

## Simulating crop phenology

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### Abstract

Understanding and predicting crop phenology and canopy development is important for many reasons including improving the efficacy of management practices and accuracy of simulation models and decision support systems. This paper reports the status of a model for predicting crop phenology (*Phenology MMS*) that can be used independently to simulate crop development or incorporated into existing crop growth models. This new model is intended to synthesize and quantify the entire developmental sequence of the shoot apex of many crops, making this information readily available to users with limited knowledge of phenology or the crop being simulated. Developmental sequences for winter wheat and corn are presented as examples of model structure, use, and performance.

### Media summary

A new crop phenology model simulates the growth stages of many crop species and cultivars for use in management and agricultural models.

### Key Words

Development, modeling, simulation.

### Introduction

Understanding crop phenology is fundamental to crop management, where timing of management practices is increasingly based on stages of crop development. Simulating canopy development is also critical for crop growth models, whether to predict the appearance of sources and sinks, determining carbon assimilation and transpiration, partitioning carbohydrates and nutrients, or determining critical life cycle events such as anthesis and maturity.

A new generation of wheat growth models began to emerge in the 1980's that changed from energy/carbon-driven to more development-driven (e.g., ARCWHEAT, Weir et al., 1984; SHOOTGRO, McMaster et al., 1992; MODWht, Rickman et al., 1996) simulations. Each new model was important in uniquely incorporating cereal development concepts lacking in the wheat growth models existing prior to their introduction. Regardless, all crop growth models benefit from good phenology submodels.

While many developmental and phenological concepts from development-driven models are transferable to other crops, one problem is assembling quantitative relationships between development and environment and genetic factors. The complete developmental sequence of the wheat shoot apex has been quantified (McMaster et al., 1992; McMaster, 1997), and extended to corn (Wilhelm and McMaster, 1998). Other than these two crops, quantitative descriptions of the developmental sequence of crops do not exist. Modifying existing plant growth models to simulate other crops in agroecosystem analyses would be easier if developmental sequences were available. Without the entire developmental sequence of a crop at least being qualitatively summarized, model developers and practitioners must search through diverse pieces of information spread throughout the literature and talk with experts, and then attempt to quantify the processes.

The objective of this paper is to present on-going work that seeks to develop a phenology simulation model (*Phenology MMS*) that outlines and quantifies the developmental sequence of many crops,

provides information relevant to each crop, and is intended to be used either independently or inserted into existing crop growth models of varying levels of detail.

## Model Overview

### Interface

A Java-based interface is used for the standalone model that allows the user to interact with the underlying Fortran simulation model. First, the user selects basic information such as the crop and weather input files (Fig. 1). Other general information is then input by the user such as planting date, method of calculating growing degree-days and phyllochron (rate of leaf appearance), and soil moisture at planting (Fig. 2). The user then either selects the default values for a crop (e.g., a generic cultivar or from a selected list of cultivars) or changes the default variables as desired (Fig. 3). The Fortran simulation module is run with these input values.

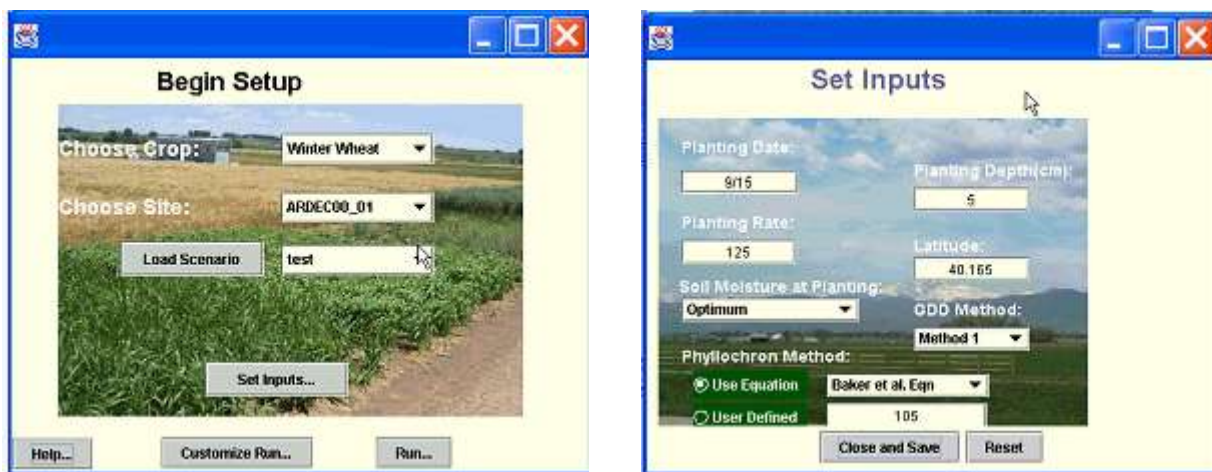


Figure 1. The beginning screen of the program for selecting crop type, location, and other basic information

Figure 2. Screen for selecting the “Set Inputs” button in Fig. 1. Basic agronomic information, initial conditions, and thermal time calculation methods are selected here.

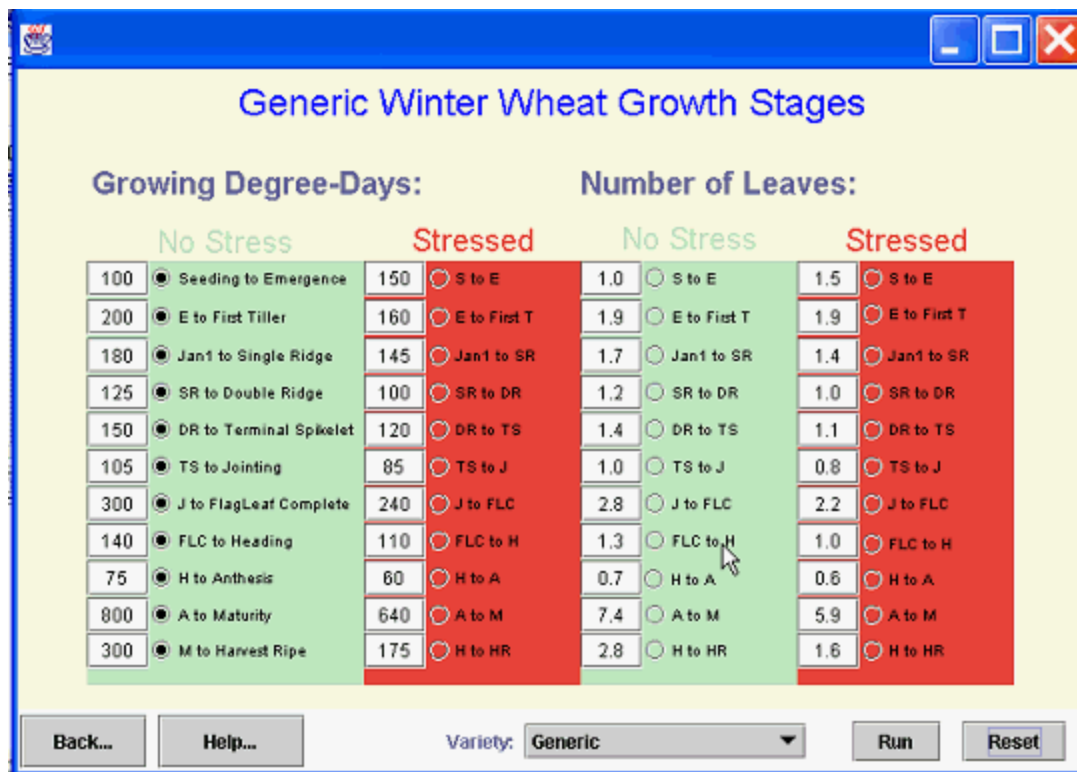


Figure 3. This screen allows the user to select the cultivar type of the selected crop and to change default parameters. The screen is accessed from the “Begin Setup” screen under the “Customize Run” button from Figure 1.

#### *Developmental sequences*

A typical approach for creating and quantifying the entire developmental sequence of each crop is to thoroughly search the literature and talk with experts of the crop. Also, certain groups of species (e.g. annual grasses) and general morphological concepts allow certain generalizations and principles to apply among crops. For instance, the grass shoot apices of wheat, barley, and rice develop very similarly with many similar growth stages. For each species, model parameters for a “generic” cultivar are provided in the *Phenology MMS* database. As cultivar-specific parameters are defined, a parameter file specific to a cultivar can be added to the database and made available on the drop-down menu. In addition, cultivar parameters can be modified to allow user to conduct “gaming” simulations with the model. Regardless of the detailed knowledge of cultivar parameters, timing or duration of a few critical stages must be known. For example, when leaves are appearing and internodes begin growth, when reproductive structures/primordia are formed, and when anthesis, physiological maturity, and harvest ripe occurs.

#### *Fortran simulation module*

Temperature is the primary factor controlling phenological development rates, with photoperiod and vernalization often being important for some crops as well (McMaster and Smika, 1988; McMaster, 1997). Factors such as water, nutrients, salinity, CO<sub>2</sub>, etc. are generally important as secondary factors, and often must exceed threshold values before influencing phenology. Thermal time is used to drive phenology. Depending on the level of resolution, understanding, and available information, the effects of stresses are addressed by different approaches. The simplest approach is to choose parameter values (see Fig. 3) for either unstressed or stressed conditions. The default approach assumes that stresses, if they have any effect, will generally hasten phenological development (Table 1). For some crops and developmental events such as tasseling and silking in corn, stress tends to decouple the synchronization

of these two events. Current trends of using the leaf number on the main shoot to predict certain growth stages (McMaster, 1997) is also provided as an option in the program, rather than using thermal time.

**Table 1. Thermal time (in growing degree-days, GDD) between growth stages pooling 12 winter wheat cultivars for 2 years and 2 locations. Adapted from McMaster and Wilhelm (2004).**

Growth stage interval	Irrigated	Dryland	Difference	
	(GDD)	(GDD)	(GDD)	(%)†
1 Jan - Jointing	484	486	-2	100.4
Jointing - Flag Leaf Complete	158	152	6	96.2
Flag Leaf Complete - Heading	164	143	21	87.2
Heading - Anthesis	133	117	16	88.0
Anthesis - Maturity	710	557	153	78.5

†  $[1 - (\text{Irrigated GDD} - \text{Dryland GDD}) / \text{Irrigated GDD}] * 100$

## Results

Developmental sequences for winter and spring wheat (Figs. 4 and 5), corn (Figs. 6 and 7), winter and spring barley, sorghum, proso millet, hay millet, sunflower, soybean, dry bean, potato, and canola have been completed for generic cultivars. A number of cultivars of wheat and corn grown in the U.S. currently have parameter files in the *Phenology MMS* database. Other crops are being researched and will be added in the future. The developmental sequence is developed in two forms for a crop (Figs. 4 and 5 for wheat, Figs. 6 and 7 for corn), and used to populate the Phenology MMS database accessed by the screen shown in Fig. 3.

# GENERIC WINTER WHEAT SHOOT APEX DEVELOPMENTAL SEQUENCE (NO STRESSES)

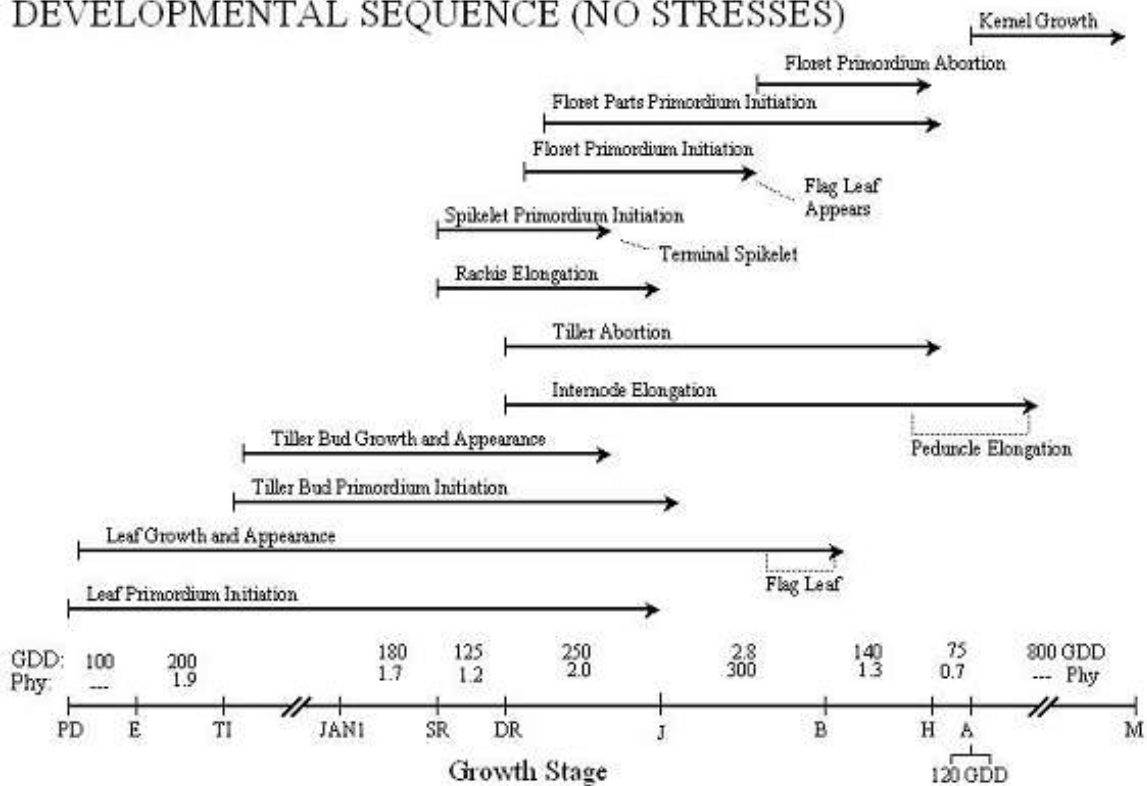


Figure 4. Developmental sequence of the winter wheat shoot apex. Adapted from McMaster (1997).

## GENERIC WINTER WHEAT GROWTH STAGES

		NO STRESSES												
		S	E	TI	1/1	SR	DR	IE/TS	J	FLC/B	H	A	PM	HR
GDD		100	200		180	125	150	105	300	140	75	800	?	
#LVS		---	1.9		1.7	1.2	1.4	1.0	2.8	1.3	0.7	---	?	
GDD		150	160		145	100	120	85	240	110	60	640	?	
#LVS		---	1.9		1.7	1.2	1.4	1.0	2.8	1.3	0.7	---	?	
		S	E	TI	1/1	SR	DR	IE/TS	J	FLC/B	H	A	PM	HR

DRYLAND

S = Sowing	DR = Double Ridge	FLC = Flag Leaf Complete	A = Anthesis
E = Emergence	IE = Internode Elongation	B = Booting	PM = Physiological Maturity
TI = Tiller Initiation	TS = Terminal Spikelet	H = Heading	HR = Harvest Ripe
SR = Single Ridge	J = Jointing		

Figure 5. Alternative representation of Fig. 4, showing stress effects.

## GENERIC MAIZE SHOOT APEX DEVELOPMENTAL SEQUENCE (NO STRESSES)

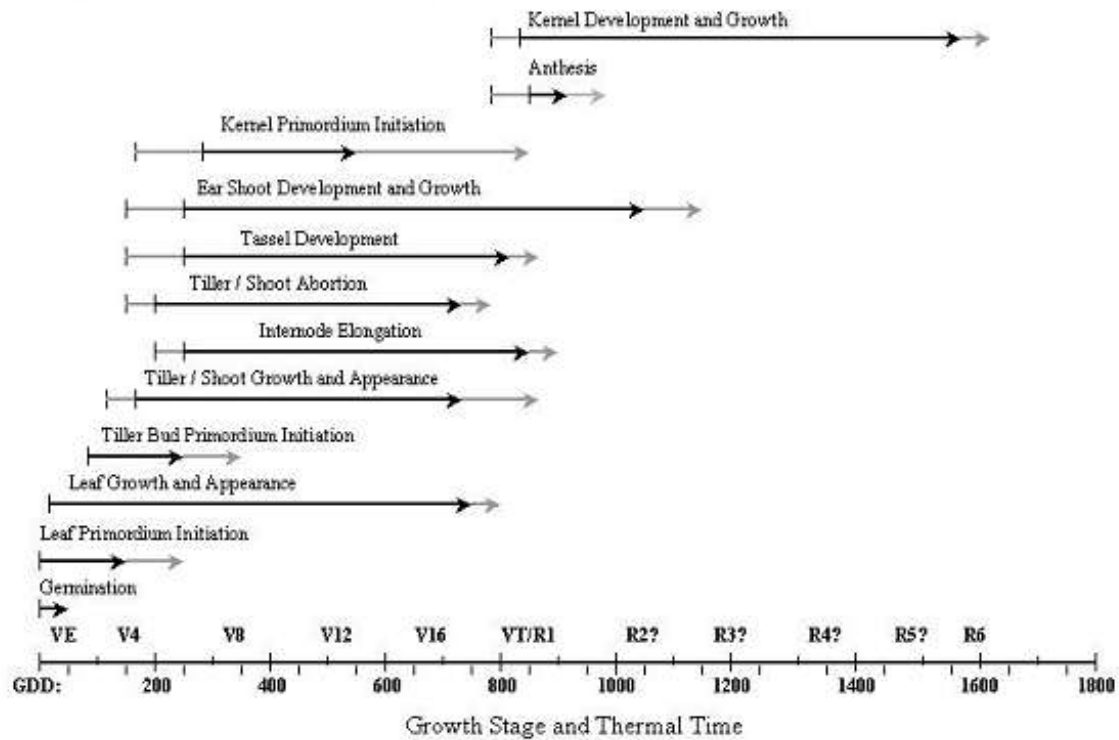
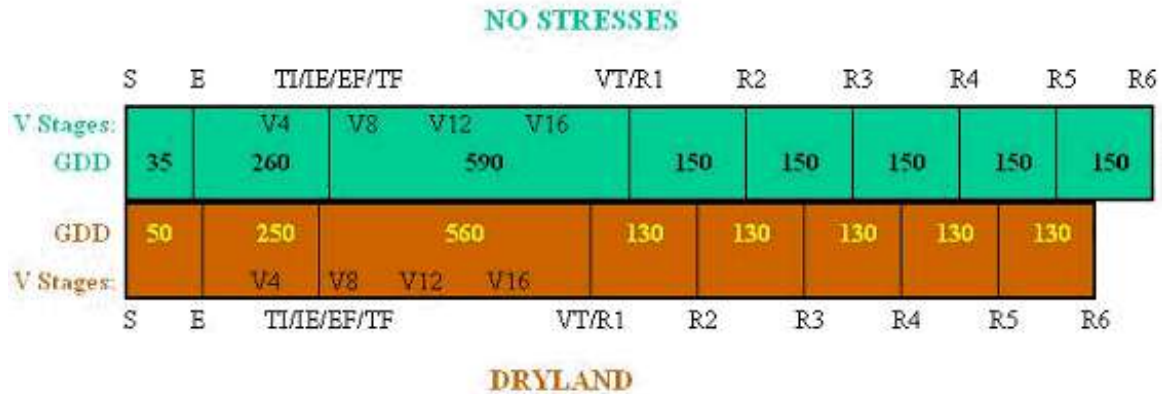


Figure 6. Developmental sequence of corn shoot apex. Adapted from Wilhelm and McMaster (1998).

## *GENERIC MAIZE GROWTH STAGES*



S = Sowing	TF = Tassel Formation	VT = Tasseling	R4 = Dough
E = Emergence	IE = Internode Elongation	R1 = Silking	R5 = Dent
TI = Tiller Initiation	V# = # of Collared Leaves	R2 = Blister	R6 = Physiological Maturity
EF = Ear Formation		R3 = Milk	

Figure 7. Alternate representation of Fig. 6, and showing stress effects.

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