* 225, 801–808.
- Goudriaan, J., van Laar, H.H., 1994. *Modelling potential crop growth processes*. Kluwer Academic Publishers, Dordrecht, The Netherlands.
- Graham, G.I., 2008. The development and use of genetic information in a breeding program. *Maize Genetics Conference Abstracts* 50, T3.
- Grimm, S.S., Jones, J.W., Boote, K.J., Herzog, D.C., 1994. Modeling the occurrence of reproductive stages after flowering for four soybean cultivars. *Agron. J.* 86, 31–38.
- Hammer, G., Cooper, M., Tardieu, F., Welch, S., Walsh, B., van Eeuwijk, F., Chapman, S., Podlich, D., 2006. Models for navigating biological complexity in breeding improved crop plants. *Trends Plant Sci.* 11, 1360–1385.
- Hammer, G.L., Broad, I.J., 2003. Genotype and environment effects on dynamics of harvest index during grain filling in sorghum. *Agron. J.* 95, 199–206.
- Hammer, G.L., Carberry, P.S., Muchow, R.C., 1993. Modelling genotypic and environmental control of leaf area dynamics in grain sorghum. I. Whole plant level. *Field Crops Res.* 33, 293–310.
- Hammer, G.L., Chapman, S., van Oosterom, E., Podlich, D.W., 2005. Trait physiology and crop modelling as a framework to link phenotypic complexity to underlying genetic systems. *Aust. J. Agric. Res.* 56, 947–960.
- Hammer, G.L., Dong, Z., McLean, G., Doherty, A., Messina, C., Schusler, J., Zinselmeier, C., Paszkiewicz, S., Cooper, M., 2009. Can changes in canopy and/or root system architecture explain historical maize yield trends in the US corn belt? *Crop Sci.* 49, 299–312.
- Hammer, G.L., Jordan, D.R., 2007. An integrated systems approach to crop improvement. In: J.H.J. Spierts, P.C. Struik and H.H. van Laar (Eds.), *Scale and Complexity in Plant Systems Research: Gene-Plant-Crop Relations*. Springer, Dordrecht, The Netherlands, pp. 45–61.
- Hammer, G.L., Kropff, M.J., Sinclair, T.R., Porter, J.R., 2002. Future contributions of crop modelling from heuristics and supporting decision making to understanding genetic regulation and aiding crop improvement. *Eur. J. Agron.* 18, 15–31.

- Hammer, G.L., Muchow, R.C., 1994. Assessing climatic risk to sorghum production in water-limited subtropical environments. I. Development and testing of a simulation model. *Field Crops Res.* 36, 221–234.
- Hammer, G.L., Sinclair, T.R., Boote, K.J., Wright, G.C., Meinke, H., Bell, M.J., 1995. A peanut simulation model: I. Model development and testing. *Agron. J.* 87, 1085–1093.
- Hammer, G.L., Sinclair, T.R., Chapman, S.C., van Oosterom, E., 2004. On systems thinking, systems biology, and the *in silico* plant. *Plant Physiol.* 134, 909–911.
- Hammer, G.L., Wright, G.C., 1994. A theoretical analysis of nitrogen and radiation use efficiency in peanut. *Aust. J. Agric. Res.* 45, 575–579.
- Hammer, G.L., Vanderlip, R.L., Gibson, G., Wade, L.J., Henzell, R.G., Younger, D.R., Warren, J., Dale, A.B., 1989. Genotype by environment interaction in grain sorghum II. Effects of temperature and photoperiod on ontogeny. *Crop Sci.* 29, 376–384.
- Hanks, J., Ritchie, J.T., 1991. *Modelling Plant and Soil Systems*, Agronomy Series 31. ASA-CSSA-SSSA, Madison, WI.
- Hoogenboom, G., White, J.W., Acosta-Gallegos, J., Gaudiel, R.G., Myers, J.R., Silbernagel, M.J., 1997. Evaluation of a crop simulation model that incorporates gene action. *Agron. J.* 89, 613–620.
- Jiang, H., Egli, D.B., 1995. Soybean seed number and crop growth rate during flowering. *Agron. J.* 87, 264–267.
- Jones, C.A., Kiniry, J.R., 1986. *CERES-Maize*, a simulation model of maize growth and development. Texas A&M University Press, College Station, TX.
- Jones, H.G., 1992. *Plants and microclimate: A quantitative approach to environmental plant physiology*, 2nd ed. Cambridge University Press, New York.
- Jones, J.W., Hoogenboom, G., Porter, C.H., Boote, K.J., Batchelor, W.D., Hunt, L.A., Wilkens, P.W., Singh, U., Gijsman, A.J., Ritchie, J.T., 2003. The DSSAT cropping system model. *Eur. J. Agron.* 18, 235–265.
- Karl, T.R., Trenberth, K.E., 2003. Modern global climate change. *Science* 302, 1719–1723.
- Kauffman, S., 1993. *The origins of order: Self-organization and selection in evolution*. Oxford University Press, New York.
- Kauffman, S., Peterson, C., Samuelsson, B., Troein, C., 2004. Genetic networks with canalizing Boolean rules are always stable. *Proc. Natl. Acad. Sci. U.S.A.* 101, 17102–17107.
- Keating, B.A., Carberry, P.S., Hammer, G.L., Probert, M.E., Robertson, M.J., Holzworth, D., Huth, N.I., Hargreaves, J.N.G., Meinke, H., Hochman, Z., McLean, G., Verburg, K., Snow, V., Dimes, J.P., Silburn, M., Wang, E., Brown, S., Bristow, K.L., Asseng, S., Chapman, S., McCown, R.L., Freebairn, D.M., Smith, C.J., 2003. An overview of APSIM, a model designed for farming systems simulation. *Eur. J. Agron.* 18, 267–288.
- Kemarian, A.R., Stockle, C.O., Huggins, D.R., 2005. Transpiration-use efficiency of barley. *Agric. For. Meteorol.* 130, 1–11.
- Koornneef, M., Alonso-Blanco, C., Peeters, A.J.M., Soppe, W., 1998. Genetic control of flowering time in *Arabidopsis*. *Annu. Rev. Plant Physiol. Plant Mol. Biol.* 49, 345–370.
- Kornegay, J., White, J.W., Dominguez, J.R., Tejada, G., Caijiao, C., 1993. Inheritance of a photoperiod response in Andean and Mesoamerican common bean. *Crop Sci.* 33, 977–984.
- Lander, E.S., Botstein, D., 1989. Mapping Mendelian factors underlying quantitative traits using RFLP linkage maps. *Genetics* 121, 185–199.
- Lander, E.S., Schork, N.J., 1994. Genetic dissection of complex traits. *Science* 265, 2037–2048.
- Lee, E.A., Tollenaar, M., 2007. Physiological basis of successful breeding strategies for maize yield. *Crop Sci.* 47, S-202–S-215.
- Lee, M., 1995. DNA markers and plant breeding programs. *Adv. Agron.* 55, 265–344.
- Lindquist, J.L., Arkebauer, T.J., Walters, D.T., Cassman, K.G., Dobermann, A., 2005. Maize radiation use efficiency under optimal growth conditions. *Agron. J.* 97, 72–78.
- Löffler, C.M., Wei, J., Fast, T., Gogerty, J., Langton, S., Bergman, M., Merrill, R.E., Cooper, M., 2005. Classification of maize environments using crop simulation and geographic information systems. *Crop Sci.* 45, 1708–1716.
- Long, S.P., Zhu, X.G., Naidu, S.L., Ort, D.R., 2006. Can improvement in photosynthesis increase crop yields? *Plant Cell Environ.* 29, 315–330.
- Loomis, R.S., Connor, D.J., 1992. *Crop Ecology. Productivity and Management in Agricultural Systems*. Cambridge University Press, Cambridge, UK.

- Loomis, R.S., Rabbinge, R., Ng, E., 1979. Explanatory models in crop physiology. *Annu. Rev. Plant Physiol.* 30, 339–367.
- Luque, S.F., Cirilo, A.G., Otegui, M.E., 2006. Genetic gains in grain yield and related physiological attributes in Argentine maize hybrids. *Field Crops Res.* 95, 383–397.
- Malosetti, M., van der Linden, C.G., Vosman, B., van Eeuwijk, F.A., 2007. Mixed-model approach to association mapping using pedigree information with an illustration of resistance to *Phytophthora infestans* in potato. *Genetics* 175, 879–889.
- Manschadi, A.M., Christopher, J., deVoil, P., Hammer, G.L., 2006. The role of root architectural traits in adaptation of wheat to water-limited environments. *Funct. Plant Biol.* 33, 823–837.
- McMaster, G.S., Wilhelm, W.W., 1997. Growing degree-days: One equation, two interpretations. *Agric. For. Meteorol.* 87, 291–300.
- Meinke, H., Hammer, G.L., Want, P., 1993. Potential soil water extraction by sunflower on a range of soils. *Field Crops Res.* 32, 59–81.
- Messina, C.D., Jones, J.W., Boote, K.J., Vallejos, C.E., 2006. A gene-based model to simulate soybean development and yield responses to environment. *Crop Sci.* 46, 456–466.
- Minorsky, P.V., 2003. Achieving the in silico plant: Systems biology and the future of plant biological research. *Plant Physiol.* 132, 404–409.
- Miralles, D.J., Slafer, G.A., 1997. Radiation interception and radiation use efficiency of near-isogenic wheat lines with different height. *Euphytica* 97, 201–208.
- Mitchell, M., 1996. *An Introduction to Genetic Algorithms*. MIT Press, Cambridge, MA.
- Monsi, M., Saeki, T., 2005. On the factor light in plant communities and its importance for matter production. *Ann. Bot.* 95, 549–567.
- Monteith, J.L., 1986. How do crops manipulate water supply and demand? *Philos. Trans. R. Soc. Lond. A* 316, 245–259.
- Monteith, J.L., 1988. Does transpiration limit the growth of vegetation or vice-versa? *J. Hydrol.* 100, 57–68.
- Muchow, R.C., Carberry, P.S., 1989. Environmental control of phenology and leaf growth in tropically adapted maize. *Field Crops Res.* 20, 221–236.
- Muchow, R.C., Sinclair, T.R., Bennett, J.M., 1990. Temperature and solar radiation effects on potential maize yield across locations. *Agron J.* 82, 338–343.
- Nobel, P., 2005. *Physicochemical and Environmental Plant Physiology*, 3rd ed. Elsevier Academic Press, Burlington, MA.
- Nowak, M.A., 2006. *Evolutionary Dynamics: Exploring the Equations of Life*. Harvard University Press, Cambridge MA.
- Otegui, M.E., Bonhomme, R., 1998. Grain yield components in maize: I. Ear growth and kernel set. *Field Crops Res.* 56, 247–256.
- Otegui, M.E., Slafer, G.A., 2000. *Physiological Basis for Maize Improvement*. The Hawthorne Press, New York.
- Pagano, E., Cela, S., Maddonni, G.A., Otegui, M.E., 2007. Intra-specific competition in maize: Ear development, flowering dynamics and kernel set of early-established plant hierarchies. *Field Crops Res.* 102, 198–209.
- Pagano, E., Maddonni, G.A., 2007. Intra-specific competition in maize: early established hierarchies differ in plant growth and biomass partitioning to the ear around silking. *Field Crops Res.* 101, 306–320.
- Parton, W.J., Ojima, D.S., Cole, C.V., Schimel, D.S., 1994. A general model for soil organic matter dynamics: Sensitivity to litter chemistry, texture and management. In: R.B. Bryant and R.W. Arnold (Eds.), *Quantitative Modelling of Soil Forming Processes*, SSSA Special Publication 39. Soil Science Society of America, Madison, WI, pp. 147–167.
- Parton, W.J., Stewart, J.W.B., Cole, C.V., 1988. Dynamics of C, N, P and S in grassland soils: A model. *Biogeochemistry* 5, 109–131.
- Passioura, J.B., 1983. Roots and drought resistance. *Agric. Water Manag.* 7, 265–280.
- Paterson, A.H., Tanksley, S.D., Sorrells, M.E., 1991. DNA markers in plant improvement. *Adv. Agron.* 46, 39–85.
- Peart, R.M., Curry, R.B., 1998. *Agricultural Systems Modelling and Simulation*. Marcel Dekker, New York.
- Peccoud, J., Vander Velden, K., Podlich, D., Winkler, C., Arthur, L., Cooper, M., 2004. The selective values of alleles in a molecular network model are context dependent. *Genetics* 166, 1715–1725.
- Pennisi, E., 2008. The blue revolution, drop by drop, gene by gene. *Science* 320, 171–173.

- Podlich, D.W., Cooper, M., 1998. QU-GENE: A simulation platform for quantitative analysis of genetic models. *Bioinformatics* 14, 632–653.
- Podlich, D.W., Cooper, M., Basford, K.E., 1999. Computer simulation of a selection strategy to accommodate genotype-environment interactions in a wheat recurrent selection programme. *Plant Breed.* 118, 17–28.
- Podlich, D.W., Winkler, C.R., Cooper, M., 2004. Mapping as you go: Effective approach for marker-assisted selection of complex traits. *Crop Sci.* 44, 1560–1571.
- Ravasz, E., Somera, A.L., Mongru, D.A., Oltavi, Z.N., Barabási, A.L., 2002. Hierarchical organization of modularity in metabolic networks. *Science* 297, 1551–1555.
- Reymond, M., Muller, B., Leonardi, A., Charcosset, A., Tardieu, F., 2003. Combining quantitative trait loci analysis and an ecophysiological model to analyze the genetic variability of the responses of maize leaf growth to temperature and water deficit. *Plant Physiol.* 131, 664–675.
- Ritchie, J.T., 1998. Soil water balance and plant water stress. In: G.Y. Tsuji, G. Hoogenboom and P.K. Thornton (Eds.), *Understanding Options for Agricultural Production*. Kluwer Academic Publishers, Dordrecht, The Netherlands, pp. 41–54.
- Ritchie, J.T., Alagarswamy, G., 2003. Model concepts to express genetic differences in maize yield components. *Agron. J.* 95, 4–9.
- Ritchie, J.T., NeSmith, D.S., 1991. Temperature and crop development. In: J. Hanks, J.T. Ritchie (Eds.), *Modelling Plant and Soil Systems*, Agronomy Series 31. ASA-CSSA-SSSA, Madison, WI, pp. 5–29.
- Robertson, M.J., Fukai, S., Ludlow, M.M., Hammer, G.L., 1993. Water extraction by grain sorghum in a sub-humid environment. I. Analysis of the water extraction pattern. *Field Crops Res.* 33, 81–97.
- Sadok, W., Naudin, P., Boussuge, B., Muller, B., Welcker, C., Tardieu, F., 2007. Leaf growth rate per unit thermal time follows QTL-dependent daily patterns in hundreds of maize lines under naturally fluctuating conditions. *Plant Cell Environ.* 30, 135–146.
- Sadras, V.O., Hall, A.J., 1988. Quantification of temperature, photoperiod and population effects on plant leaf area in sunflower crops. *Field Crops Res.* 18, 185–196.
- Simpson, G.G., Gendall, A.R., Dean, C., 1999. When to switch to flowering. *Annu. Rev. Plant Physiol. Plant Mol. Biol.* 15, 519–550.
- Sinclair, T., Purcell, L., Sneller, C.H., 2004. Crop transformation and the challenge to increase yield potential. *Trends Plant Sci.* 9, 70–75.
- Sinclair, T.R., 1986. Water and nitrogen limitations in soybean grain production. I. Model development. *Field Crops Res.* 15, 125–141.
- Sinclair, T.R., 1996. Limits to crop yield? In: K.J. Boote, J.M. Bennett, T.R. Sinclair and G.M. Paulsen (Eds.), *Physiology and Determination of Crop Yield*. ASA-CSSA-SSSA, Madison, WI, pp. 509–531.
- Sinclair, T.R., Horie, T., 1989. Leaf nitrogen, photosynthesis, and crop radiation use efficiency: A review. *Crop Sci.* 29, 90–98.
- Sinclair, T.R., Muchow, R.C., 1999. Radiation use efficiency. *Adv. Agron.* 65, 215–265.
- Sinclair, T.R., Muchow, R.C., 2001. System analysis of plant traits to increase grain yield on limited water supplies. *Agron. J.* 93, 263–270.
- Sinclair, T.R., Seligman, N.G., 1996. Crop modeling: From infancy to maturity. *Agron. J.* 88, 698–704.
- Sinclair, T.R., Tanner, C.B., Bennett, J.M., 1984. Water-use efficiency in crop production. *Bioscience* 34, 36–40.
- Slafer, G.A., 1994. *Genetic improvement of field crops*. Marcel Dekker, New York.
- Soltani, A., Hammer, G.L., Torabi, B., Robertson, M.J., Zeinali, E., 2006. Modelling chickpea growth and development: Phenological development. *Field Crops Res.* 99, 1–13.
- Stöckle, C.O., Donatelli, M., Nelson, R., 2003. CropSyst, a cropping systems simulation model. *Eur. J. Agron.* 18, 289–307.
- Tamaki, S., Matsuo, S., Wong, H.L., Yokoi, S., Shimamoto, K., 2007. Hd3a protein is a mobile flowering signal in rice. *Science* 316, 1033–1036.

- Tanner, C.B., Sinclair, T.R., 1983. Efficient water use in crop production: Research or re-search? In: H.M. Taylor, W.R. Jordan and T.R. Sinclair (Eds.), *Limitations to Efficient Water Use in Crop Production*. ASA-CSSA-SSSA, Madison, WI, pp. 1–27.
- Tardieu, F., 2003. Virtual plants: Modelling as a tool for the genomics of tolerance to water deficit. *Trends Plant Sci.* 8, 9–14.
- Tardieu, F., Granier, C., Muller, B., 1999. Modelling leaf expansion in a fluctuating environment: Are changes in specific leaf area a consequence of changes in expansion rate? *New Phytol.* 143, 33–43.
- Thomas, Fukai, S., Hammer, G.L., 1995. Growth and yield response of barley and chickpea to water stress under three environments in southeast Queensland. II. Root growth and soil water extraction pattern. *Aust. J. Agric. Res.* 46, 35–48.
- Thornley, J.H.M., Johnson, I.R., 2000. *Plant and Crop Modelling*. The Blackburn Press, New Jersey.
- Tollenaar, M., Dwyer, L.M., Stewart, D.W., 1992. Ear and kernel formation in maize hybrids representing three decades of grain yield improvement in Ontario. *Crop Sci.* 32, 432–438.
- Tuberosa, R., Salvi, S., 2006. Genomics-based approaches to improve drought tolerance of crops. *Trends Plant Sci.* 11, 405–412.
- Tuberosa, R., Salvi, S., Giuliani, S., Sanguinetti, M.C., Bellotti, M., Conti, S., Landi, P., 2007. Genome-wide approaches to investigate and improve maize response to drought. *Crop Sci.* 47, S-120–S-141.
- Tuberosa, R., Salvi, S., Sanguinetti, M.C., Landi, P., Maccaferri, M., Conti, S., 2002. Mapping QTLs regulating morpho-physiological traits and yield: Case studies, shortcomings and perspectives in drought-stressed maize. *Ann. Bot.* 89, 941–963.
- van Eeuwijk, F.A., Malosetti, M., Yin, X., Struik, P.C., Stam, P., 2005. Statistical models for genotype by environment data: From conventional ANOVA models to eco-physiological QTL models. *Aust. J. Agric. Res.* 56, 883–894.
- van Ittersum, M.K., Leffelaar, P.A., van Keulen, H., Kropff, M.J., Bastiaans, L., Goudriaan, J., 2003. On approaches and applications of the Wageningen crop models. *Eur. J. Agron.* 18, 201–234.
- van Oosterom, E.J., Hammer, G.L., 2008. Determination of grain number in sorghum. *Field Crops Res.* 108, 259–268.
- Vega, C.R.C., Andrade, F.H., Sadras, V.O., Uhart, S.A., Valentinuz, O.R., 2001. Seed number as a function of growth. A comparative study in soybean, sunflower, and maize. *Crop Sci.* 41, 748–754.
- Villalobos, F.J., Hall, A.J., Ritchie, J.T., Orgaz, F., 1996. Oilcrop-sun: A development, growth and yield model of the sunflower crop. *Agron. J.* 88, 403–415.
- Wang, J., van Ginkel, M., Podlich, D., Ye, G., Trethowan, R., Pfeiffer, W., DeLacy, I.H., Cooper, M., Rajaram, S., 2003. Comparison of two breeding strategies by computer simulation. *Crop Sci.* 43, 1764–1773.
- Wardlaw, I.F., 1990. Tansley Review No. 27: The control of carbon partitioning in plants. *New Phytol.* 116, 341–381.
- White, J.W., Hoogenboom, G., 1996. Simulating effects of genes for physiological traits in a process-oriented crop model. *Agron. J.* 88, 416–422.
- White, J.W., Laing, D.R., 1989. Photoperiod response of flowering in diverse genotypes of common bean (*Phaseolus vulgaris*). *Field Crops Res.* 22, 113–128.
- Wright, S., 1932. The roles of mutation, inbreeding, crossbreeding and selection in evolution. In: *Proceedings of the 6th International Congress of Genetics*. Ithaca, New York, pp. 356–366.
- Yin, X., Stam, P., Kropff, M.J., Schapendonk, A.H.C.M., 2003. Crop modelling, QTL mapping, and their complementary role in plant breeding. *Agron. J.* 95, 90–98.
- Yin, X., Struik, P.C., van Eeuwijk, F.A., Stam, P., Tang, J., 2005. QTL analysis and QTL-based prediction of flowering phenology in recombinant inbred lines of barley. *J. Exp. Bot.* 56, 967–976.
- Yuan, J.S., Galbraith, D.W., Dai, S.Y., Griffin, P., Stewart, N. Jr., 2008. Plant systems biology comes of age. *Trends Plant Sci.* 13, 165–171.