

0.0.0.0

## 1 The APSIM Soybean Model

The APSIM Soybean model has been developed using the Plant Modelling Framework (PMF) of ([Brown et al., 2014](#)). This new framework provides a library of plant organ and process submodels that can be coupled, at runtime, to construct a model in much the same way that models can be coupled to construct a simulation. This means that dynamic composition of lower level process and organ classes (e.g. photosynthesis, leaf) into larger constructions (e.g. maize, wheat, sorghum) can be achieved by the model developer without additional coding.

The model consists of:

- a phenology model to simulate development between growth phases
- a structure model to simulate plant morphology
- a collection of organs to simulate the various plant parts
- an arbitrator to allocate resources (N, biomass) to the various plant organs

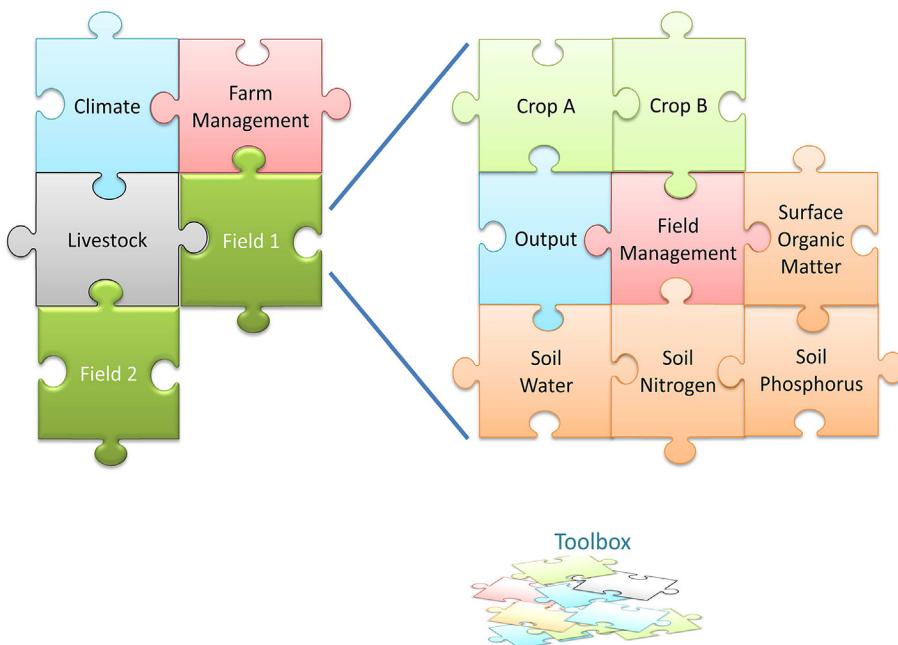
## 2 APSIM Description

The Agricultural Production Systems sIMulator (APSIM) is a farming systems modelling framework that is being actively developed by the APSIM Initiative.

It is comprised of

1. a set of biophysical models that capture the science and management of the system being modelled,
2. a software framework that allows these models to be coupled together to facilitate data exchange between the models,
3. a set of input models that capture soil characteristics, climate variables, genotype information, field management etc,
4. a community of developers and users who work together, to share ideas, data and source code,
5. a data platform to enable this sharing and
6. a user interface to make it accessible to a broad range of users.

The literature contains numerous papers outlining the many uses of APSIM applied to diverse problem domains. In particular, [Holzworth et al., 2014](#); [Keating et al., 2003](#); [McCown et al., 1996](#); [McCown et al., 1995](#) have described earlier versions of APSIM in detail, outlining the key APSIM crop and soil process models and presented some examples of the capabilities of APSIM.



**Figure 2:** This conceptual representation of an APSIM simulation shows a “top level” farm (with climate, farm management and livestock) and two fields. The farm and each field are built from a combination of models found in the toolbox. The APSIM infrastructure connects all selected model pieces together to form a coherent simulation.\*

The APSIM Initiative has begun developing a next generation of APSIM (APSIM Next Generation) that is written from scratch and designed to run natively on Windows, LINUX and MAC OSX. The new framework incorporates the best of the APSIM 7.x framework with an improved supporting framework. The Plant Modelling Framework (a generic collection of plant building blocks) was ported from the existing APSIM to bring a rapid development pathway for plant models. The user interface paradigm has been kept the same as the existing APSIM version, but completely rewritten to support new application domains and the newer Plant Modelling Framework. The ability to describe experiments has been added which can also be used for rapidly building factorials of simulations. The ability to write C# scripts to control farm and paddock management has been retained. Finally, all simulation outputs are written to an SQLite database to make it easier and quicker to query, filter and graph outputs.

The model described in this documentation is for APSIM Next Generation.

APSIM is freely available for non-commercial purposes. Non-commercial use of APSIM means public-good research & development and educational activities. It includes the support of policy development and/or implementation by, or on behalf of, government bodies and industry-good work where the research outcomes are to be made publicly available. For more information visit the [licensing page on the APSIM web site](#)

### 3 Model description

The Soybean model is constructed from the following list of software components. Details of the implementation and model parameterisation are provided in the following sections.

#### List of Plant Model Components.

Component Name	Component Type
Arbitrator	Models.PMF.OrganArbitrator
Phenology	Models.PMF.Phen.Phenology
Leaf	Models.PMF.Organs.SimpleLeaf
Grain	Models.PMF.Organs.ReproductiveOrgan
Root	Models.PMF.Organs.Root
Nodule	Models.PMF.Organs.Nodule
Shell	Models.PMF.Organs.GenericOrgan

Component Name	Component Type
Stem	Models.PMF.Organs.GenericOrgan
MortalityRate	Models.Functions.Constant

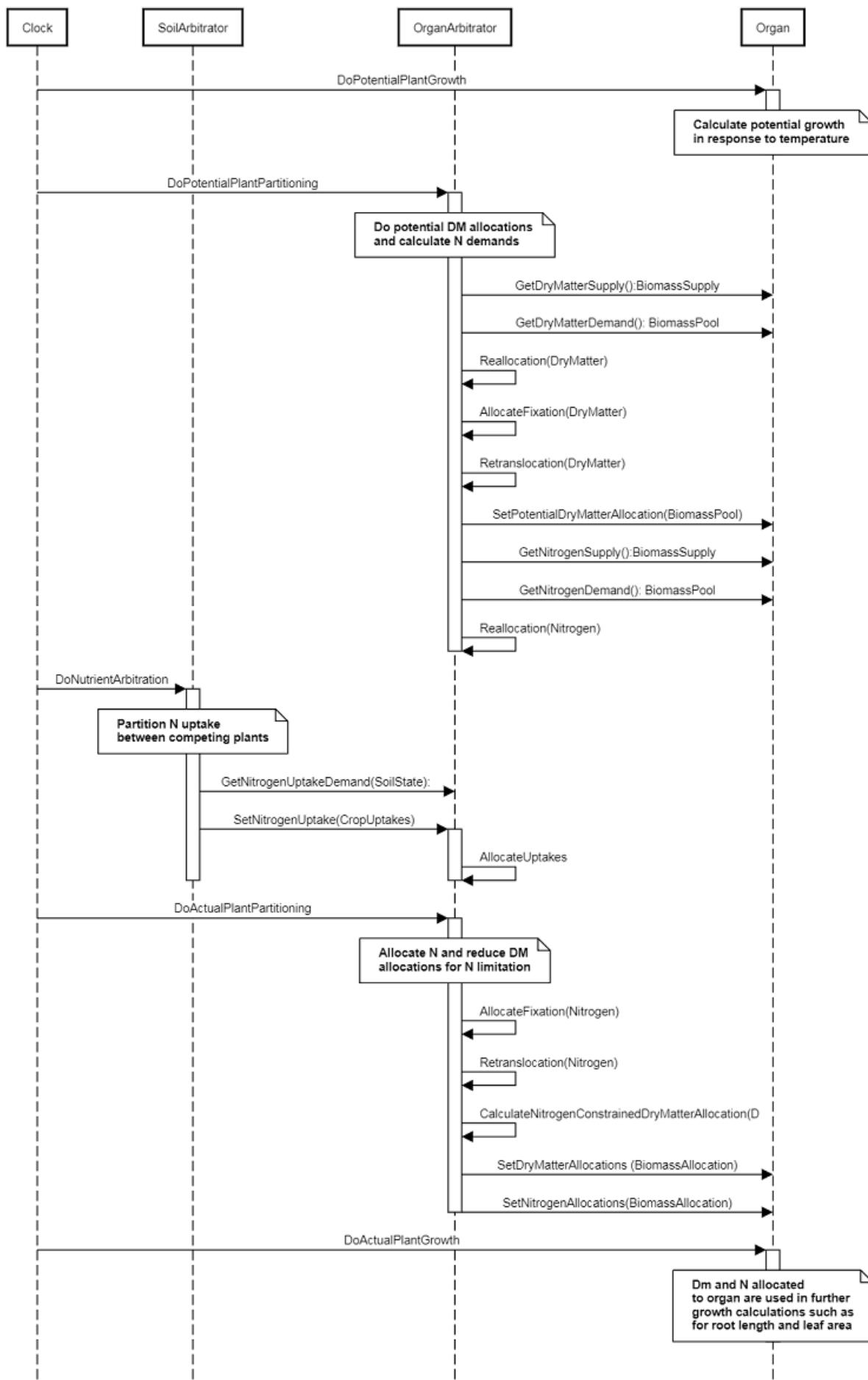
### 3.1 Arbitrator

The Arbitrator class determines the allocation of dry matter (DM) and Nitrogen between each of the organs in the crop model. Each organ can have up to three different pools of biomass:

- **Structural biomass** which is essential for growth and remains within the organ once it is allocated there.
- **Metabolic biomass** which generally remains within an organ but is able to be re-allocated when the organ senesces and may be retranslocated when demand is high relative to supply.
- **Storage biomass** which is partitioned to organs when supply is high relative to demand and is available for retranslocation to other organs whenever supply from uptake, fixation, or re-allocation is lower than demand.

The process followed for biomass arbitration is shown in Figure 3. Arbitration calculations are triggered by a series of events (shown below) that are raised every day. For these calculations, at each step the Arbitrator exchange information with each organ, so the basic computations of demand and supply are done at the organ level, using their specific parameters.

1. **doPotentialPlantGrowth.** When this event occurs, each organ class executes code to determine their potential growth, biomass supplies and demands. In addition to demands for structural, non-structural and metabolic biomass (DM and N) each organ may have the following biomass supplies:
  2. **Fixation supply.** From photosynthesis (DM) or symbiotic fixation (N)
  3. **Uptake supply.** Typically uptake of N from the soil by the roots but could also be uptake by other organs (eg foliage application of N).
  4. **Retranslocation supply.** Storage biomass that may be moved from organs to meet demands of other organs.
  5. **Reallocation supply.** Biomass that can be moved from senescing organs to meet the demands of other organs.
6. **doPotentialPlantPartitioning.** On this event the Arbitrator first executes the DoDMSetup() method to gather the DM supplies and demands from each organ, these values are computed at the organ level. It then executes the DoPotentialDMAAllocation() method which works out how much biomass each organ would be allocated assuming N supply is not limiting and sends these allocations to the organs. Each organ then uses their potential DM allocation to determine their N demand (how much N is needed to produce that much DM) and the arbitrator calls DoNSetup() to gather the N supplies and demands from each organ and begin N arbitration. Firstly DoNReallocation() is called to redistribute N that the plant has available from senescing organs. After this step any unmet N demand is considered as plant demand for N uptake from the soil (N Uptake Demand).
  7. **doNutrientArbitration.** When this event occurs, the soil arbitrator gets the N uptake demands from each plant (where multiple plants are growing in competition) and their potential uptake from the soil and determines how much of their demand that the soil is able to provide. This value is then passed back to each plant instance as their Nuptake and doNUptakeAllocation() is called to distribute this N between organs.
  8. **doActualPlantPartitioning.** On this event the arbitrator call DoNRetranslocation() and DoNFixation() to satisfy any unmet N demands from these sources. Finally, DoActualDMAAllocation is called where DM allocations to each organ are reduced if the N allocation is insufficient to achieve the organs minimum N concentration and final allocations are sent to organs.



**Figure 3:** Schematic showing the procedure for arbitration of biomass partitioning. Pink boxes represent events that occur every day and their numbering shows the order of calculations. Blue boxes represent the methods that are called when these events occur. Orange boxes contain properties that make up the organ/arbitrator interface. Green boxes are organ specific properties.

## 3.2 Phenology

This model simulates the development of the crop through successive developmental *phases*. Each phase is bound by distinct growth *stages*. Phases often require a target to be reached to signal movement to the next phase. Differences between cultivars are specified by changing the values of the default parameters shown below.

In the new model we simplified phenology by taking out stages that are not measurable (e.g. end of juvenile stage) and by adding new stages that are measurable (e.g. start pod). The new phenology follows the V/R staging system.

The key differences for cultivars are mostly phenological parameters (e.g., Vegetative.Target, ReproductivePhotoperiodModifier). In some cases, some additional parameters have been changed, see parameter values in the cultivar section.

### List of stages and phases used in the simulation of crop phenological development

Phase Number	Phase Name	Initial Stage	Final Stage
1	Germinating	Sowing	Germination
2	Emerging	Germination	Emergence
3	Vegetative	Emergence	StartFlowering
4	EarlyFlowering	StartFlowering	StartPodDevelopment
5	EarlyPodDevelopment	StartPodDevelopment	StartGrainFilling
6	EarlyGrainFilling	StartGrainFilling	EndCanopyDevelopment
7	MidGrainFilling	EndCanopyDevelopment	EndPodDevelopment
8	LateGrainFilling	EndPodDevelopment	EndGrainFill
9	Maturing	EndGrainFill	Maturity
10	Ripening	Maturity	HarvestRipe
11	ReadyForHarvesting	HarvestRipe	Unused

### 3.2.1 Phenological Phases

#### 3.2.1.1 Germinating Phase

The model assumes that germination will be completed on the day after sowing, provided that the extractable soil water is greater than zero.

#### 3.2.1.2 Emerging Phase

This phase goes from Germination to Emergence and simulates time to emergence as a function of sowing depth. The *ThermalTime Target* for ending this phase is given by:

$$\text{Target} = \text{SowingDepth} \times \text{ShootRate} + \text{ShootLag}$$

Where:

$$\text{ShootRate} = 1 \text{ (deg day/mm)},$$

$$\text{ShootLag} = 10 \text{ (deg day)},$$

and *SowingDepth* (mm) is sent from the manager with the sowing event.

Progress toward emergence is driven by Thermal time accumulation, where thermal time is calculated as:

$$\text{ThermalTime} = [\text{Phenology}].\text{VegetativeThermalTime}$$

#### 3.2.1.3 Vegetative Phase

This *phase* goes from Emergence to StartFlowering. It uses a *Target* to determine the duration between development *Stages*. Daily *progress* is accumulated until the *Target* is met and remaining fraction of the day is forwarded to the next phase.

The *Target* and the daily *Progression* toward StartFlowering are described as follow:

#### 3.2.1.3.1 Target

*Target* = 200

*Progression* = [Phenology].ThermalTime

#### 3.2.1.4 EarlyFlowering Phase

This *phase* goes from StartFlowering to StartPodDevelopment. It uses a *Target* to determine the duration between development *Stages*. Daily *progress* is accumulated until the *Target* is met and remaining fraction of the day is forwarded to the next phase.

The duration of the grain filling phase has been taken from the model of Robertson et al (2002).

The *Target* and the daily *Progression* toward StartPodDevelopment are described as follow:

#### 3.2.1.4.1 Target

*Target* = 200

*Progression* = [Phenology].ThermalTime

#### 3.2.1.5 EarlyPodDevelopment Phase

This *phase* goes from StartPodDevelopment to StartGrainFilling. It uses a *Target* to determine the duration between development *Stages*. Daily *progress* is accumulated until the *Target* is met and remaining fraction of the day is forwarded to the next phase.

The duration of the grain filling phase has been taken from the model of Robertson et al (2002).

The *Target* and the daily *Progression* toward StartGrainFilling are described as follow:

#### 3.2.1.5.1 Target

*Target* = 140

*Progression* = [Phenology].ThermalTime

#### 3.2.1.6 EarlyGrainFilling Phase

This *phase* goes from StartGrainFilling to EndCanopyDevelopment. It uses a *Target* to determine the duration between development *Stages*. Daily *progress* is accumulated until the *Target* is met and remaining fraction of the day is forwarded to the next phase.

The *Target* and the daily *Progression* toward EndCanopyDevelopment are described as follow:

#### 3.2.1.6.1 Target

*Target* = FractionofGrainfilling × [Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue

Where:

FractionofGrainfilling = 0.05

*Progression* = [Phenology].ThermalTime

#### 3.2.1.7 MidGrainFilling Phase

This *phase* goes from EndCanopyDevelopment to EndPodDevelopment. It uses a *Target* to determine the duration between development *Stages*. Daily *progress* is accumulated until the *Target* is met and remaining fraction of the day is forwarded to the next phase.

The *Target* and the daily *Progression* toward EndPodDevelopment are described as follow:

#### 3.2.1.7.1 Target

*Target* = FractionofMidToLateGrainfilling × MidToLateGrainfilling

Where:

*FractionofMidToLateGrainfilling* = 0.5

### 3.2.1.7.1.1 MidToLateGrainfilling

*MidToLateGrainfilling* = [*Phenology*].*LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue* - [*Phenology*].*EarlyGrainFilling.Target*

*Progression* = [*Phenology*].*ThermalTime*

### 3.2.1.8 LateGrainFilling Phase

This *phase* goes from EndPodDevelopment to EndGrainFill. It uses a *Target* to determine the duration between development *Stages*. Daily *progress* is accumulated until the *Target* is met and remaining fraction of the day is forwarded to the next phase.

The *Target* and the daily *Progression* toward EndGrainFill are described as follow:

#### 3.2.1.8.1 Target

*Target* = *EntireGrainfillPeriod* - [*Phenology*].*EarlyGrainFilling.Target* - [*Phenology*].*MidGrainFilling.Target*

Where:

*EntireGrainfillPeriod* = 500

*Progression* = [*Phenology*].*ThermalTime*

### 3.2.1.9 Maturing Phase

This *phase* goes from EndGrainFill to Maturity. It uses a *Target* to determine the duration between development *Stages*. Daily *progress* is accumulated until the *Target* is met and remaining fraction of the day is forwarded to the next phase.

The *Target* and the daily *Progression* toward Maturity are described as follow:

#### 3.2.1.9.1 Target

*Target* = 45

*Progression* = [*Phenology*].*ThermalTime*

### 3.2.1.10 Ripening Phase

This *phase* goes from Maturity to HarvestRipe. It uses a *Target* to determine the duration between development *Stages*. Daily *progress* is accumulated until the *Target* is met and remaining fraction of the day is forwarded to the next phase.

The *Target* and the daily *Progression* toward HarvestRipe are described as follow:

#### 3.2.1.10.1 Target

*Target* = 45

*Progression* = [*Phenology*].*ThermalTime*

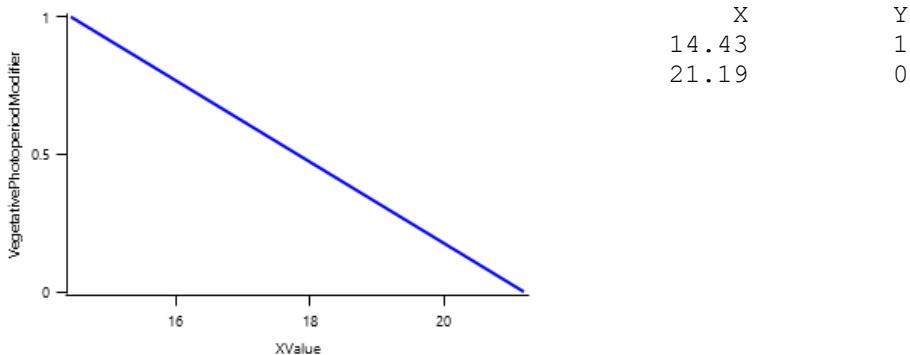
It is the end phase in phenology and the crop will sit, unchanging, in this phase until it is harvested or removed by other method

*ThermalTime* = [*Phenology*].*ThermalTime*

## 3.2.2 VegetativePhotoperiodModifier

These parameters are overridden by cultivar parameter descriptions to capture the difference between individual cultivars in terms of their phenological development. Responses shown here are only indicative. See cultivar descriptions for more information.

*VegetativePhotoperiodModifier* is calculated using linear interpolation



*XValue* = [Phenology].Photoperiod

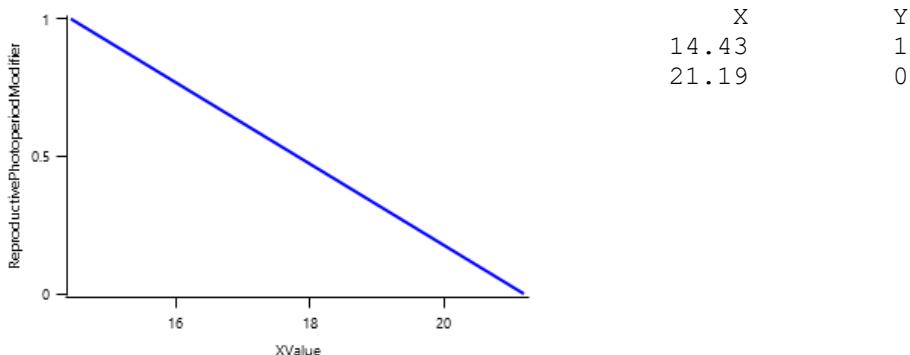
### 3.2.3 ReproductiveThermalTime

Cardinal temperatures for vegetative and reproductive thermal time are the same except the range of 0-15° C, see graph. A base temperature of 10° C is used for vegetative phase, which temperature has been used to calibrate 56 soybean cultivars in the USA (Archontoulis et al., 2014) and 72 soybean cultivars in China (Wu et al., 2019). The small changes in cardinal temperatures for reproductive thermal time was important for solving issues related to photoperiod response for some Australian cultivars. Such a differentiation in base temperature between V and R stages is supported by Boote et al. (1998), DSSAT-CROPGRO soybean model, who showed that cardinal temperatures may differ for vegetative and reproductive development for soybean. This is something to further explore as new data from other environments are added to the APSIM NG database.

### 3.2.4 ReproductivePhotoperiodModifier

These parameters are overridden by cultivar parameter descriptions to capture the difference between individual cultivars in terms of their phenological development. Responses shown here are only indicative. See cultivar descriptions for more information.

*ReproductivePhotoperiodModifier* is calculated using linear interpolation



*XValue* = [Phenology].Photoperiod

### 3.2.5 ThermalTime

#### 3.2.5.1 PreEmergence

The value of ThermalTime from Sowing to Emergence is calculated as follows:

$$\text{Base} = [\text{Phenology}].\text{VegetativeThermalTime}$$

#### 3.2.5.2 VegetativeGrowth

The value of ThermalTime from Emergence to EndCanopyDevelopment is calculated as follows:

##### 3.2.5.2.1 TT

$$TT = [\text{Phenology}].\text{VegetativeThermalTime} \times [\text{Phenology}].\text{VegetativePhotoperiodModifier}$$

### 3.2.5.3 ReproductiveGrowth

The value of ThermalTime from EndCanopyDevelopment to HarvestRipe is calculated as follows:

#### 3.2.5.3.1 TT

$$TT = [\text{Phenology}].\text{ReproductiveThermalTime} \times [\text{Phenology}].\text{ReproductivePhotoperiodModifier}$$

ThermalTime has a value of zero for phases not specified above

### 3.2.6 Photoperiod

Returns the duration of the day, or photoperiod, in hours. This is calculated using the specified latitude (given in the weather file) and twilight sun angle threshold. If a variable called ClimateControl.PhotoPeriod is found in the simulation, it will be used instead.

$$\text{Twilight} = 0 \text{ (degrees)}$$

### 3.2.7 EmergenceDAS

A function is used to provide emergence date as days after sowing (DAS).

Before Emergence

$$\text{PreEventValue} = 0$$

On Emergence the value is set to:

$$\text{PostEventValue} = [\text{Plant}].\text{DaysAfterSowing}$$

### 3.2.8 FloweringDAS

A function is used to provide flowering date as days after sowing(DAS).

Before StartFlowering

$$\text{PreEventValue} = 0$$

On StartFlowering the value is set to:

$$\text{PostEventValue} = [\text{Plant}].\text{DaysAfterSowing}$$

### 3.2.9 MaturityDAS

A function is used to provide maturity date as days after sowing(DAS).

Before Maturity

$$\text{PreEventValue} = 0$$

On Maturity the value is set to:

$$\text{PostEventValue} = [\text{Plant}].\text{DaysAfterSowing}$$

## 3.3 Leaf

This organ is simulated using a SimpleLeaf organ type. It provides the core functions of intercepting radiation, producing biomass through photosynthesis, and determining the plant's transpiration demand. The model also calculates the growth, senescence, and detachment of leaves. SimpleLeaf does not distinguish leaf cohorts by age or position in the canopy.

Radiation interception and transpiration demand are computed by the MicroClimate model. This model takes into account competition between different plants when more than one is present in the simulation. The values of canopy Cover, LAI, and plant Height (as defined below) are passed daily by SimpleLeaf to the MicroClimate model. MicroClimate uses an implementation of the Beer-Lambert equation to compute light interception and the Penman-Monteith equation to calculate potential evapotranspiration. These values are then given back to SimpleLeaf which uses them to calculate photosynthesis and soil water demand.

### 3.3.1 InitialWt

$$\text{InitialWt} = 1$$

### 3.3.2 Dry Matter Demand

The dry matter demand for the organ is calculated as defined in DMDemands, based on the DMDemandFunction and partition fractions for each biomass pool.

#### 3.3.2.1 DMDemands

This is the collection of functions for calculating the demands for each of the biomass pools (Structural, Metabolic, and Storage).

##### 3.3.2.1.1 Structural

Growth in leaf area is used to calculate the leaf dry matter demand. The same was assumed in the original crop models in APSIM. Further model development can be taken once new experimental data for metabolic, structural and storage forms are provided.

DeltaLAI describes the LAI variation over the cycle and is calculated using the Area of Largest Leaf, relative leaf area, plant number, branch number and leaf appearance rate (thermal time/phyllochron).

$$\text{Structural} = [\text{Leaf}].\text{DeltaLAI} / [\text{Leaf}].\text{SpecificArea}$$

##### 3.3.2.1.2 Storage

$$\text{Storage} = 0 \text{ (g/m}^2\text{)}$$

##### 3.3.2.1.3 Metabolic

$$\text{Metabolic} = 0 \text{ (g/m}^2\text{)}$$

### 3.3.3 Nitrogen Demand

The N demand is calculated as defined in NDemands, based on DM demand the N concentration of each biomass pool.

#### 3.3.3.1 NDemands

This is the collection of functions for calculating the demands for each of the biomass pools (Structural, Metabolic, and Storage).

##### 3.3.3.1.1 Structural

$$\text{Structural} = [\text{Leaf}].\text{minimumNconc} \times [\text{Leaf}].\text{potentialDMAlocation.Structural}$$

##### 3.3.3.1.2 Metabolic

$$\text{Metabolic} = \text{MetabolicNconc} \times [\text{Leaf}].\text{potentialDMAlocation.Structural}$$

Where:

##### 3.3.3.1.2.1 MetabolicNconc

$$\text{MetabolicNconc} = [\text{Leaf}].\text{criticalNConc} - [\text{Leaf}].\text{minimumNconc}$$

##### 3.3.3.1.3 Storage

The partitioning of daily growth to storage biomass attempts to bring the organ's N content to the maximum concentration.

$$\text{Storage} = [\text{Leaf}].\text{maximumNconc} \times ([\text{Leaf}].\text{Live.Wt} + \text{potentialAllocationWt}) - [\text{Leaf}].\text{Live.N}$$

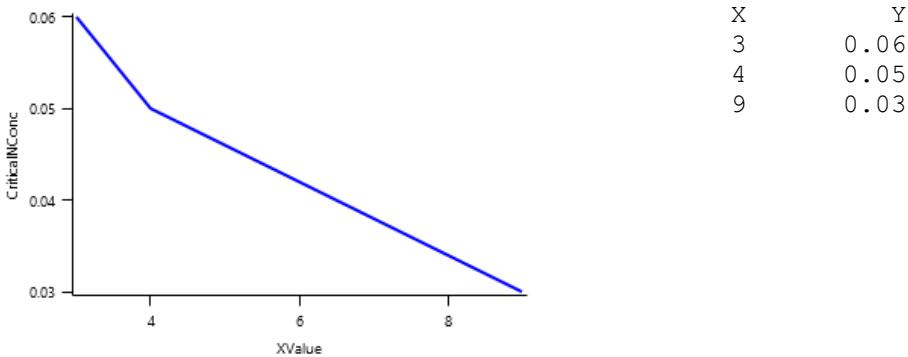
The demand for storage N is further reduced by a factor specified by the [Leaf].NitrogenDemandSwitch.

#### 3.3.3.2 MinimumNConc

$$\text{MinimumNConc} = 0.02$$

#### 3.3.3.3 CriticalNConc

CriticalNConc is calculated using linear interpolation

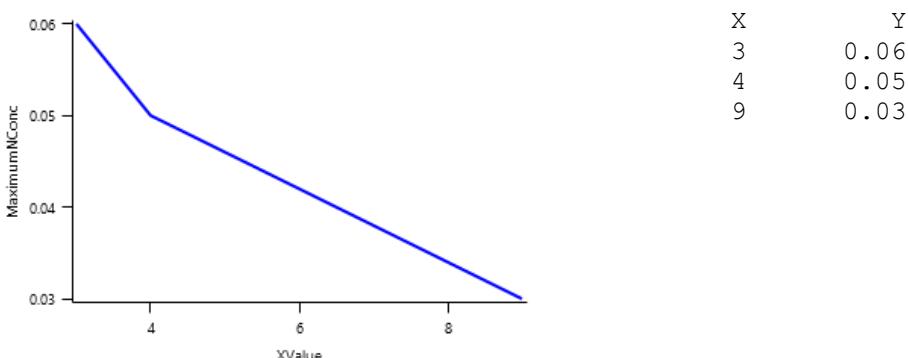


*XValue = [Phenology].Stage*

### 3.3.3.4 MaximumNConc

These values have been fitted to the available data. The fitted values are within the observed maximum and minimum values obtained in the FACTS soybean experiments (Archontoulis et al., 2020).

*MaximumNConc* is calculated using linear interpolation



*XValue = [Phenology].Stage*

The demand for N is reduced by a factor specified by the NitrogenDemandSwitch.

### 3.3.4 Dry Matter Supply

Leaf does not reallocate DM when senescence of the organ occurs.

Leaf does not retranslocate non-structural DM.

#### 3.3.4.1 Photosynthesis

Biomass fixation is modelled as the product of intercepted radiation and its conversion efficiency, the radiation use efficiency (RUE) (Monteith et al., 1977). This approach simulates net photosynthesis rather than providing separate estimates of growth and respiration. The potential photosynthesis calculated using RUE is then adjusted according to stress factors, these account for plant nutrition (FN), air temperature (FT), vapour pressure deficit (FVPD), water supply (FW) and atmospheric CO<sub>2</sub> concentration (FCO<sub>2</sub>). NOTE: RUE in this model is expressed as g/MJ for a whole plant basis, including both above and below ground growth.

*RUE = 1.2*

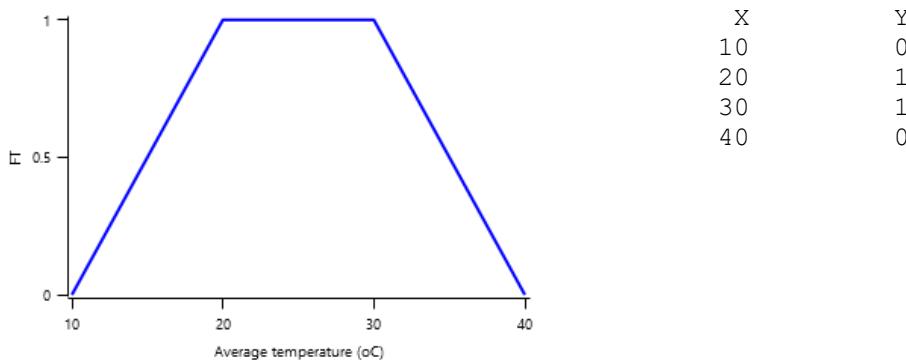
This value has been fitted to available data. In contrast to Classic, the RUE value in NG refers to the whole plant (above and below ground) and the calibrated value is 1.2 g/MJ. There are no literature references for whole plant RUE in soybean. To come up with this value we considered: RUE for above ground biomass (Sinclair and Horie 1989, van Roekel et al., 2014), biomass and root data from Iowa FACTS experiments and model fitting to available data.

##### 3.3.4.1.1 FT

*FT is calculated as a function of daily min and max temperatures, these are weighted toward max temperature according to the specified MaximumTemperatureWeighting factor. A value equal to 1.0 means it will use max temperature, a value of 0.5 means average temperature.*

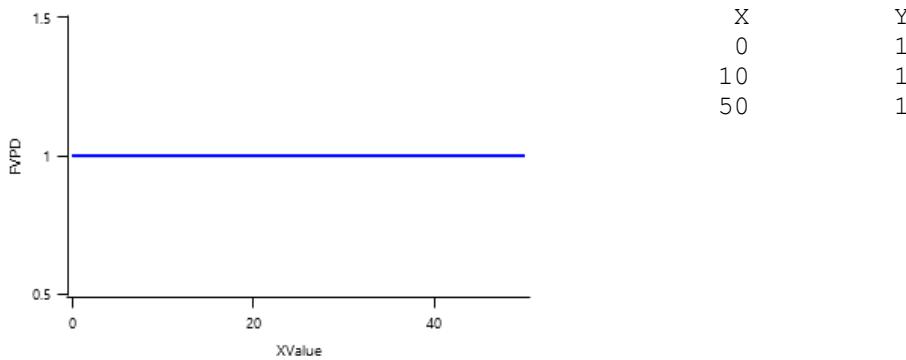
*MaximumTemperatureWeighting = 0.5*

The function for temperature effect on RUE comes from APSIM classic, which seems to work well across diverse environments. We did not find any comments/suggestions in the published papers suggesting alternative ones, so for now we used the same function. As more data from different environments are added to APSIM database, it will be possible to further test the photosynthetic temperature response in the future.



### 3.3.4.1.2 FVPD

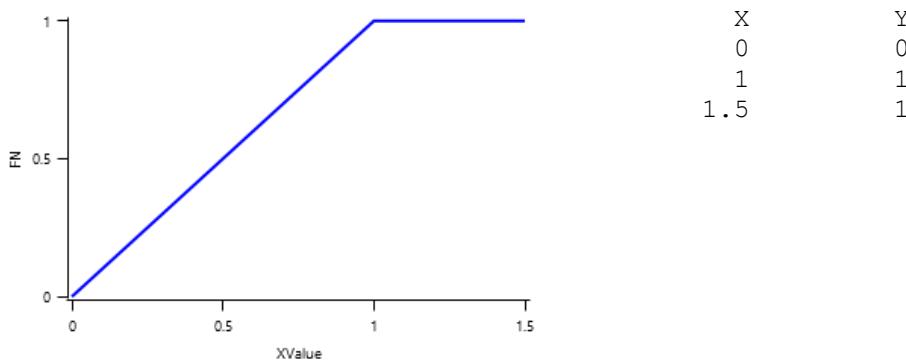
*FVPD* is calculated using linear interpolation



*XValue = [Leaf].Photosynthesis.VPD*

### 3.3.4.1.3 FN

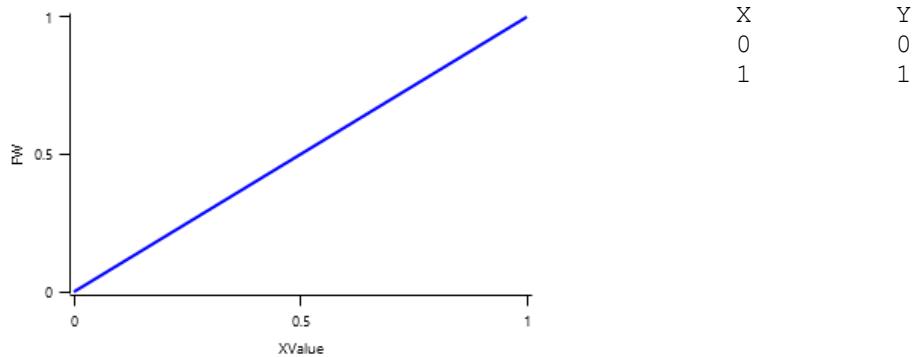
*FN* is calculated using linear interpolation



*XValue = [Leaf].Fn*

### 3.3.4.1.4 FW

*FW* is calculated using linear interpolation



*XValue = [Leaf].Fw*

#### 3.3.4.1.5 FCO2

This model calculates the CO<sub>2</sub> impact on RUE using the approach of Reyenga et al., 1999.

*RadnInt = [Leaf].RadiationIntercepted*

### 3.3.5 Nitrogen Supply

Leaf will reallocate 100% of N that senesces each day.

Leaf will retranslocate 50% of non-structural N each day.

### 3.3.6 Canopy Properties

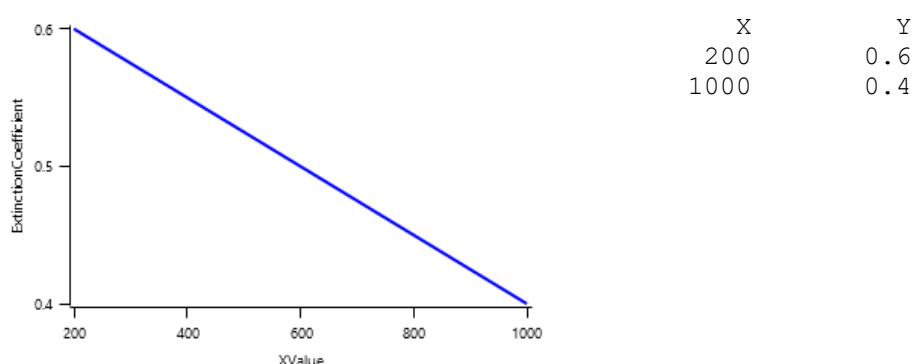
Leaf has been defined with a LAIFunction, cover is calculated using the Beer-Lambert equation.

#### 3.3.6.1 Area

*Area = [Leaf].SpecificArea × [Leaf].Live.Wt*

#### 3.3.6.2 ExtinctionCoefficient

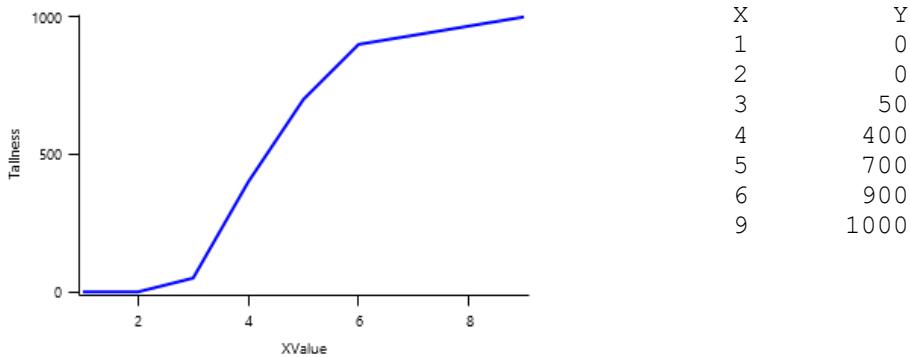
*ExtinctionCoefficient* is calculated using linear interpolation



*XValue = [Soybean].SowingData.RowSpacing*

#### 3.3.6.3 Tallness

*Tallness* is calculated using linear interpolation



*XValue* = [Phenology].Stage

### 3.3.7 Senescence and Detachment

The proportion of live biomass that senesces and moves into the dead pool each day is quantified by the SenescenceRate.

#### 3.3.7.1 SenescenceRate

##### 3.3.7.1.1 Vegetative

The value of SenescenceRate from Emergence to EndCanopyDevelopment is calculated as follows:

$$\text{Rate} = 0$$

##### 3.3.7.1.2 Reproductive

Leaf senescence rate is calculated to ensure that all leaves are senesced by crop maturity.

There is no data on detachment rates and so a simple value was chosen to ensure that leaves were not retained in the canopy. In the future, with more data available a thermal time basis leaf detachment rate will be explored.

The value of SenescenceRate from EndCanopyDevelopment to Maturity is calculated as follows:

##### 3.3.7.1.2.1 Rate

$$\text{Rate} = [\text{Phenology}].\text{ThermalTime} / \text{TTRemaining}$$

Where:

$$\text{TTRemaining} = \text{TTRequired} - \text{TTComplete}$$

Where:

$$\begin{aligned} \text{TTRequired} &= [\text{Phenology}].\text{MidGrainFilling.Target} + \\ &[\text{Phenology}].\text{LateGrainFilling.Target} + [\text{Phenology}].\text{Maturing.Target} \end{aligned}$$

$$\begin{aligned} \text{TTComplete} &= [\text{Phenology}].\text{MidGrainFilling.ProgressThroughPhase} + \\ &[\text{Phenology}].\text{LateGrainFilling.ProgressThroughPhase} + \\ &[\text{Phenology}].\text{Maturing.ProgressThroughPhase} \end{aligned}$$

SenescenceRate has a value of zero for phases not specified above

Leaf detaches 5% of its dead biomass each day, passing it to the surface organic matter model for decomposition.

### 3.3.8 BiomassRemovalDefaults

This organ will respond to certain management actions by either removing some of its biomass from the system or transferring some of its biomass to the soil surface residues. The following table describes the default proportions of live and dead biomass that are transferred out of the simulation using "Removed" or to soil surface residue using "To Residue" for a range of management actions. The total percentage removed for live or dead must not exceed 100%. The difference between the total and 100% gives the biomass remaining on the plant. These can be changed during a simulation using a manager script.

Method	% Live Removed	% Dead Removed	% Live To Residue	% Dead To Residue
Harvest	0	0	100	100
Cut	0	0	100	100

## 3.4 Grain

This organ uses a generic model for plant reproductive components. Yield is calculated from its components in terms of organ number and size (for example, grain number and grain size).

### 3.4.1 PotentialHarvestIndex

$$\text{PotentialHarvestIndex} = 0.5$$

### 3.4.2 FillingDuration

$$\text{FillingDuration} = [\text{Phenology}].\text{EarlyGrainFilling.Target} + [\text{Phenology}].\text{MidGrainFilling.Target} + [\text{Phenology}].\text{LateGrainFilling.Target}$$

### 3.4.3 DMDemandFunction

#### 3.4.3.1 GrainFilling

The value of DMDemandFunction from StartGrainFilling to EndGrainFill is calculated as follows:

##### 3.4.3.1.1 HIGrainDemand

$$\text{HIGrainDemand} = [\text{AboveGround}].\text{Wt} \times \text{HarvestIndexIncrease} \times [\text{Phenology}].\text{ThermalTime}$$

Where:

##### 3.4.3.1.1.1 HarvestIndexIncrease

$$\text{HarvestIndexIncrease} = [\text{Grain}].\text{PotentialHarvestIndex} / [\text{Grain}].\text{FillingDuration}$$

DMDemandFunction has a value of zero for phases not specified above

### 3.4.4 MinimumNConc

$$\text{MinimumNConc} = 0.05 \text{ (g/g)}$$

### 3.4.5 MaximumNConc

$$\text{MaximumNConc} = 0.058 \text{ (g/g)}$$

### 3.4.6 WaterContent

$$\text{WaterContent} = 0.12 \text{ (g/g)}$$

Water content used to calculate a fresh weight.

### 3.4.7 NFillingRate

$$\text{NFillingRate} = [\text{Grain}].\text{MaximumNConc} \times [\text{Grain}].\text{DMDemandFunction} \times [\text{Grain}].\text{DMConversionEfficiency}$$

### 3.4.8 BiomassRemovalDefaults

This organ will respond to certain management actions by either removing some of its biomass from the system or transferring some of its biomass to the soil surface residues. The following table describes the default proportions of live and dead biomass that are transferred out of the simulation using "Removed" or to soil surface residue using "To Residue" for a range of management actions. The total percentage removed for live or dead must not exceed 100%. The difference between the total and 100% gives the biomass remaining on the plant. These can be changed during a simulation using a manager script.

Method	% Live Removed	% Dead Removed	% Live To Residue	% Dead To Residue
Harvest	100	100	0	0
Cut	0	0	100	100

### 3.4.9 DMConversionEfficiency

*DMConversionEfficiency* = 0.89

### 3.4.10 RemobilisationCost

*RemobilisationCost* = 0

### 3.4.11 CarbonConcentration

*CarbonConcentration* = 0.4

### 3.4.12 HarvestIndex

*HarvestIndex* = [Grain].Wt / [AboveGround].Wt

### 3.4.13 MaximumPotentialGrainSize

*MaximumPotentialGrainSize* = 0

This parameter is not used. Grain growth is calculated from harvest index increase.

### 3.4.14 NumberFunction

*NumberFunction* = 0 (/m<sup>2</sup>)

Grain number is not estimated by this model.

## 3.5 Root

The generic root model calculates root growth in terms of rooting depth, biomass accumulation and subsequent root length density in each soil layer.

### Root Growth

Roots grow downwards through the soil profile, with initial depth determined by sowing depth and the growth rate determined by *RootFrontVelocity*. The *RootFrontVelocity* is modified by multiplying it by the soil's XF value; which represents any resistance posed by the soil to root extension. Root depth is also constrained by a maximum root depth.

Root length growth is calculated using the daily DM partitioned to roots and a specific root length. Root proliferation in layers is calculated using an approach similar to the generalised equimarginal criterion used in economics. The uptake of water and N per unit root length is used to partition new root material into layers of higher 'return on investment'.

### Dry Matter Demands

A daily DM demand is provided to the organ arbitrator and a DM supply returned. By default, 100% of the dry matter (DM) demanded from the root is structural. The daily loss of roots is calculated using a *SenescenceRate* function. All senesced material is automatically detached and added to the soil FOM.

### Nitrogen Demands

The daily structural N demand from root is the product of total DM demand and the minimum N concentration. Any N above this is considered Storage and can be used for retranslocation and/or reallocation as the respective factors are set to values other than zero.

### Nitrogen Uptake

Potential N uptake by the root system is calculated for each soil layer (i) that the roots have extended into. In each layer potential uptake is calculated as the product of the mineral nitrogen in the layer, a factor controlling

the rate of extraction ( $k\text{NO}_3$  or  $k\text{NH}_4$ ), the concentration of N form (ppm), and a soil moisture factor ( $\text{NUptakeSWFactor}$ ) which typically decreases as the soil dries.

$$\text{NO}_3 \text{ uptake} = \text{NO}_3_i \times k\text{NO}_3 \times \text{NO}_3_{\text{ppm}, i} \times \text{NUptakeSWFactor}$$

$$\text{NH}_4 \text{ uptake} = \text{NH}_4_i \times k\text{NH}_4 \times \text{NH}_4_{\text{ppm}, i} \times \text{NUptakeSWFactor}$$

Nitrogen uptake demand is limited to the maximum daily potential uptake ( $\text{MaxDailyNUptake}$ ) and the plants N demand. The demand for soil N is then passed to the soil arbitrator which determines how much of the N uptake demand each plant instance will be allowed to take up.

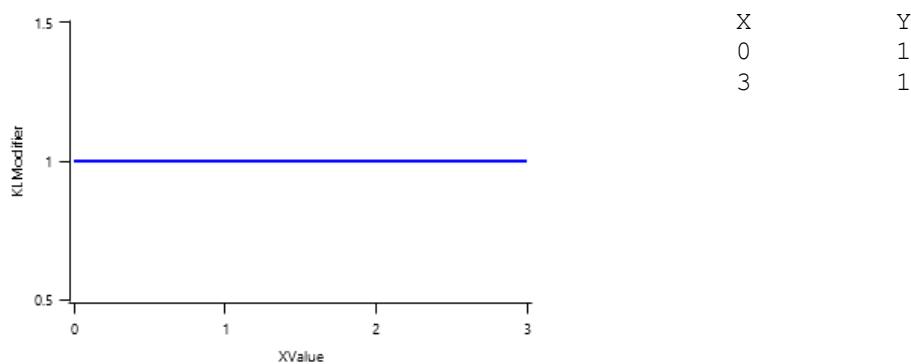
### Water Uptake

Potential water uptake by the root system is calculated for each soil layer that the roots have extended into. In each layer potential uptake is calculated as the product of the available water in the layer (water above LL limit) and a factor controlling the rate of extraction (KL). The values of both LL and KL are set in the soil interface and KL may be further modified by the crop via the KLModifier function.

$$\text{SW uptake} = (\text{SW}_i - \text{LL}_i) \times \text{KL}_i \times \text{KLModifier}$$

#### 3.5.1 KLModifier

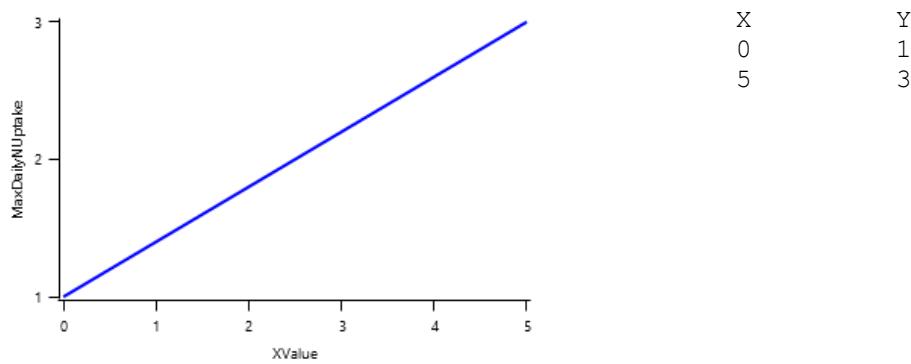
$\text{KLModifier}$  is calculated using linear interpolation



$$XValue = [\text{Leaf}].\text{LAI}$$

#### 3.5.2 MaxDailyNUptake

$\text{MaxDailyNUptake}$  is calculated using linear interpolation



$$XValue = [\text{Leaf}].\text{LAI}$$

#### 3.5.3 SenescenceRate

$$\text{SenescenceRate} = 0.005$$

#### 3.5.4 MaximumRootDepth

$$\text{MaximumRootDepth} = 1000000$$

### **3.5.5 RootFrontVelocity**

#### **3.5.5.1 PreEmergence**

The value of RootFrontVelocity from Germination to Emergence is calculated as follows:

$$\text{Function} = 5$$

#### **3.5.5.2 early**

The value of RootFrontVelocity from Emergence to StartGrainFilling is calculated as follows:

$$\text{Function} = 30$$

#### **3.5.5.3 late**

The value of RootFrontVelocity from StartGrainFilling to Maturity is calculated as follows:

$$\text{Function} = 5$$

RootFrontVelocity has a value of zero for phases not specified above

### **3.5.6 MaximumNConc**

$$\text{MaximumNConc} = 0.01$$

### **3.5.7 MinimumNConc**

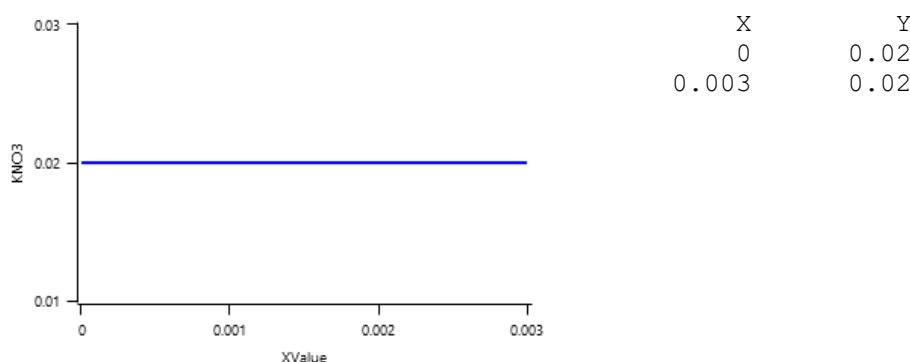
$$\text{MinimumNConc} = 0.005$$

### **3.5.8 NitrogenDemandSwitch**

1 between Emergence and EndGrainFill and a value of zero outside of this period

### **3.5.9 KNO3**

KNO3 is calculated using linear interpolation

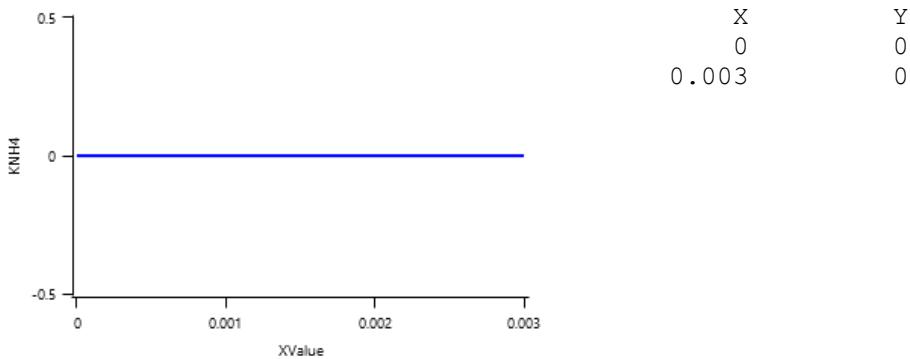


$$XValue = [\text{Root}].LengthDensity$$

### **3.5.10 KNH4**

The current model version considers only NO3 uptake but NH4 option can be activated by the user (e.g. [Root].KNH4.XYPairs.Y=0.01,0.01). We do not expect activation of NH4 to change total plant N uptake because the nitrification rate (conversion of NH4 to NO3) is very fast in the model. In the future we will re-evaluate this.

KNH4 is calculated using linear interpolation



*XValue = [Root].LengthDensity*

### 3.5.11 BiomassRemovalDefaults

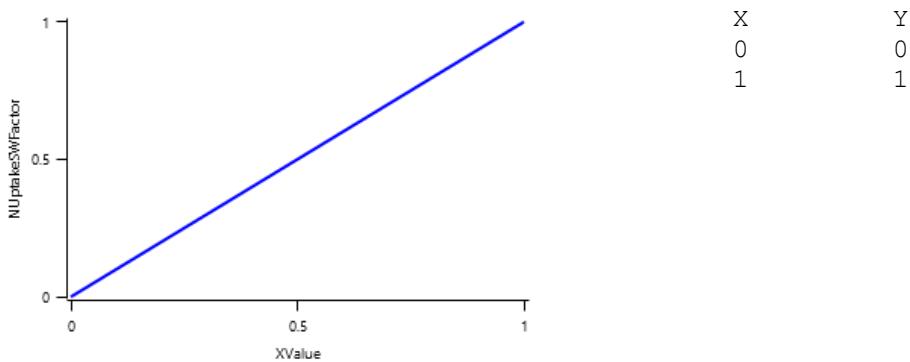
This organ will respond to certain management actions by either removing some of its biomass from the system or transferring some of its biomass to the soil surface residues. The following table describes the default proportions of live and dead biomass that are transferred out of the simulation using "Removed" or to soil surface residue using "To Residue" for a range of management actions. The total percentage removed for live or dead must not exceed 100%. The difference between the total and 100% gives the biomass remaining on the plant. These can be changed during a simulation using a manager script.

Default values for biomass removals for Root are only estimates with no data behind them. They are just to consider potential root senescence in response to damage.

Method	% Live Removed	% Dead Removed	% Live To Residue	% Dead To Residue
Harvest	0	0	20	0
Cut	0	0	20	0

### 3.5.12 NUptakeSWFactor

*NUptakeSWFactor* is calculated using linear interpolation



*XValue = [Root].RWC*

### 3.5.13 SpecificRootLength

*SpecificRootLength = 40 (m/g)*

### 3.5.14 DMConversionEfficiency

*DMConversionEfficiency = 1*

### 3.5.15 MaintenanceRespirationFunction

*MaintenanceRespirationFunction = 1*

### **3.5.16 RemobilisationCost**

*RemobilisationCost = 0*

### **3.5.17 CarbonConcentration**

*CarbonConcentration = 0.4*

### **3.5.18 DMDemands**

This is the collection of functions for calculating the demands for each of the biomass pools (Structural, Metabolic, and Storage).

#### **3.5.18.1 Structural**

*Structural = DMDemandFunction × StructuralFraction*

Where:

##### **3.5.18.1.1 DMDemandFunction**

*DMDemandFunction = PartitionFraction [Arbitrator].DM.TotalFixationSupply*

Where:

###### **3.5.18.1.1.1 PartitionFraction**

The value of PartitionFraction from Emergence to StartFlowering is calculated as follows:

*Function = 0.2*

The value of PartitionFraction from StartFlowering to StartGrainFilling is calculated as follows:

*Function = 0.2*

The value of PartitionFraction from StartGrainFilling to Maturity is calculated as follows:

*Function = 0.05*

PartitionFraction has a value of zero for phases not specified above

*StructuralFraction = 1*

#### **3.5.18.2 Metabolic**

*Metabolic = 0 (g/m<sup>2</sup>)*

#### **3.5.18.3 Storage**

The partitioning of daily growth to storage biomass is based on a storage fraction.

##### **3.5.18.3.1 StorageFraction**

*StorageFraction = 1 - [Root].DMDemands.Structural.StructuralFraction*

### **3.5.19 NDemands**

This is the collection of functions for calculating the demands for each of the biomass pools (Structural, Metabolic, and Storage).

#### **3.5.19.1 Structural**

*Structural = [Root].minimumNconc × [Root].potentialDMAAllocation.Structural*

#### **3.5.19.2 Metabolic**

*Metabolic = MetabolicNconc × [Root].potentialDMAAllocation.Structural*

Where:

### **3.5.19.2.1 MetabolicNconc**

$MetabolicNconc = [Root].criticalNConc - [Root].minimumNconc$

### **3.5.19.3 Storage**

The partitioning of daily growth to storage biomass attempts to bring the organ's N content to the maximum concentration.

$Storage = [Root].maximumNconc \times ([Root].Live.Wt + potentialAllocationWt) - [Root].Live.N$

The demand for storage N is further reduced by a factor specified by the [Root].NitrogenDemandSwitch.

$CriticalNConc = [Root].MinimumNConc$

## **3.5.20 InitialWt**

This is the collection of functions for calculating the demands for each of the biomass pools (Structural, Metabolic, and Storage).

### **3.5.20.1 Structural**

$Structural = 0.2 \text{ (g/plant)}$

### **3.5.20.2 Metabolic**

$Metabolic = 0 \text{ (g/m}^2\text{)}$

### **3.5.20.3 Storage**

$Storage = 0 \text{ (g/m}^2\text{)}$

## **3.5.21 RootDepthStressFactor**

$RootDepthStressFactor = 1$

## **3.6 Nodule**

This organ simulates the root structure associate with symbiotic N-fixing bacteria. It provides the core functions of determining N fixation supply and related costs. It also calculates the growth, senescence and detachment of nodules.

### **3.6.1 Dry Matter Demand**

The dry matter demand for the organ is calculated as defined in DMDemands, based on the DMDemandFunction and partition fractions for each biomass pool.

#### **3.6.1.1 DMDemands**

This is the collection of functions for calculating the demands for each of the biomass pools (Structural, Metabolic, and Storage).

##### **3.6.1.1.1 Structural**

$Structural = DMDemandFunction \times StructuralFraction$

Where:

###### **3.6.1.1.1.1 DMDemandFunction**

$DMDemandFunction = PartitionFraction \times [Arbitrator].DM.TotalFixationSupply$

Where:

The value of PartitionFraction from Emergence to StartFlowering is calculated as follows:

$Function = 0.03$

The value of PartitionFraction from StartFlowering to StartGrainFilling is calculated as follows:

$Function = 0.02$

The value of PartitionFraction from StartGrainFilling to Maturity is calculated as follows:

$$\text{Function} = 0$$

PartitionFraction has a value of zero for phases not specified above

$$\text{StructuralFraction} = 1 \text{ (g/g)}$$

### 3.6.1.1.2 Metabolic

$$\text{Metabolic} = 0 \text{ (g/m2)}$$

### 3.6.1.1.3 Storage

The partitioning of daily growth to storage biomass is based on a storage fraction.

#### 3.6.1.1.3.1 StorageFraction

$$\text{StorageFraction} = 1 - [\text{Nodule}].\text{DMDemands}.Structural.\text{StructuralFraction}$$

## 3.6.2 Nitrogen Demand

The N demand is calculated as defined in NDemand, based on DM demand the N concentration of each biomass pool.

### 3.6.2.1 NDemand

This is the collection of functions for calculating the demands for each of the biomass pools (Structural, Metabolic, and Storage).

#### 3.6.2.1.1 Structural

$$\text{Structural} = [\text{Nodule}].\text{minimumNconc} \times [\text{Nodule}].\text{potentialDMAlocation}.Structural$$

#### 3.6.2.1.2 Metabolic

$$\text{Metabolic} = \text{MetabolicNconc} \times [\text{Nodule}].\text{potentialDMAlocation}.Structural$$

Where:

#### 3.6.2.1.2.1 MetabolicNconc

$$\text{MetabolicNconc} = [\text{Nodule}].\text{criticalNConc} - [\text{Nodule}].\text{minimumNconc}$$

#### 3.6.2.1.3 Storage

The partitioning of daily growth to storage biomass attempts to bring the organ's N content to the maximum concentration.

$$\text{Storage} = [\text{Nodule}].\text{maximumNconc} \times ([\text{Nodule}].\text{Live.Wt} + \text{potentialAllocationWt}) - [\text{Nodule}].\text{Live.N}$$

The demand for storage N is further reduced by a factor specified by the [Nodule].NitrogenDemandSwitch.

### 3.6.2.2 MinimumNConc

$$\text{MinimumNConc} = 0.01$$

$$\text{CriticalNConc} = [\text{Nodule}].\text{MinimumNConc}$$

### 3.6.2.3 MaximumNConc

$$\text{MaximumNConc} = 0.02$$

The demand for N is reduced by a factor specified by the NitrogenDemandSwitch.

### 3.6.2.4 NitrogenDemandSwitch

1 between Emergence and EndGrainFill and a value of zero outside of this period

## 3.6.3 Dry Matter Supply

Nodule does not reallocate DM when senescence of the organ occurs.

Nodule does not retranslocate non-structural DM.

### 3.6.4 Nitrogen Supply

Nodule does not reallocate N when senescence of the organ occurs.

Nodule does not retranslocate non-structural N.

### 3.6.5 FixationRate

FixationRate is the same as DailyPotentialFixationRate until it reaches StartGrainFilling stage when it fixes its value

#### 3.6.5.1 DailyPotentialFixationRate

$$\text{DailyPotentialFixationRate} = \min(\text{PotentialFixationRate}, \text{MaximumFixationRate})$$

Where:

##### 3.6.5.1.1 PotentialFixationRate

$$\text{PotentialFixationRate} = [\text{AboveGroundLive}].\text{Wt} \times \text{SpecificFixationRate}$$

Where:

###### 3.6.5.1.1.1 SpecificFixationRate

The value of SpecificFixationRate from Emergence to StartFlowering is calculated as follows:

$$\text{Rate} = 0.006$$

The value of SpecificFixationRate from StartFlowering to EndGrainFill is calculated as follows:

$$\text{Rate} = 0.002$$

SpecificFixationRate has a value of zero for phases not specified above

$$\text{MaximumFixationRate} = 0.6 \text{ (g/g)}$$

### 3.6.6 Senescence and Detachment

Nodule has senescence parameterised to zero so all biomass in this organ will remain alive.

Nodule has detachment parameterised to zero so all biomass in this organ will remain with the plant until a defoliation or harvest event occurs.

### 3.6.7 BiomassRemovalDefaults

This organ will respond to certain management actions by either removing some of its biomass from the system or transferring some of its biomass to the soil surface residues. The following table describes the default proportions of live and dead biomass that are transferred out of the simulation using "Removed" or to soil surface residue using "To Residue" for a range of management actions. The total percentage removed for live or dead must not exceed 100%. The difference between the total and 100% gives the biomass remaining on the plant. These can be changed during a simulation using a manager script.

Default values for biomass removals for Nodule are only estimates with no data behind them. They are just to consider potential root senescence in response to damage.

Method	% Live Removed	% Dead Removed	% Live To Residue	% Dead To Residue
Harvest	0	0	20	0
Cut	0	0	20	0

## 3.7 Shell

This organ is simulated using a GenericOrgan type. It is parameterised to calculate the growth, senescence, and detachment of any organ that does not have specific functions.

### 3.7.1 Dry Matter Demand

The dry matter demand for the organ is calculated as defined in DMDemands, based on the DMDemandFunction and partition fractions for each biomass pool.

#### 3.7.1.1 DMDemands

This is the collection of functions for calculating the demands for each of the biomass pools (Structural, Metabolic, and Storage).

##### 3.7.1.1.1 Structural

Shell harvest index is used to calculate shell biomass demand, which follows the same approach than grain harvest index. It represents the fraction of shell biomass in relation to total aboveground biomass.

$$\text{Structural} = \text{DMDemandFunction} \times \text{StructuralFraction}$$

Where:

###### 3.7.1.1.1.1 DMDemandFunction

The value of DMDemandFunction from StartPodDevelopment to EndPodDevelopment is calculated as follows:

$$\text{HIPodDemand} = [\text{AboveGround}].\text{Wt} \times \text{HarvestIndexIncrease} \times [\text{Phenology}].\text{ThermalTime}$$

Where:

$$\text{HarvestIndexIncrease} = [\text{Shell}].\text{PotentialHarvestIndex} / [\text{Shell}].\text{FillingDuration}$$

DMDemandFunction has a value of zero for phases not specified above

$$\text{StructuralFraction} = 1$$

###### 3.7.1.1.1.2 Metabolic

$$\text{Metabolic} = 0 \text{ (g/m2)}$$

###### 3.7.1.1.1.3 Storage

The partitioning of daily growth to storage biomass is based on a storage fraction.

###### 3.7.1.1.1.3.1 StorageFraction

$$\text{StorageFraction} = 1 - [\text{Shell}].\text{DMDemands}. \text{Structural}. \text{StructuralFraction}$$

## 3.7.2 Nitrogen Demand

The N demand is calculated as defined in NDemands, based on DM demand the N concentration of each biomass pool.

### 3.7.2.1 NDemands

This is the collection of functions for calculating the demands for each of the biomass pools (Structural, Metabolic, and Storage).

#### 3.7.2.1.1 Structural

$$\text{Structural} = [\text{Shell}].\text{minimumNconc} \times [\text{Shell}].\text{potentialDMAlocation}. \text{Structural}$$

#### 3.7.2.1.2 Storage

The partitioning of daily growth to storage biomass attempts to bring the organ's N content to the maximum concentration.

$$\text{Storage} = [\text{Shell}].\text{maximumNconc} \times ([\text{Shell}].\text{Live}. \text{Wt} + \text{potentialAllocationWt}) - [\text{Shell}].\text{Live}. \text{N}$$

The demand for storage N is further reduced by a factor specified by the [Shell].NitrogenDemandSwitch.

### 3.7.2.1.3 Metabolic

*Metabolic* = 0 (g/m<sup>2</sup>)

### 3.7.2.2 MinimumNConc

*MinimumNConc* = 0.01

*CriticalNConc* = [Shell].MinimumNConc

### 3.7.2.3 MaximumNConc

*MaximumNConc* = 0.045

The demand for N is reduced by a factor specified by the NitrogenDemandSwitch.

### 3.7.2.4 NitrogenDemandSwitch

1 between StartPodDevelopment and EndPodDevelopment and a value of zero outside of this period

## 3.7.3 Dry Matter Supply

Shell does not reallocate DM when senescence of the organ occurs.

Shell will retranslocate 10% of non-structural DM each day.

## 3.7.4 Nitrogen Supply

Shell will reallocate 100% of N that senesces each day.

Shell will retranslocate 50% of non-structural N each day.

## 3.7.5 Senescence and Detachment

The proportion of live biomass that senesces and moves into the dead pool each day is quantified by the SenescenceRate.

### 3.7.5.1 SenescenceRate

#### 3.7.5.1.1 ReproductivePhase

The value of SenescenceRate from StartPodDevelopment to Maturity is calculated as follows:

##### 3.7.5.1.1.1 Rate

*Rate* = minimum (*Fraction*, *One*)

Where:

*Fraction* = [Phenology].ThermalTime / *TTRemaining*

Where:

*TTRemaining* = *ReproductiveTT* - *ReproductiveTT1Complete*

Where:

*ReproductiveTT* =

[Phenology].EarlyPodDevelopment.Target + [Phenology].EarlyGrainFilling.Target + [Phenology].Mi

*ReproductiveTT1Complete* =

[Phenology].EarlyPodDevelopment.ProgressThroughPhase + [Phenology].EarlyGrainFilling.Progr

*One* = 1

SenescenceRate has a value of zero for phases not specified above

Shell has detachment parameterised to zero so all biomass in this organ will remain with the plant until a defoliation or harvest event occurs.

### 3.7.6 BiomassRemovalDefaults

This organ will respond to certain management actions by either removing some of its biomass from the system or transferring some of its biomass to the soil surface residues. The following table describes the default proportions of live and dead biomass that are transferred out of the simulation using "Removed" or to soil surface residue using "To Residue" for a range of management actions. The total percentage removed for live or dead must not exceed 100%. The difference between the total and 100% gives the biomass remaining on the plant. These can be changed during a simulation using a manager script.

Method	% Live Removed	% Dead Removed	% Live To Residue	% Dead To Residue
Harvest	0	0	100	100
Cut	0	0	100	100

## 3.8 Stem

This organ is simulated using a GenericOrgan type. It is parameterised to calculate the growth, senescence, and detachment of any organ that does not have specific functions.

### 3.8.1 Dry Matter Demand

The dry matter demand for the organ is calculated as defined in DMDemands, based on the DMDemandFunction and partition fractions for each biomass pool.

#### 3.8.1.1 DMDemands

This is the collection of functions for calculating the demands for each of the biomass pools (Structural, Metabolic, and Storage).

##### 3.8.1.1.1 Structural

$$\text{Structural} = \text{Fraction} \times [\text{Stem}].\text{PotentialGrowth}$$

Where:

###### 3.8.1.1.1.1 Fraction

The value of Fraction from Emergence to StartPodDevelopment is calculated as follows:

$$\text{Fraction} = 0.75$$

The value of Fraction from StartPodDevelopment to EndGrainFill is calculated as follows:

$$\text{Fraction} = 0$$

Fraction has a value of zero for phases not specified above

###### 3.8.1.1.2 Metabolic

$$\text{Metabolic} = 0 \text{ (g/m2)}$$

###### 3.8.1.1.3 Storage

$$\text{Storage} = [\text{Stem}].\text{PotentialGrowth} \times \text{StorageFraction}$$

Where:

###### 3.8.1.1.3.1 StorageFraction

$$\text{StorageFraction} = 1 - [\text{Stem}].\text{DMDemands}. \text{Structural}. \text{Fraction}$$

## 3.8.2 Nitrogen Demand

The N demand is calculated as defined in NDemands, based on DM demand the N concentration of each biomass pool.

### 3.8.2.1 NDemands

This is the collection of functions for calculating the demands for each of the biomass pools (Structural, Metabolic, and Storage).

#### 3.8.2.1.1 Structural

$$\text{Structural} = [\text{Stem}].\text{minimumNconc} \times [\text{Stem}].\text{potentialDMAAllocation.Structural}$$

#### 3.8.2.1.2 Metabolic

$$\text{Metabolic} = \text{MetabolicNconc} \times [\text{Stem}].\text{potentialDMAAllocation.Structural}$$

Where:

##### 3.8.2.1.2.1 MetabolicNconc

$$\text{MetabolicNconc} = [\text{Stem}].\text{criticalNConc} - [\text{Stem}].\text{minimumNconc}$$

#### 3.8.2.1.3 Storage

The partitioning of daily growth to storage biomass attempts to bring the organ's N content to the maximum concentration.

$$\text{Storage} = [\text{Stem}].\text{maximumNconc} \times ([\text{Stem}].\text{Live.Wt} + \text{potentialAllocationWt}) - [\text{Stem}].\text{Live.N}$$

The demand for storage N is further reduced by a factor specified by the [Stem].NitrogenDemandSwitch.

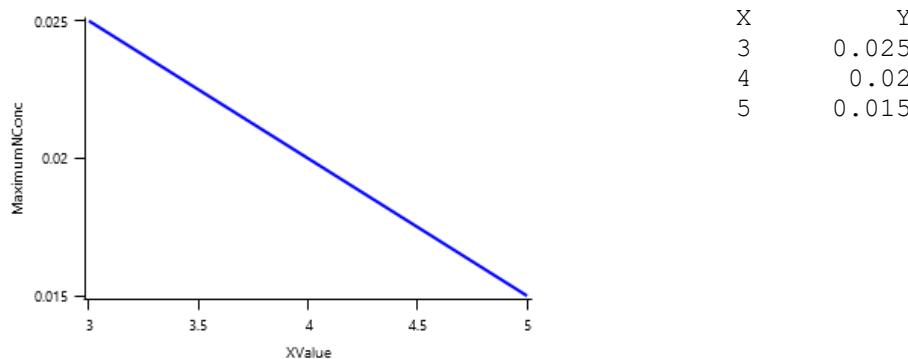
### 3.8.2.2 MinimumNConc

$$\text{MinimumNConc} = 0.006$$

$$\text{CriticalNConc} = [\text{Stem}].\text{MinimumNConc}$$

### 3.8.2.3 MaximumNConc

*MaximumNConc* is calculated using linear interpolation



$$XValue = [\text{Phenology}].\text{Stage}$$

The demand for N is reduced by a factor specified by the NitrogenDemandSwitch.

### 3.8.2.4 NitrogenDemandSwitch

There is no evidence of stem N storage during grain filling. Also, there is no stem structural growth during this time.

1 between Emergence and StartGrainFilling and a value of zero outside of this period

### 3.8.3 Dry Matter Supply

Stem does not reallocate DM when senescence of the organ occurs.

The proportion of non-structural DM that is allocated each day is quantified by the DMReallocationFactor.

### 3.8.3.1 DMRetranslocationFactor

#### 3.8.3.1.1 GrainFilling

The value of DMRetranslocationFactor from EndCanopyDevelopment to EndGrainFill is calculated as follows:

$$\text{RetranslocationFactor} = 0.2$$

DMRetranslocationFactor has a value of zero for phases not specified above

### 3.8.4 Nitrogen Supply

Stem will reallocate 100% of N that senesces each day.

Stem will retranslocate 50% of non-structural N each day.

### 3.8.5 Senescence and Detachment

The proportion of live biomass that senesces and moves into the dead pool each day is quantified by the SenescenceRate.

#### 3.8.5.1 SenescenceRate

##### 3.8.5.1.1 PostCanopyPhase

The value of SenescenceRate from EndCanopyDevelopment to Maturity is calculated as follows:

###### 3.8.5.1.1.1 Rate

$$\text{Rate} = \min(\text{Fraction}, 1)$$

Where:

$$\text{Fraction} = [\text{Phenology}].\text{ThermalTime} / \text{TTRemaining}$$

Where:

$$\text{TTRemaining} = \text{PostCanopyTT} - \text{PostCanopyTTComplete}$$

Where:

$$\begin{aligned} \text{PostCanopyTT} &= \\ &[\text{Phenology}].\text{EarlyPodDevelopment.Target} + [\text{Phenology}].\text{EarlyGrainFilling.Target} + [\text{Phenology}].\text{MidGrainFilling.Target} + [\text{Phenology}].\text{LateGrainFilling.Target} \end{aligned}$$

$$\begin{aligned} \text{PostCanopyTTComplete} &= \\ &[\text{Phenology}].\text{MidGrainFilling.ProgressThroughPhase} + [\text{Phenology}].\text{LateGrainFilling.ProgressThroughPhase} \end{aligned}$$

$$1 = 1$$

SenescenceRate has a value of zero for phases not specified above

Stem has detachment parameterised to zero so all biomass in this organ will remain with the plant until a defoliation or harvest event occurs.

### 3.8.6 BiomassRemovalDefaults

This organ will respond to certain management actions by either removing some of its biomass from the system or transferring some of its biomass to the soil surface residues. The following table describes the default proportions of live and dead biomass that are transferred out of the simulation using "Removed" or to soil surface residue using "To Residue" for a range of management actions. The total percentage removed for live or dead must not exceed 100%. The difference between the total and 100% gives the biomass remaining on the plant. These can be changed during a simulation using a manager script.

Method	% Live Removed	% Dead Removed	% Live To Residue	% Dead To Residue
Harvest	0	0	100	100
Cut	0	0	100	100

## **3.9 AboveGround Biomass**

This is a composite biomass class, representing the sum of 1 or more biomass objects.

AboveGround summarises the following biomass objects:

- [Leaf].Live
- [Leaf].Dead
- [Stem].Live
- [Stem].Dead
- [Grain].Live
- [Grain].Dead
- [Shell].Live
- [Shell].Dead

## **3.10 BelowGround Biomass**

This is a composite biomass class, representing the sum of 1 or more biomass objects.

BelowGround summarises the following biomass objects:

- [Root].Live
- [Root].Dead
- [Nodule].Live
- [Nodule].Dead

## **3.11 AboveGroundLive Biomass**

This is a composite biomass class, representing the sum of 1 or more biomass objects.

AboveGroundLive summarises the following biomass objects:

- [Leaf].Live
- [Stem].Live
- [Grain].Live
- [Shell].Live

## **3.12 Total Biomass**

This is a composite biomass class, representing the sum of 1 or more biomass objects.

Total summarises the following biomass objects:

- [Leaf].Live
- [Leaf].Dead
- [Stem].Live
- [Stem].Dead
- [Grain].Live
- [Grain].Dead
- [Shell].Live
- [Shell].Dead
- [Root].Live
- [Root].Dead
- [Nodule].Live
- [Nodule].Dead

## **3.13 TotalLive Biomass**

This is a composite biomass class, representing the sum of 1 or more biomass objects.

TotalLive summarises the following biomass objects:

- [Leaf].Live
- [Stem].Live
- [Grain].Live
- [Shell].Live

- [Root].Live
- [Nodule].Live

## 3.14 TotalDead Biomass

This is a composite biomass class, representing the sum of 1 or more biomass objects.

TotalDead summarises the following biomass objects:

- [Leaf].Dead
- [Stem].Dead
- [Grain].Dead
- [Shell].Dead
- [Root].Dead
- [Nodule].Dead

## 3.15 Pod Biomass

This is a composite biomass class, representing the sum of 1 or more biomass objects.

Pod summarises the following biomass objects:

- [Shell].Live
- [Shell].Dead
- [Grain].Live
- [Grain].Dead

## 3.16 Australia

Bowyer, Buchanan, Bunya, Cowrie, Davis, Djakal, Djakal1, F148\_7, FiskebyV, Hooper\_MG40, Leichhardt, Manark, Soya791, Stephens\_MG40, Warrigal

### 3.16.1 Buchanan

This cultivar is defined by overriding some of the base parameters of the plant model.

Buchanan makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 480
[Phenology].EarlyFlowering.Target.FixedValue = 100
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.015
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 467
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.39, 15.61
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.39, 15.61
[Phenology].MidGrainFilling.Target.FractionofMidToLateGrainfilling.FixedValue=0.33
[Grain].MaximumNConc.FixedValue = 0.067
[Stem].PotentialGrowth.PartitionFraction.StemGrowthPhase.StemFraction.FixedValue = 0.5
[Leaf].AreaLargestLeaf.FixedValue=0.009
```

### 3.16.2 Djakal

This cultivar is defined by overriding some of the base parameters of the plant model.

Djakal makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 380
[Phenology].EarlyFlowering.Target.FixedValue = 100
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 405
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.75, 17
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 11.9, 15.5
[Leaf].AreaLargestLeaf.FixedValue=0.009
```

### 3.16.3 Davis

This cultivar is defined by overriding some of the base parameters of the plant model.

Davis makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 480
[Phenology].EarlyFlowering.Target.FixedValue = 100
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.015
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 467
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.39, 15.61
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.39, 15.61
[Phenology].MidGrainFilling.Target.FractionofMidToLateGrainfilling.FixedValue=0.33
[Grain].MaximumNConc.FixedValue = 0.067
[Stem].PotentialGrowth.PartitionFraction.StemGrowthPhase.StemFraction.FixedValue = 0.5
[Leaf].AreaLargestLeaf.FixedValue=0.012
```

### **3.16.4 Hooper\_MG40**

This cultivar is defined by overriding some of the base parameters of the plant model.

Hooper\_MG40 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 380
[Phenology].EarlyFlowering.Target.FixedValue = 80
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 440
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.26, 16.67
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.26, 16.67
[Leaf].AreaLargestLeaf.FixedValue=0.009
```

### **3.16.5 Stephens\_MG40**

This cultivar is defined by overriding some of the base parameters of the plant model.

Stephens\_MG40 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 360
[Phenology].EarlyFlowering.Target.FixedValue = 80
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 440
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.26, 16.67
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.26, 16.67
[Leaf].AreaLargestLeaf.FixedValue=0.009
```

### **3.16.6 FiskebyV**

This cultivar is defined by overriding some of the base parameters of the plant model.

FiskebyV makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 285
[Phenology].EarlyFlowering.Target.FixedValue = 80
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 405
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.75, 18
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.75, 18
```

### **3.16.7 F148\_7**

This cultivar is defined by overriding some of the base parameters of the plant model.

F148\_7 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 314
[Phenology].EarlyFlowering.Target.FixedValue = 80
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 485
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.75, 17
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12, 18
[Leaf].AreaLargestLeaf.FixedValue=0.009
```

### **3.16.8 Bowyer**

This cultivar is defined by overriding some of the base parameters of the plant model.

Bowyer makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 377  
[Phenology].EarlyFlowering.Target.FixedValue = 80  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 405  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.75, 15.5  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 11.9, 15.5
```

### 3.16.9 Bunya

This cultivar is defined by overriding some of the base parameters of the plant model.

Bunya makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 550  
[Phenology].EarlyFlowering.Target.FixedValue = 80  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 405  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.75, 18  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 10.9, 15.5  
[Leaf].AreaLargestLeaf.FixedValue=0.009
```

### 3.16.10 Cowrie

This cultivar is defined by overriding some of the base parameters of the plant model.

Cowrie makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 390  
[Phenology].EarlyFlowering.Target.FixedValue = 80  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 425  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.75, 16  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.75, 16  
[Leaf].AreaLargestLeaf.FixedValue=0.009
```

### 3.16.11 Soya791

This cultivar is defined by overriding some of the base parameters of the plant model.

Soya791 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 430  
[Phenology].EarlyFlowering.Target.FixedValue = 80  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 425  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.75, 15.3  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.75, 15.3  
[Leaf].AreaLargestLeaf.FixedValue=0.009
```

### 3.16.12 Manark

This cultivar is defined by overriding some of the base parameters of the plant model.

Manark makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 440  
[Phenology].EarlyFlowering.Target.FixedValue = 80  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 425  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.75, 15  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.75, 15  
[Leaf].AreaLargestLeaf.FixedValue=0.009
```

### 3.16.13 Warrigal

This cultivar is defined by overriding some of the base parameters of the plant model.

Warrigal makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 490
[Phenology].EarlyFlowering.Target.FixedValue = 80
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 425
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.75, 15
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.75, 15
[Leaf].AreaLargestLeaf.FixedValue=0.009
```

### 3.16.14 Leichhardt

This cultivar is defined by overriding some of the base parameters of the plant model.

Leichhardt makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 806
[Phenology].EarlyFlowering.Target.FixedValue = 80
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 425
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.75, 14.7
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.75, 14.7
[Leaf].AreaLargestLeaf.FixedValue=0.009
```

### 3.16.15 Djakal1

This cultivar is defined by overriding some of the base parameters of the plant model.

Djakal1 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 332
[Phenology].EarlyFlowering.Target.FixedValue = 80
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 440
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.26, 16.67
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.26, 16.67
[Leaf].AreaLargestLeaf.FixedValue=0.009
```

## 3.17 USA

AsgrowAG4403\_MG40, AsgrowAG5701\_MG50, Becks321NRR\_MG32, Becks367NRR\_MG37, HornbeckHBK4891\_MG40, Hutcheson\_MG50, IA1006\_MG10, IA2008\_MG20, Lambert\_MG0, Macon\_MG30, NK622\_MG60, Pioneer92MGI\_MG26, Pioneer94B01\_MG40, PioneerP22T61\_MG22, PioneerP22T69R\_MG22, PioneerP92Y75\_MG27, PioneerP932T16R\_MG32, PioneerP93M11\_MG31, PioneerP9504\_MG50, Trial\_MG00

### 3.17.1 Trial\_MG00

This cultivar is defined by overriding some of the base parameters of the plant model.

Trial\_MG00 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 268
[Phenology].EarlyFlowering.Target.FixedValue = 76
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 432
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 14.43, 21.19
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 14.43, 21.19
```

### 3.17.2 Lambert\_MG0

This cultivar is defined by overriding some of the base parameters of the plant model.

Lambert\_MG0 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 294
[Phenology].EarlyFlowering.Target.FixedValue = 81
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 442
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 14.29, 20.14
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 14.29, 20.14
```

### **3.17.3 IA1006\_MG10**

This cultivar is defined by overriding some of the base parameters of the plant model.

IA1006\_MG10 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 336  
[Phenology].EarlyFlowering.Target.FixedValue = 118  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05  
[Phenology].LateGrainFilling.Target.EntireGrainfillIPeriod.FixedValue = 518  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 14.37, 19.30  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 14.37, 19.30
```

### **3.17.4 IA2008\_MG20**

This cultivar is defined by overriding some of the base parameters of the plant model.

IA2008\_MG20 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 329  
[Phenology].EarlyFlowering.Target.FixedValue = 150  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.05  
[Phenology].LateGrainFilling.Target.EntireGrainfillIPeriod.FixedValue = 580  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.92, 17.93  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.92, 17.93
```

### **3.17.5 PioneerP22T61\_MG22**

This cultivar is defined by overriding some of the base parameters of the plant model.

PioneerP22T61\_MG22 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 328  
[Phenology].EarlyFlowering.Target.FixedValue = 106  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.3  
[Phenology].LateGrainFilling.Target.EntireGrainfillIPeriod.FixedValue = 499  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.59, 17.6  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.59, 17.6
```

### **3.17.6 PioneerP22T69R\_MG22**

This cultivar is defined by overriding some of the base parameters of the plant model.

PioneerP22T69R\_MG22 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 328  
[Phenology].EarlyFlowering.Target.FixedValue = 106  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.35  
[Phenology].LateGrainFilling.Target.EntireGrainfillIPeriod.FixedValue = 580  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.59, 17.6  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.59, 17.6
```

### **3.17.7 Pioneer92MGI\_MG26**

This cultivar is defined by overriding some of the base parameters of the plant model.

Pioneer92MGI\_MG26 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 271  
[Phenology].EarlyFlowering.Target.FixedValue = 120  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.125  
[Phenology].LateGrainFilling.Target.EntireGrainfillIPeriod.FixedValue = 529  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.77, 17.57  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.77, 17.57
```

### **3.17.8 PioneerP92Y75\_MG27**

This cultivar is defined by overriding some of the base parameters of the plant model.

PioneerP92Y75\_MG27 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 328  
[Phenology].EarlyFlowering.Target.FixedValue = 106  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.14  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 499  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.59, 17.6  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.59, 17.6
```

### **3.17.9 Macon\_MG30**

This cultivar is defined by overriding some of the base parameters of the plant model.

Macon\_MG30 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 367  
[Phenology].EarlyFlowering.Target.FixedValue = 163  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.175  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 607  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 14.05, 17.56  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 14.05, 17.56
```

### **3.17.10 PioneerP93M11\_MG31**

This cultivar is defined by overriding some of the base parameters of the plant model.

PioneerP93M11\_MG31 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 250  
[Phenology].EarlyFlowering.Target.FixedValue = 110  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.30  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 457  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.4, 16.0  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.4, 16.0  
[Grain].MaximumNConc.FixedValue = 0.065  
[Shell].PotentialHarvestIndex.FixedValue = 0.5  
[Leaf].AreaLargestLeaf.FixedValue=0.013
```

### **3.17.11 Becks321NRR\_MG32**

This cultivar is defined by overriding some of the base parameters of the plant model.

Becks321NRR\_MG32 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 272  
[Phenology].EarlyFlowering.Target.FixedValue = 117  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.20  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 522  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.45, 18.0  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.45, 18.0
```

### **3.17.12 PioneerP932T16R\_MG32**

This cultivar is defined by overriding some of the base parameters of the plant model.

PioneerP932T16R\_MG32 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 328  
[Phenology].EarlyFlowering.Target.FixedValue = 106  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.40  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 499  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.59, 17.6  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.59, 17.6
```

### **3.17.13 Becks367NRR\_MG37**

This cultivar is defined by overriding some of the base parameters of the plant model.

Becks367NRR\_MG37 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 267  
[Phenology].EarlyFlowering.Target.FixedValue = 112
```

```
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.26  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 506  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.27, 17.2  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.27, 17.2
```

### **3.17.14 AsgrowAG4403\_MG40**

This cultivar is defined by overriding some of the base parameters of the plant model.

AsgrowAG4403\_MG40 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 292  
[Phenology].EarlyFlowering.Target.FixedValue = 123  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.30  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 535  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.09, 16.49  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.09, 16.49
```

### **3.17.15 HornbeckHBK4891\_MG40**

This cultivar is defined by overriding some of the base parameters of the plant model.

HornbeckHBK4891\_MG40 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 292  
[Phenology].EarlyFlowering.Target.FixedValue = 123  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.30  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 535  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.09, 16.49  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.09, 16.49
```

### **3.17.16 Pioneer94B01\_MG40**

This cultivar is defined by overriding some of the base parameters of the plant model.

Pioneer94B01\_MG40 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 322  
[Phenology].EarlyFlowering.Target.FixedValue = 143  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.30  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 567  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.05, 16.46  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.05, 16.46
```

### **3.17.17 PioneerP9504\_MG50**

This cultivar is defined by overriding some of the base parameters of the plant model.

PioneerP9504\_MG50 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 404  
[Phenology].EarlyFlowering.Target.FixedValue = 112  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.30  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 505  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.83, 16.13  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.83, 16.13
```

### **3.17.18 AsgrowAG5701\_MG50**

This cultivar is defined by overriding some of the base parameters of the plant model.

AsgrowAG5701\_MG50 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 404  
[Phenology].EarlyFlowering.Target.FixedValue = 131  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.30  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 549  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.83, 16.13  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.83, 16.13
```

### **3.17.19 Hutcheson\_MG50**

This cultivar is defined by overriding some of the base parameters of the plant model.

Hutcheson\_MG50 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 438  
[Phenology].EarlyFlowering.Target.FixedValue = 112  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.30  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 505  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.58, 15.88  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.58, 15.88
```

### **3.17.20 NK622\_MG60**

This cultivar is defined by overriding some of the base parameters of the plant model.

NK622\_MG60 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 436  
[Phenology].EarlyFlowering.Target.FixedValue = 93  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.30  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 467  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.39, 15.61  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.39, 15.61
```

## **3.18 Generic**

Generic\_MG0, Generic\_MG00, Generic\_MG000, Generic\_MG1, Generic\_MG10, Generic\_MG2, Generic\_MG3, Generic\_MG4, Generic\_MG5, Generic\_MG6, Generic\_MG7, Generic\_MG8, Generic\_MG9

### **3.18.1 Generic\_MG000**

This cultivar is defined by overriding some of the base parameters of the plant model.

Generic\_MG000 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 310  
[Phenology].EarlyFlowering.Target.FixedValue = 100  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.475  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 590  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 14.6, 22.35  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 14.6, 22.35
```

### **3.18.2 Generic\_MG00**

This cultivar is defined by overriding some of the base parameters of the plant model.

Generic\_MG00 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 320  
[Phenology].EarlyFlowering.Target.FixedValue = 100  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.467  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 600  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 14.35, 21.11  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 14.35, 21.11
```

### **3.18.3 Generic\_MG0**

This cultivar is defined by overriding some of the base parameters of the plant model.

Generic\_MG0 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 336  
[Phenology].EarlyFlowering.Target.FixedValue = 120  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.422  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 616  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 14.1, 19.95  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 14.1, 19.95
```

### **3.18.4 Generic\_MG1**

This cultivar is defined by overriding some of the base parameters of the plant model.

Generic\_MG1 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 340  
[Phenology].EarlyFlowering.Target.FixedValue = 120  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.411  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 632  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.84, 18.77  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.84, 18.77
```

### **3.18.5 Generic\_MG2**

This cultivar is defined by overriding some of the base parameters of the plant model.

Generic\_MG2 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 348  
[Phenology].EarlyFlowering.Target.FixedValue = 120  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.386  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 648  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.59, 17.61  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.59, 17.61
```

### **3.18.6 Generic\_MG3**

This cultivar is defined by overriding some of the base parameters of the plant model.

Generic\_MG3 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 380  
[Phenology].EarlyFlowering.Target.FixedValue = 120  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.361  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 664  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.4, 16.91  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.4, 16.91
```

### **3.18.7 Generic\_MG4**

This cultivar is defined by overriding some of the base parameters of the plant model.

Generic\_MG4 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 388  
[Phenology].EarlyFlowering.Target.FixedValue = 140  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.324  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 664  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.1, 16.49  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.1, 16.49
```

### **3.18.8 Generic\_MG5**

This cultivar is defined by overriding some of the base parameters of the plant model.

Generic\_MG5 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 396  
[Phenology].EarlyFlowering.Target.FixedValue = 160  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.072  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 696  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.83, 16.13  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.83, 16.13
```

### **3.18.9 Generic\_MG6**

This cultivar is defined by overriding some of the base parameters of the plant model.

Generic\_MG6 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 404  
[Phenology].EarlyFlowering.Target.FixedValue = 180  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.056  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 712  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.58, 15.8  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.58, 15.8
```

### **3.18.10 Generic\_MG7**

This cultivar is defined by overriding some of the base parameters of the plant model.

Generic\_MG7 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 416  
[Phenology].EarlyFlowering.Target.FixedValue = 200  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.055  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 728  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.33, 15.46  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.33, 15.46
```

### **3.18.11 Generic\_MG8**

This cultivar is defined by overriding some of the base parameters of the plant model.

Generic\_MG8 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 430  
[Phenology].EarlyFlowering.Target.FixedValue = 200  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.054  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 744  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.07, 15.1  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.07, 15.1
```

### **3.18.12 Generic\_MG9**

This cultivar is defined by overriding some of the base parameters of the plant model.

Generic\_MG9 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 460  
[Phenology].EarlyFlowering.Target.FixedValue = 200  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.053  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 748  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 11.88, 14.82  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 11.88, 14.82
```

### **3.18.13 Generic\_MG10**

This cultivar is defined by overriding some of the base parameters of the plant model.

Generic\_MG10 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 470  
[Phenology].EarlyFlowering.Target.FixedValue = 200  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.053  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 748  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 11.78, 14.65  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 11.78, 14.65
```

## **3.19 China**

Hedou19, Jiuyuehuang, Nandou12, Texuan13

### **3.19.1 Nandou12**

This cultivar is defined by overriding some of the base parameters of the plant model.

Nandou12 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 500  
[Phenology].EarlyFlowering.Target.FixedValue = 120  
[Phenology].EarlyPodDevelopment.Target.FixedValue = 180  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.2  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 440  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.63, 15.13  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.63, 15.13  
[Phenology].MidGrainFilling.Target.FractionofMidToLateGrainfilling.FixedValue=0.45  
[Leaf].AreaLargestLeaf.FixedValue=0.013  
[Grain].PotentialHarvestIndex.FixedValue=0.35
```

### 3.19.2 Texuan13

This cultivar is defined by overriding some of the base parameters of the plant model.

Texuan13 makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 500  
[Phenology].EarlyFlowering.Target.FixedValue = 200  
[Phenology].EarlyPodDevelopment.Target.FixedValue = 170  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.2  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 460  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.63, 15.13  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.63, 15.13  
[Phenology].MidGrainFilling.Target.FractionofMidToLateGrainfilling.FixedValue=0.45  
[Leaf].AreaLargestLeaf.FixedValue=0.013  
[Grain].PotentialHarvestIndex.FixedValue=0.35
```

### 3.19.3 Jiuyuehuang

This cultivar is defined by overriding some of the base parameters of the plant model.

Jiuyuehuang makes the following changes:

```
[Phenology].Vegetative.Target.FixedValue = 540  
[Phenology].EarlyFlowering.Target.FixedValue = 140  
[Phenology].EarlyPodDevelopment.Target.FixedValue = 140  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.2  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 420  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 12.94, 15.44  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 12.94, 15.44  
[Phenology].MidGrainFilling.Target.FractionofMidToLateGrainfilling.FixedValue=0.45  
[Leaf].AreaLargestLeaf.FixedValue=0.013  
[Grain].PotentialHarvestIndex.FixedValue=0.25
```

### 3.19.4 Hedou19

This cultivar is defined by overriding some of the base parameters of the plant model.

Hedou19 makes the following changes:

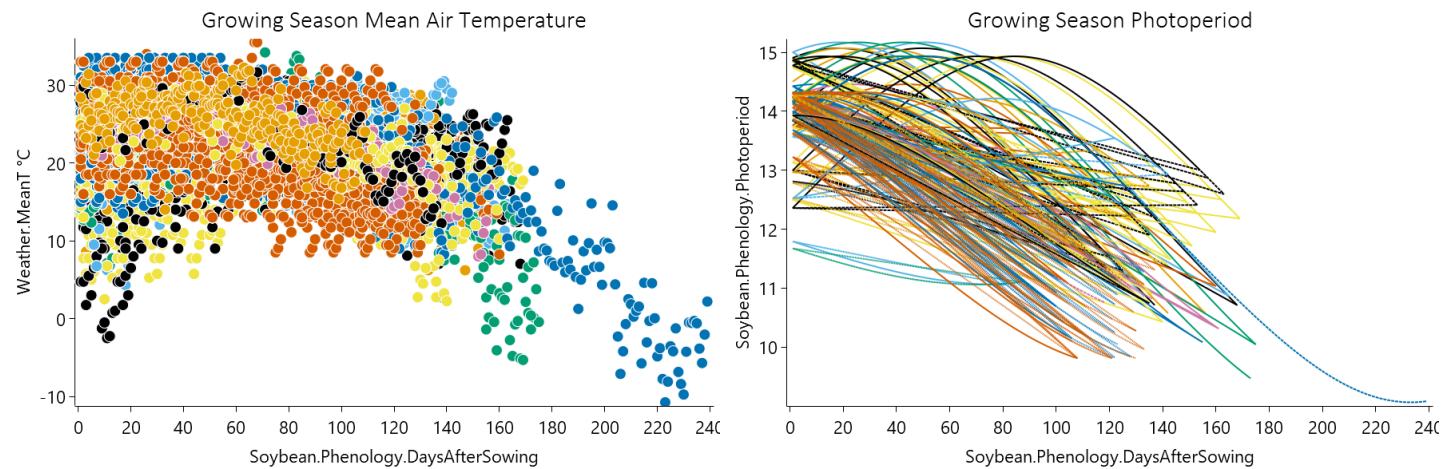
```
[Phenology].Vegetative.Target.FixedValue = 370  
[Phenology].EarlyFlowering.Target.FixedValue = 120  
[Phenology].EarlyPodDevelopment.Target.FixedValue = 180  
[Phenology].EarlyGrainFilling.Target.FractionofGrainfilling.FixedValue = 0.361  
[Phenology].LateGrainFilling.Target.EntireGrainfillPeriod.FixedValue = 600  
[Phenology].VegetativePhotoperiodModifier.XYPairs.X = 13.57, 16.07  
[Phenology].ReproductivePhotoperiodModifier.XYPairs.X = 13.57, 16.07  
[Phenology].MidGrainFilling.Target.FractionofMidToLateGrainfilling.FixedValue=0.45  
[Leaf].AreaLargestLeaf.FixedValue=0.02  
[Leaf].Phyllochron.FixedValue=45
```

## 3.20 MortalityRate

*MortalityRate* = 0

## 4 Validation

The soybean model has been tested across a range of planting and agronomic conditions. These include datasets from Australia, USA and China covering a wide range of weather conditions (See graphs that follow) and agronomic factors (irrigation, fertiliser, sowing dates).



### 4.1 Map



## 4.2 USA

### 4.2.1 FACTS

This trial was conducted on deep fertile soils, in central Iowa (Ames) and in northwest Iowa (Sutherland), USA, in years 2015, 2016 and 2017. In each year two planting date were studied, early versus late. Row spacing was 76 cm, and plant population was around 35 plants/m<sup>2</sup> (see details in APSIM managers). No nitrogen or irrigation applied. This region has shallow water tables (about 1.2 m below surface, range 0.3 to 3m) and the soil has no subsurface drainage. Data from years 2015 and 2017 have been incorporated while data from year 2016 will be added later. Local weather data (the station was positioned 10 m from the trial) and actual soil profile data (measured in Nov 2014 up to 1.2 meter, soil organic matter, texture, and pH by layer) were used. Additional soil data were taken from ssurgo. The following measurements were taken per plot (each treatment was replicated 3 times): Phenology (visual observations in the field using the V/R coding system); biomass samplings 6-9 times per season and per treatment (destructive sampling of 1 m<sup>2</sup> per plot); biomass partitioning and dry weight of each plant tissue including green and yellow leaves, stem plus petioles, and pod-walls plus seeds (note that seeds were separated at the final harvest only); carbon and nitrogen concentration of each plant tissue (LECO CN analyzer); green leaf area index (LI Area Meter); node number and pod number per plant; leaf area per node in year 2015 only; root front depth over time (manual soil core technique) and maximum root depth, mass and length (mechanical gidding probe technique, depth of 240 cm) at approximately middle grain fill stage; daily soil water and temperature at two depths, 15 and 45 cm (5TM sensors placed horizontally, METEO group), daily water table depth (CTD-10 sensors, METEO group), and soil nitrate and ammonium approximately 10 times over each season and treatment at two depths 0-30 and 30-60 cm (sample was extracted in 2 M potassium chloride), and N-fixation over time (Isotope dilution method); soybean leaf senescence (gages to measure drop leaves dry matter and CN concentration, 1m<sup>2</sup> size, 3-4 measurements per season per treatment); crop residue dry matter, soil cover and soil nitrogen and water measurements (manual samplings 10 times from crop harvest to planting of the next crop). This dataset is licensed by the Iowa State University Research Foundation.

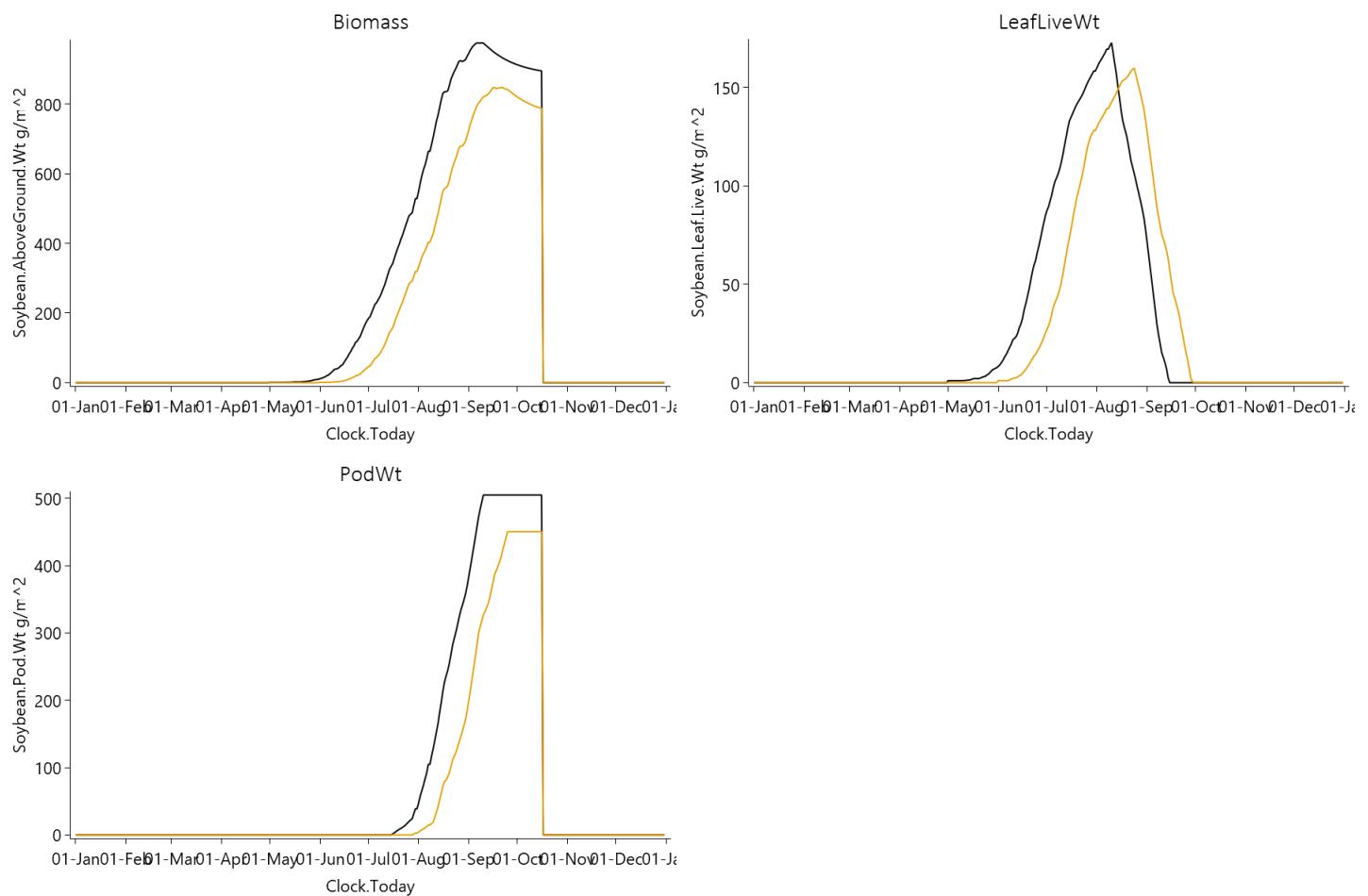
#### List of experiments.

Experiment Name	Design (Number of Treatments)
Ames2015	Sow (2)
Ames2017	Sow (2)
Sutherland2015	Sow (2)
Sutherland2017	Sow (2)

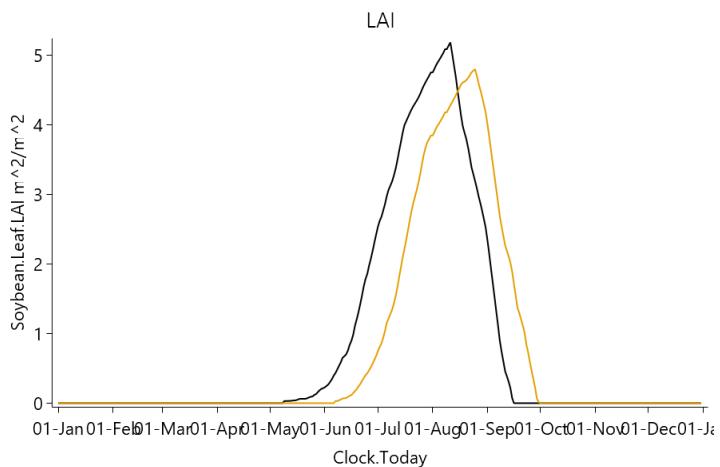
## 4.2.1.1 Ames2015

### 4.2.1.1.1 Graphs

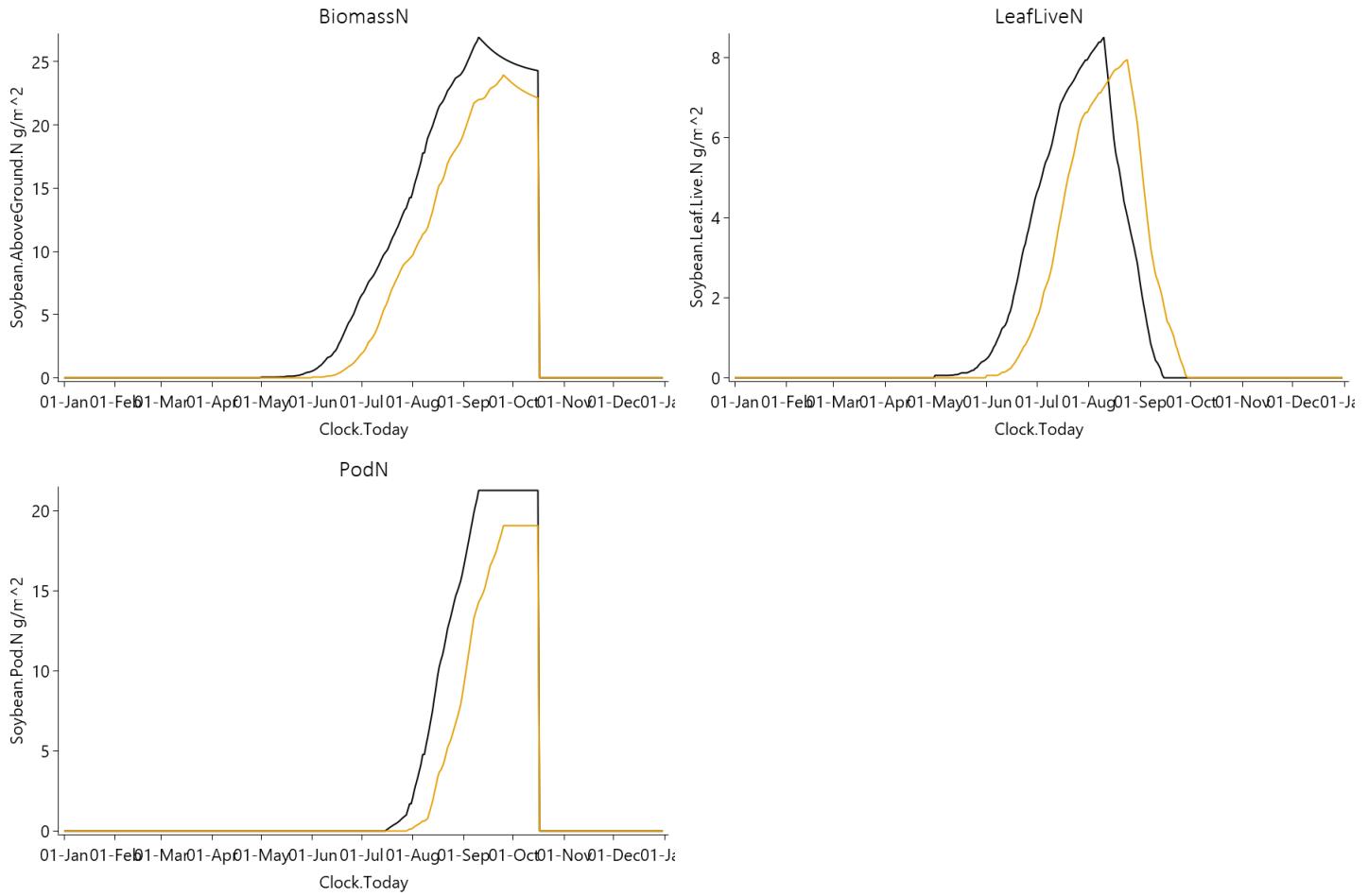
#### 4.2.1.1.1.1 Biomass



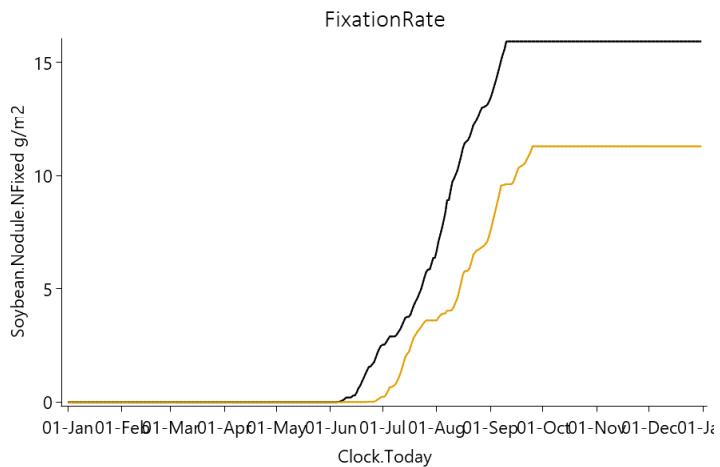
#### 4.2.1.1.1.2 Canopy



#### 4.2.1.1.3 Nitrogen



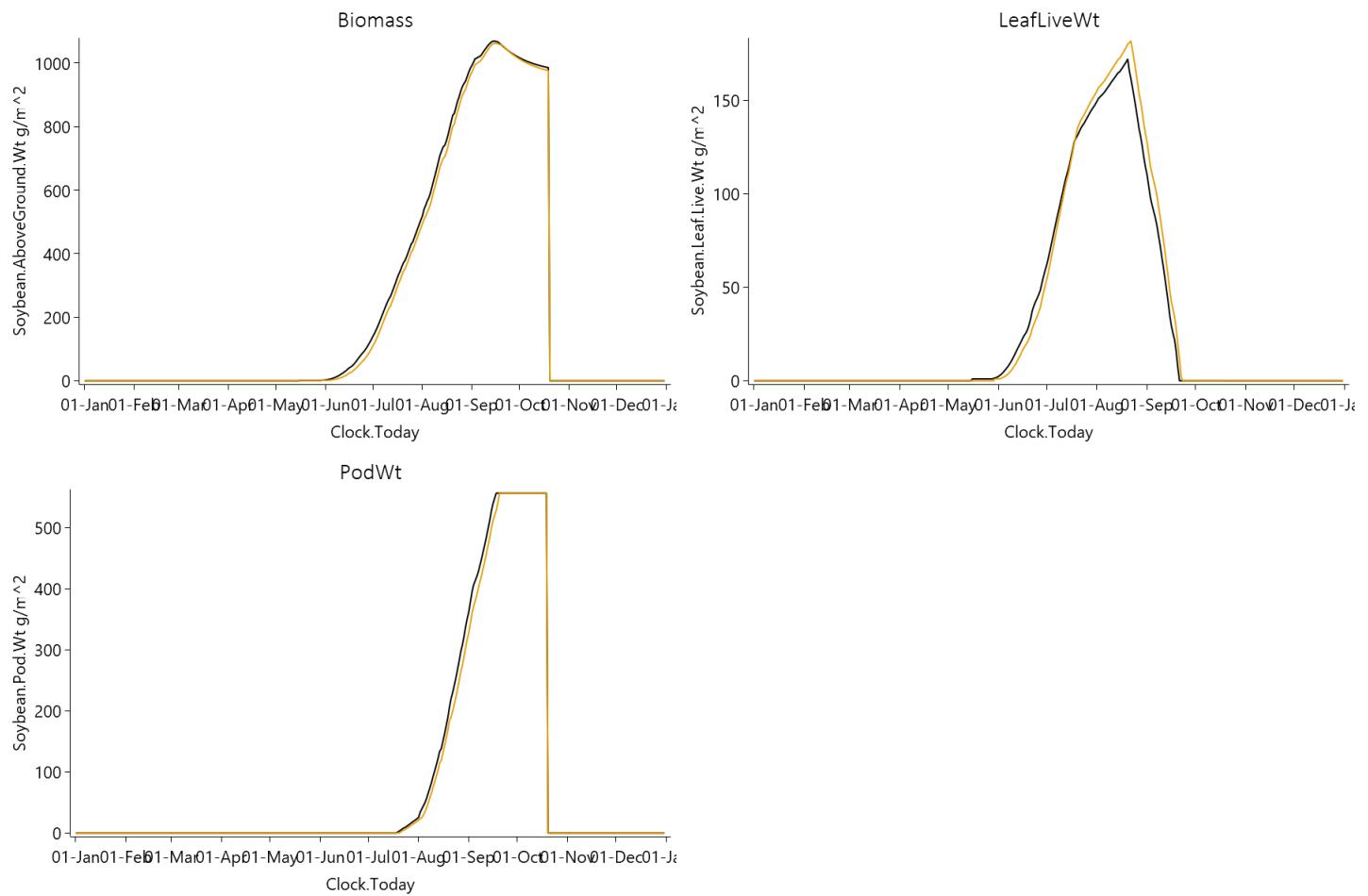
#### 4.2.1.1.4 Fixation



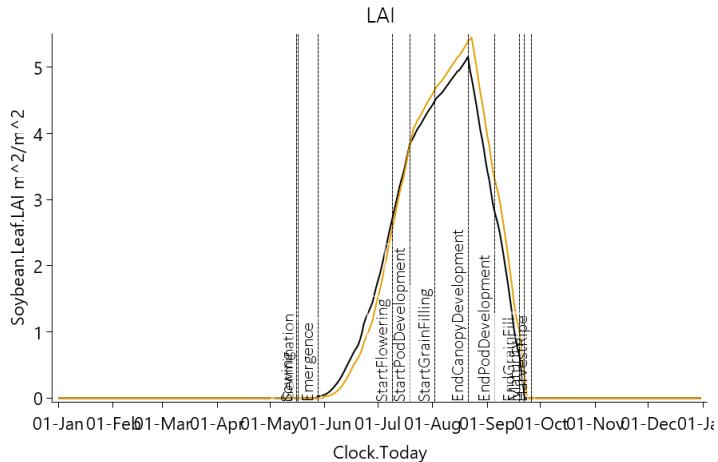
## 4.2.1.2 Ames2017

### 4.2.1.2.1 Graphs

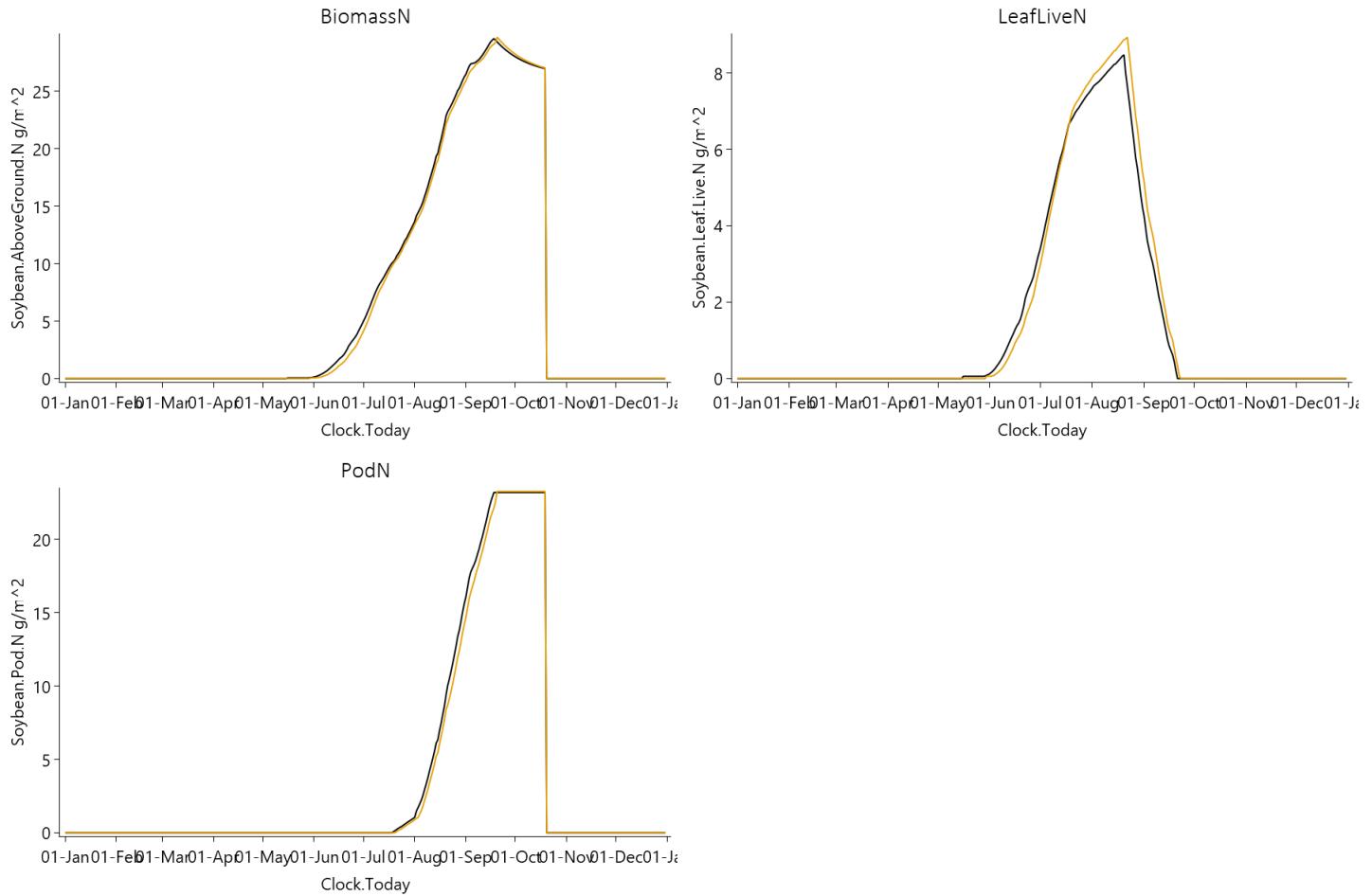
#### 4.2.1.2.1.1 Biomass



#### 4.2.1.2.1.2 Canopy



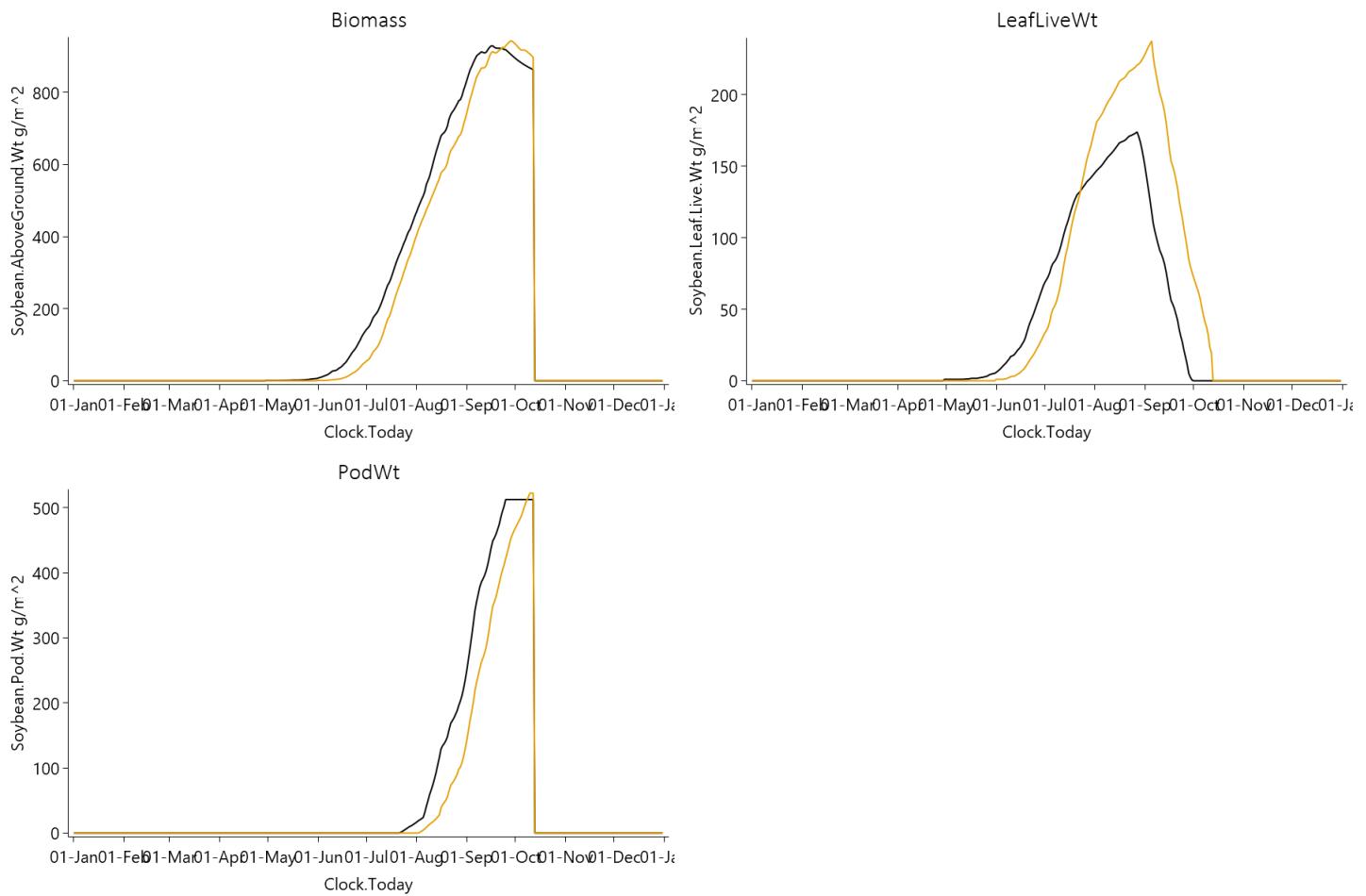
#### 4.2.1.2.1.3 Nitrogen



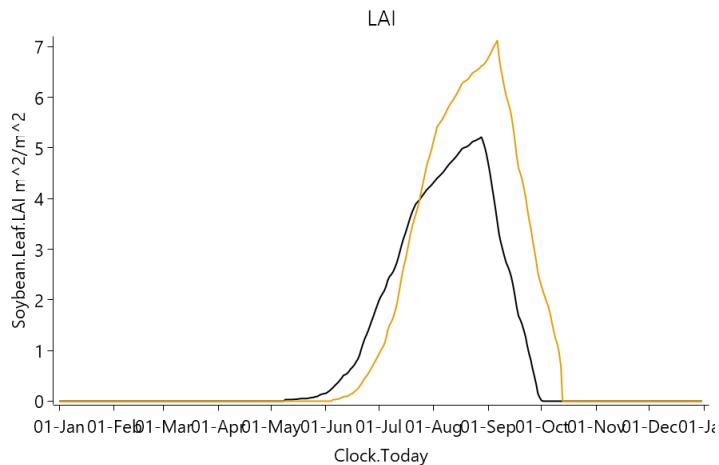
### 4.2.1.3 Sutherland2015

#### 4.2.1.3.1 Graphs

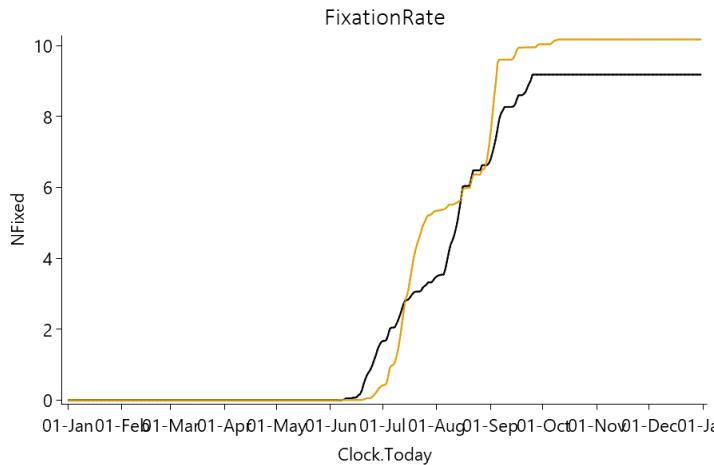
##### 4.2.1.3.1.1 Biomass



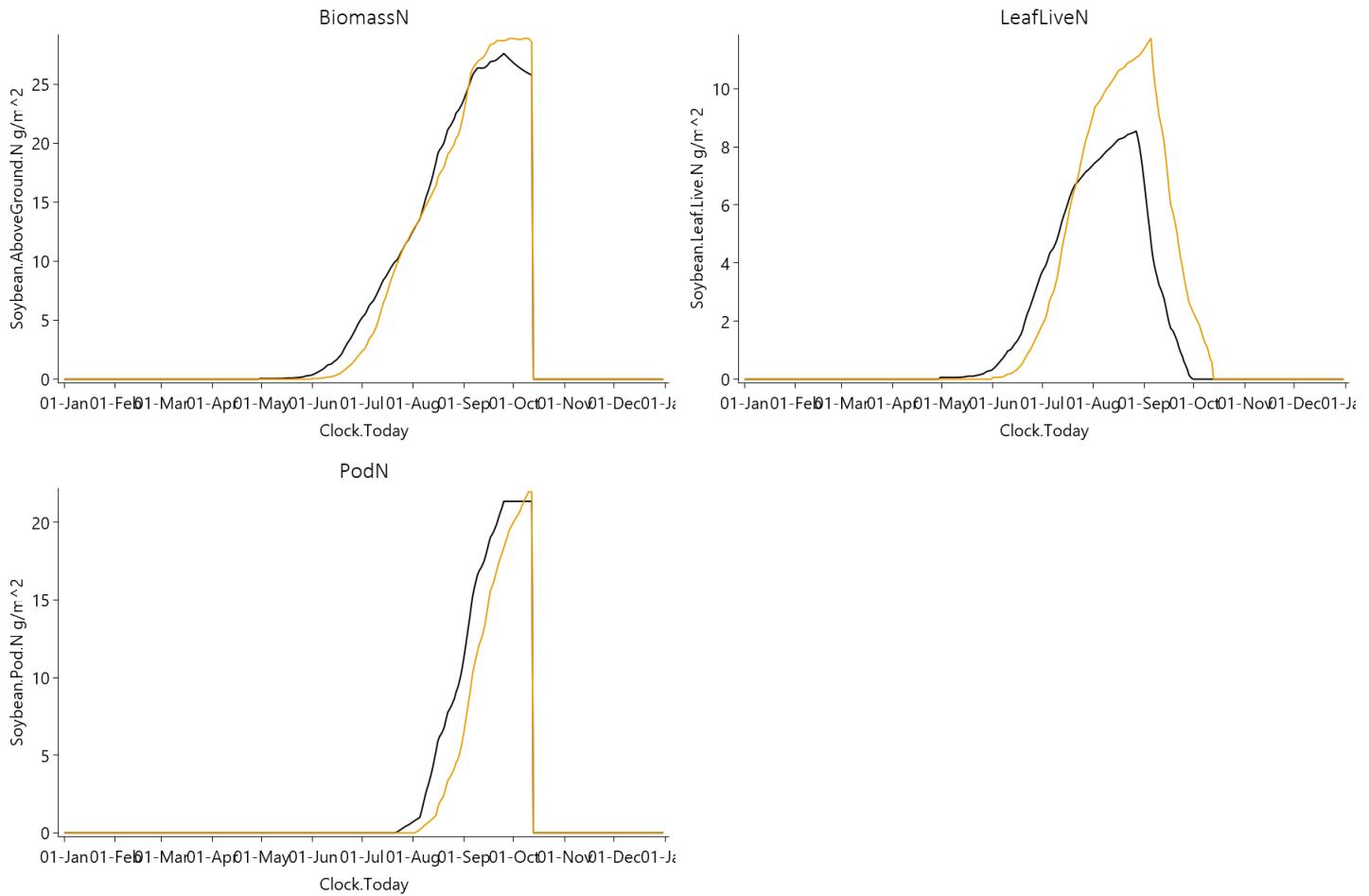
##### 4.2.1.3.1.2 Canopy



#### 4.2.1.3.1.3 Fixation



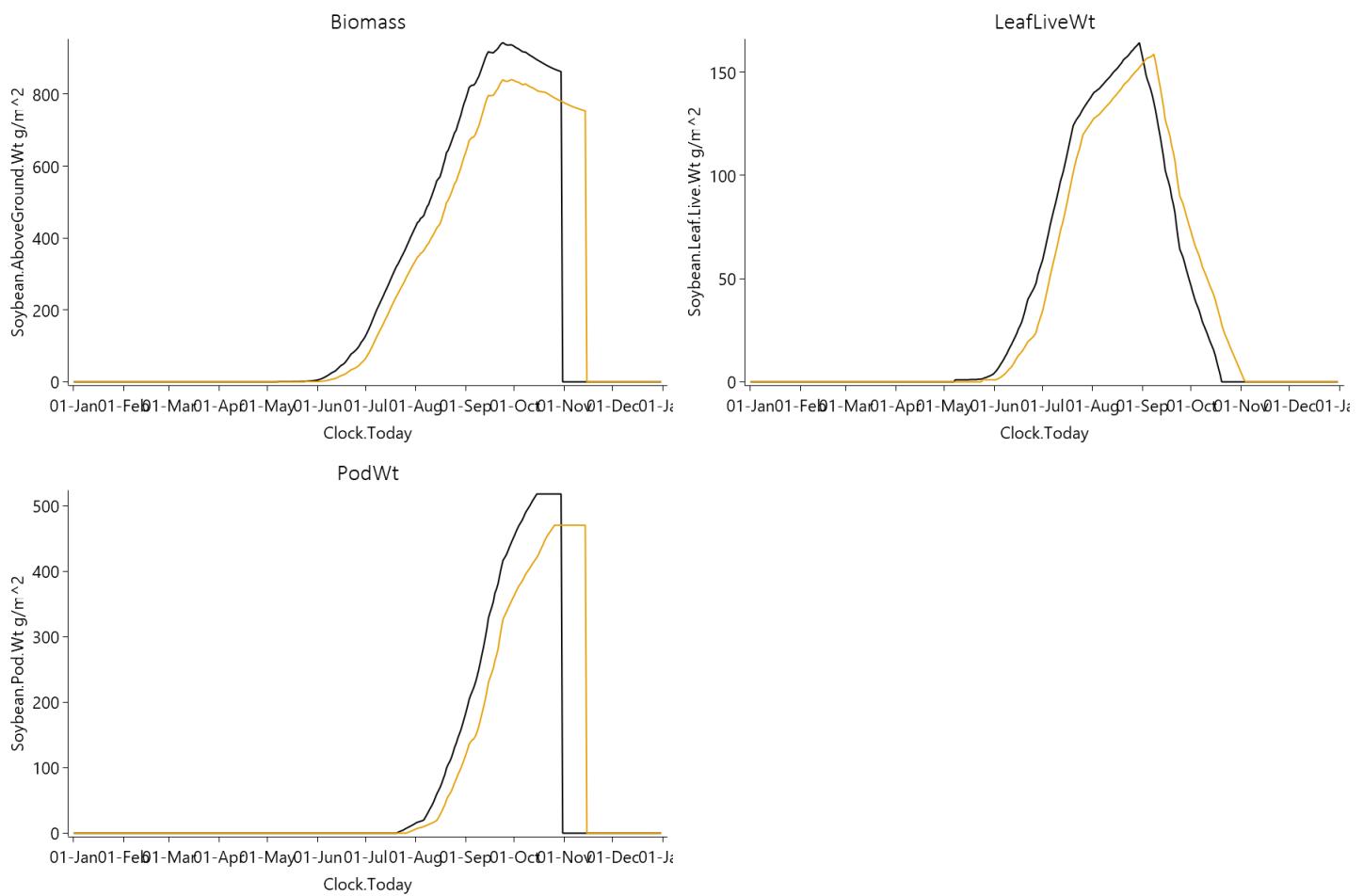
#### 4.2.1.3.1.4 Nitrogen



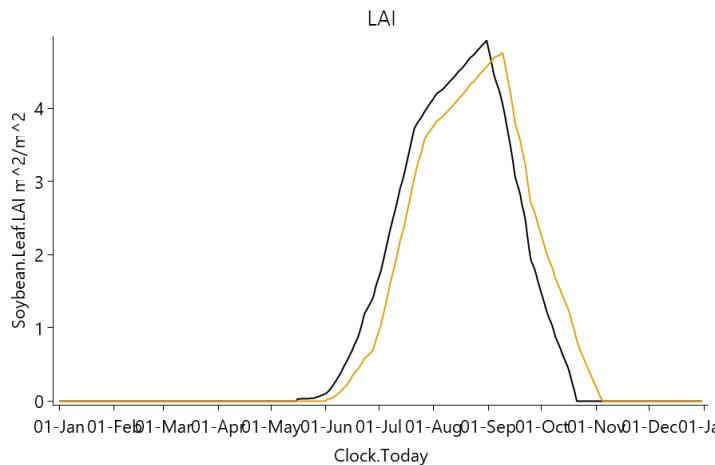
## 4.2.1.4 Sutherland2017

### 4.2.1.4.1 Graphs

#### 4.2.1.4.1.1 Biomass



#### 4.2.1.4.1.2 Canopy

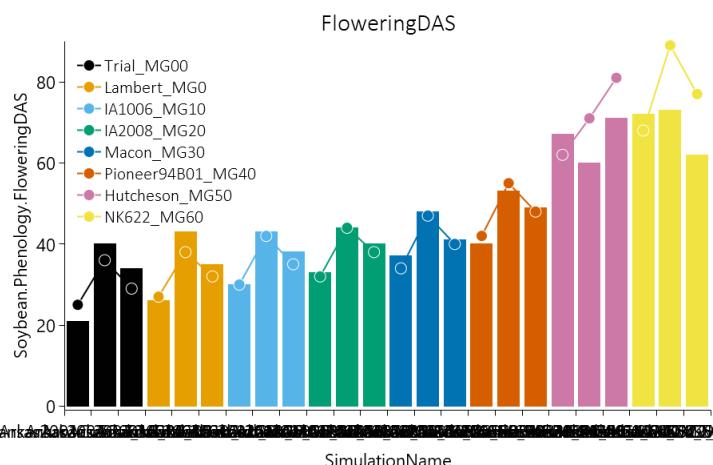


## 4.2.2 Arkansas

This trial ([Edwards, 2005](#)) was conducted on a silt loam soil in Fayetteville Arkansas, USA, in years 2001, 2002 and 2003. The factor studied were seven soybean maturity groups (from mg 00 to mg 6) and in some year multiple varieties within a maturity group. Crops were irrigated. No N fertilization was applied. This region has no shallow water tables. Phenology data were collected at different growth stages and were used in this work. Weather and soil data for the site were estimated from public sources. For additional information about this trial, see Archountolis et al. (2014).

### List of experiments.

Experiment Name	Design (Number of Treatments)
Arkansas2001	Cv (8)
Arkansas2002	Cv (8)
Arkansas2003	Cv (8)

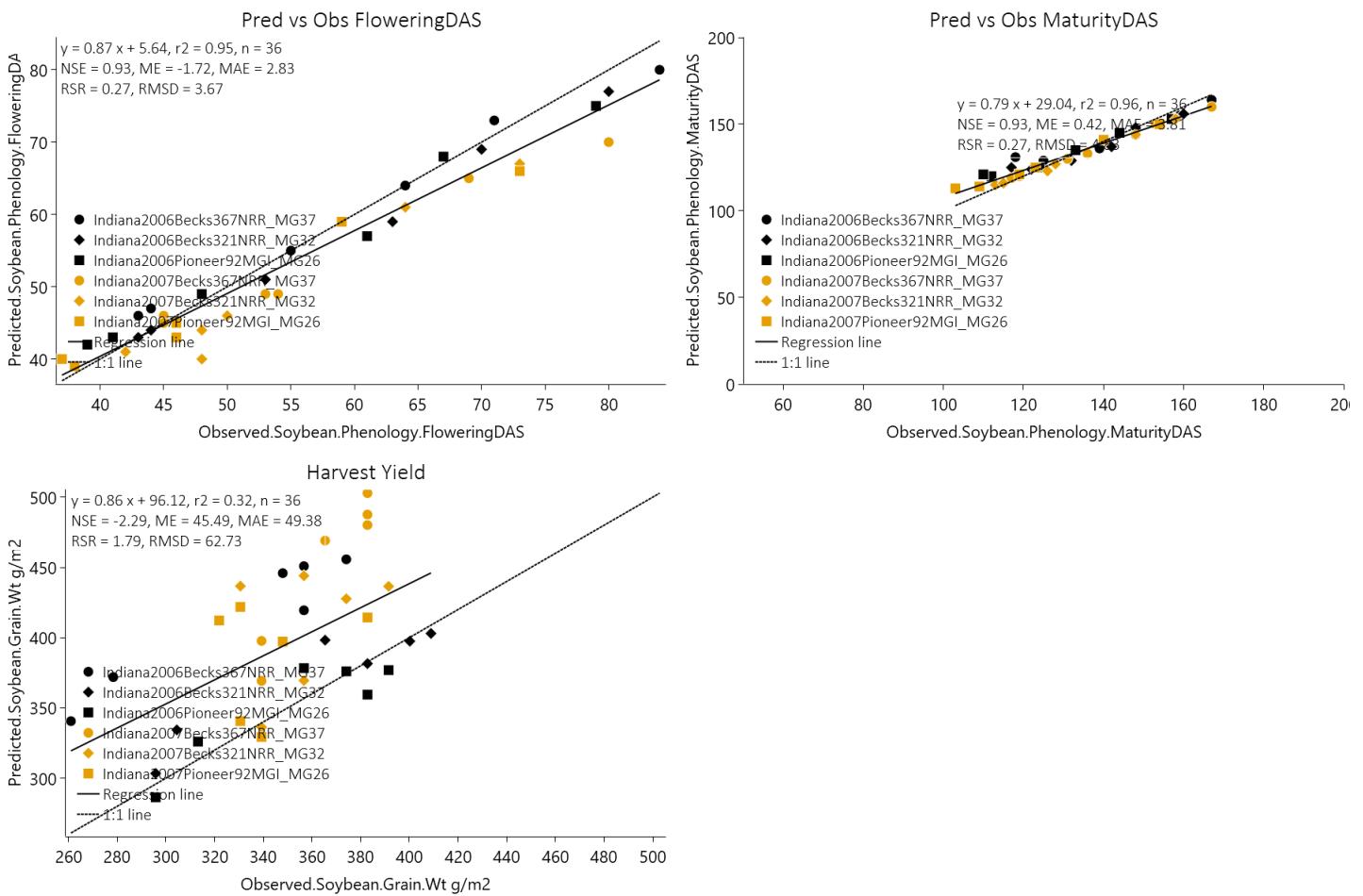


#### 4.2.3 Indiana

This trial ([Robinson, 2009](#)) conducted in West Lafayette Indiana, USA, in years 2006 and 2007. The factors studied were six planting dates x three varieties (from mg 2.6 to mg 3.7). No irrigation or fertilization applied. Phenology, gravimetric soil moisture at three depth (manual soil cores), pod numbers, seed size, grain yield, protein and oil data were collected. Weather and soil data for the site were estimated from public sources. For additional information about this trial, see Archountolis et al. (2014).

#### List of experiments.

Experiment Name	Design (Number of Treatments)
Indiana2006	(18)
Indiana2007	(18)

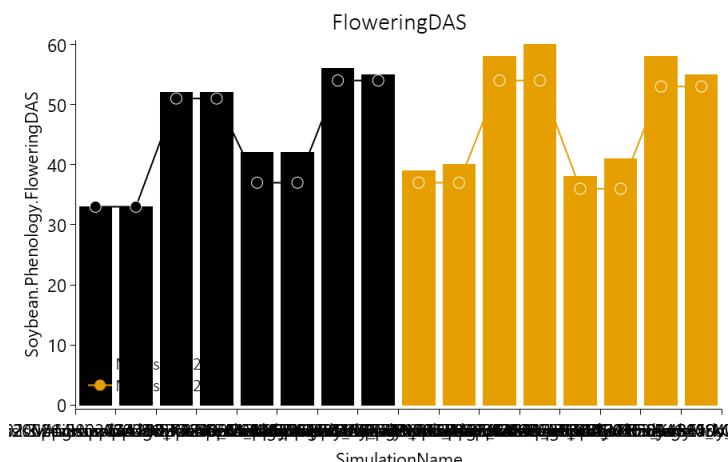


#### **4.2.4 Mississippi**

This trial ([Zhang, 2004](#)) was conducted in Stoneville Mississippi USA, in years 1998 to 2002. The factors studied were planting dates (ranged from early March to early July) and varieties (from mg 3.4 to mg 5.6). Crops were irrigated. Phenological measurements were obtained in the field following the V/R staging system. For additional information about this trial, see Archountolis et al. (2014).

## List of experiments.

Experiment Name	Design (Number of Treatments)
Mississippi2002	(8)
Mississippi2003	(8)



## 4.2.5 Nebraska

This trial ([Salvagiotti, 2009](#)) was conducted on a deep silt loam soil in Lincoln Nebraska USA, in years 2006 and 2007. The factors studied were different crop histories (normal N applied to corn-soy rotation and high N applied

to the rotation) and 4 N fertilization treatments to the soybean crop (zero N, 180 kg N/ha at planting, 180 kg N/ha as split between preplanting and V6 leaf stage, and 180 kg N/ha at R5 stage). Crops were irrigated. Row spacing was 76 cm, plant density about 31 pl/m<sup>2</sup> and planting date around late April to early May. The following measurements were taken: initial soil nitrate, destructive biomass samples six times during the season (size 0.46 m<sup>2</sup> per plot) per year and per treatment, biomass partitioning, dry weight and N concentrations of each tissue (Dumas method in Rapid N Cube; Elementer, Germany), fallen leaves, phenology, and N-fixation during the growing season using the ureide method. Local weather data and public soil data were used to drive the simulations.

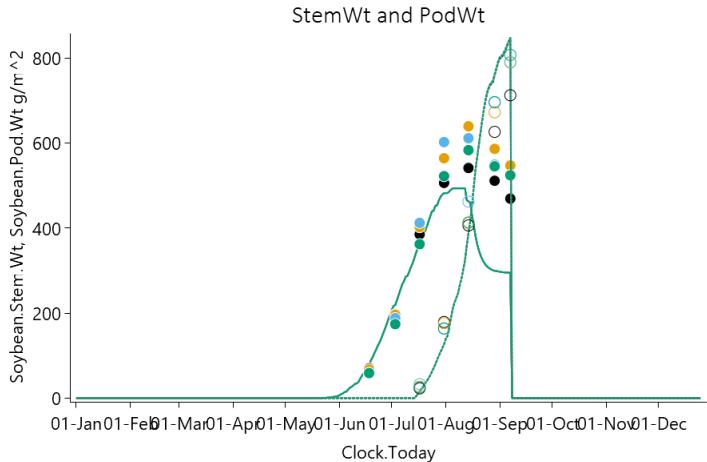
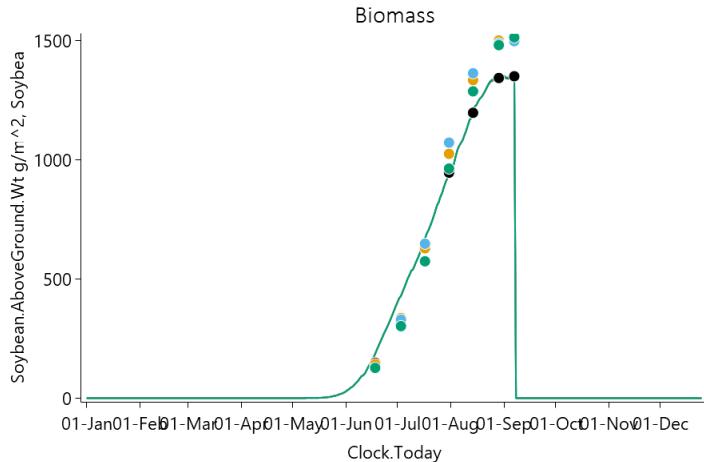
## List of experiments.

Experiment Name	Design (Number of Treatments)
Nebraska2006	N (4)
Nebraska2007	N (4)

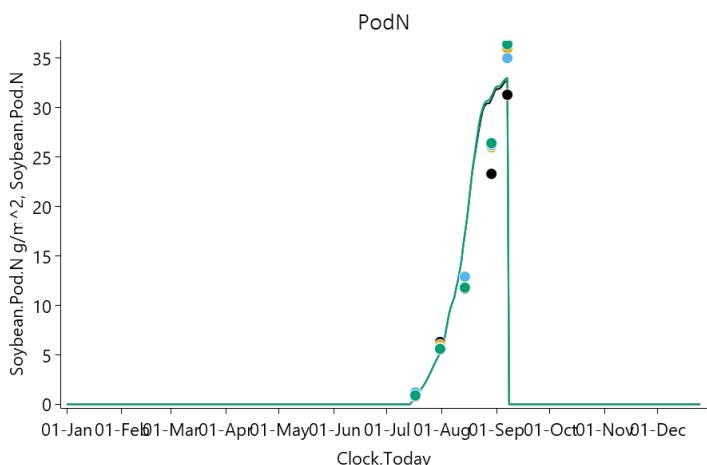
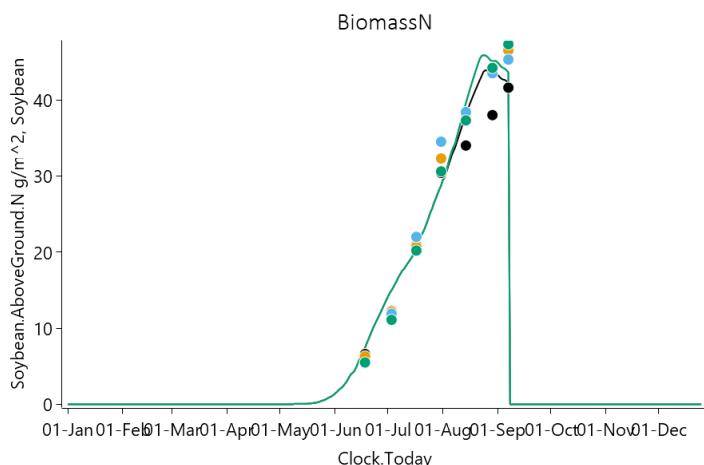
### 4.2.5.1 Nebraska2006

#### 4.2.5.1.1 Graphs

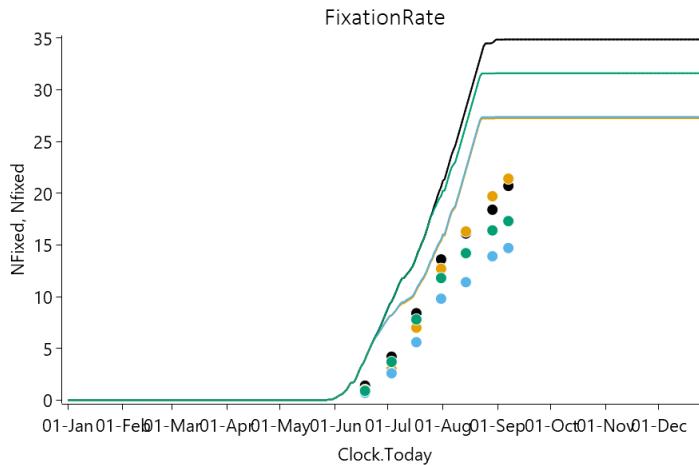
##### 4.2.5.1.1.1 Biomass



##### 4.2.5.1.1.2 Nitrogen



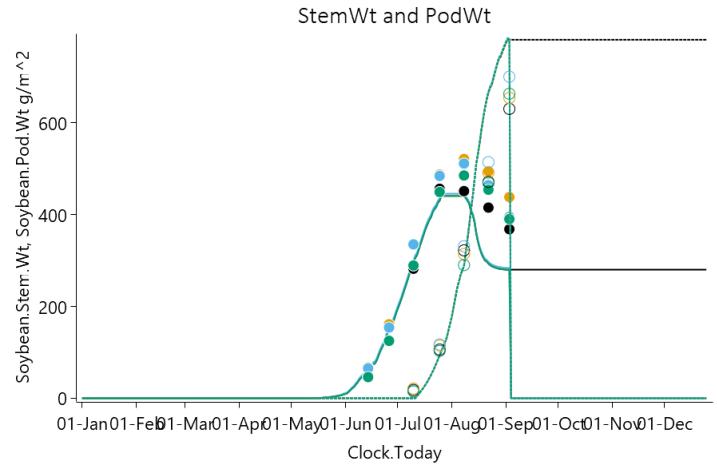
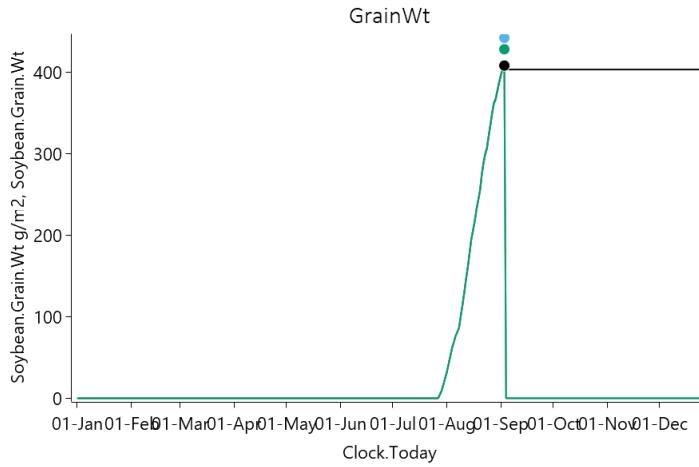
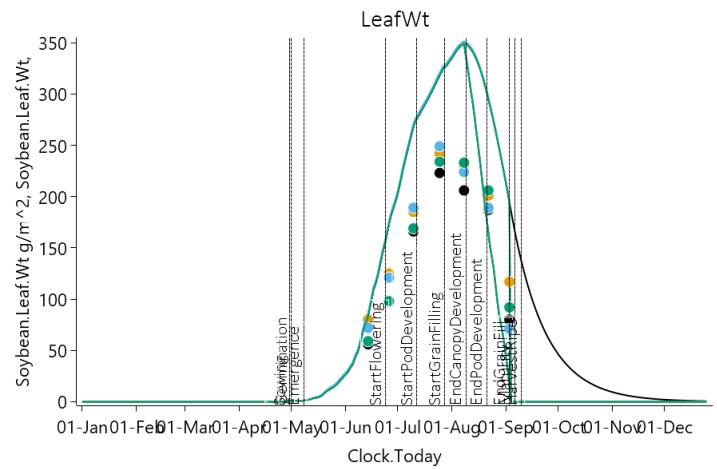
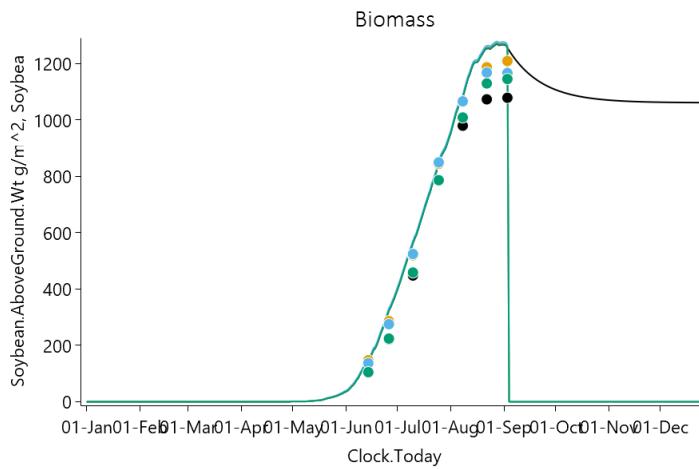
#### 4.2.5.1.1.3 Fixation



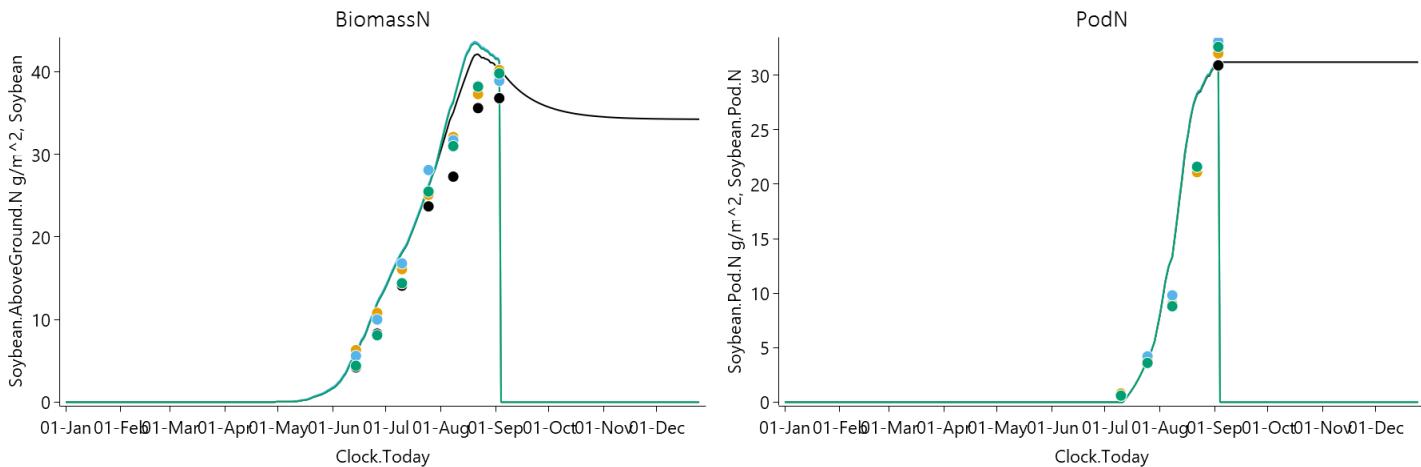
#### 4.2.5.2 Nebraska2007

##### 4.2.5.2.1 Graphs

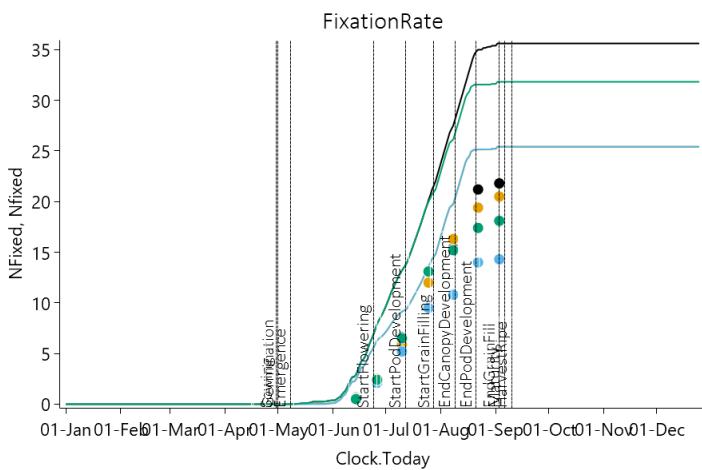
###### 4.2.5.2.1.1 Biomass



#### 4.2.5.2.1.2 Nitrogen



#### 4.2.5.2.1.3 Fixation



### 4.3 Australia

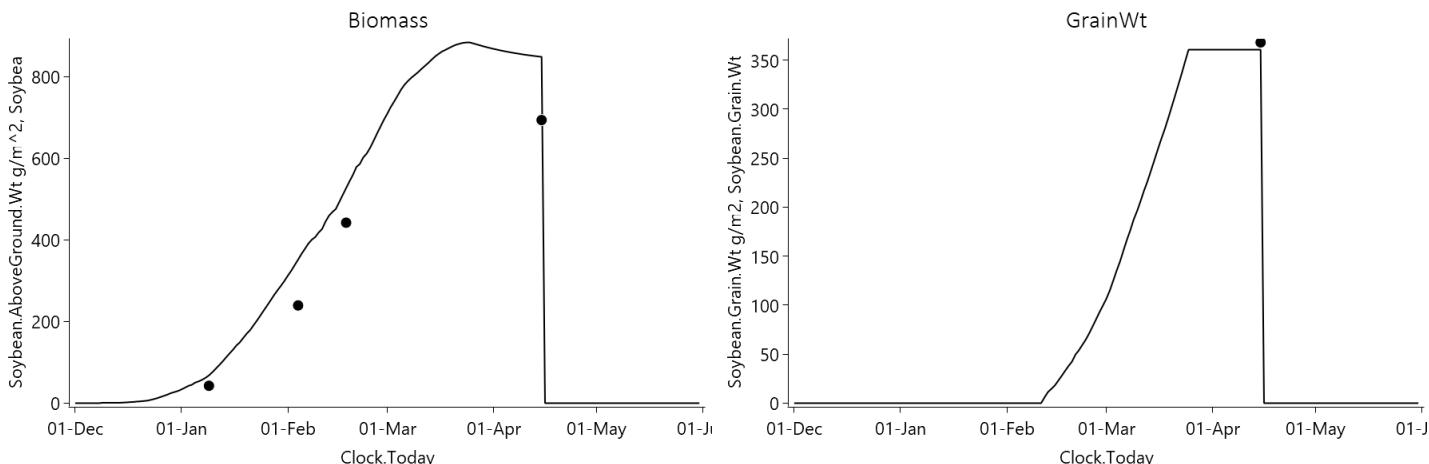
#### 4.3.1 Coleambally

##### List of experiments.

Experiment Name	Design (Number of Treatments)
Coleambally	Sow (1)

#### 4.3.1.1 Graphs

##### 4.3.1.1.1 Biomass



### 4.3.2 Gatton

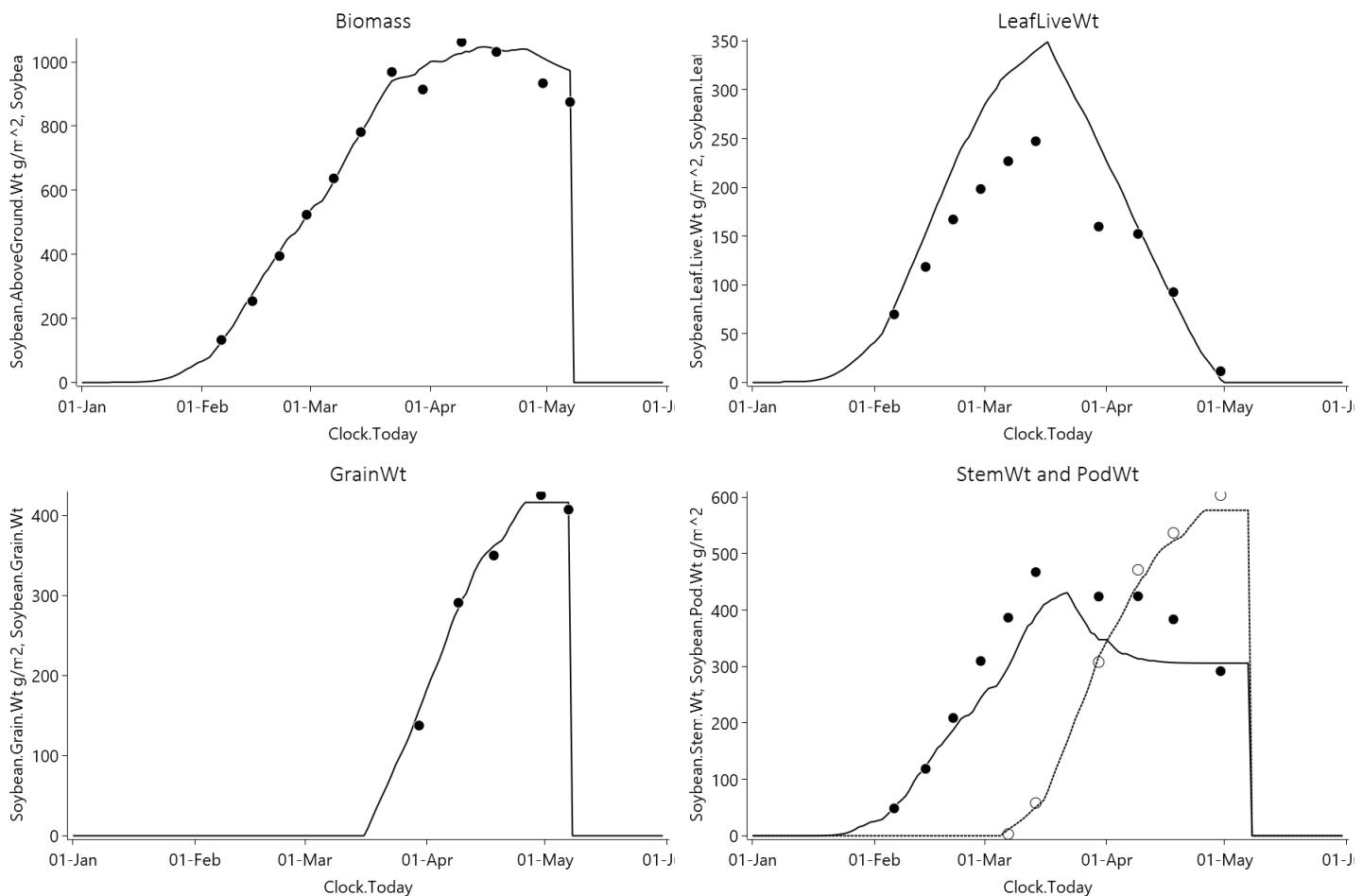
This dataset ([Muchow et al., 1993](#)) includes the cultvar "Davis" grown under irrigated conditions in a subtropical environment at the Gatton Research Station in southeastern Queensland, Australia. Plants were sampled almost weekly for biomass partitioning, nitrogen and plant development.

#### List of experiments.

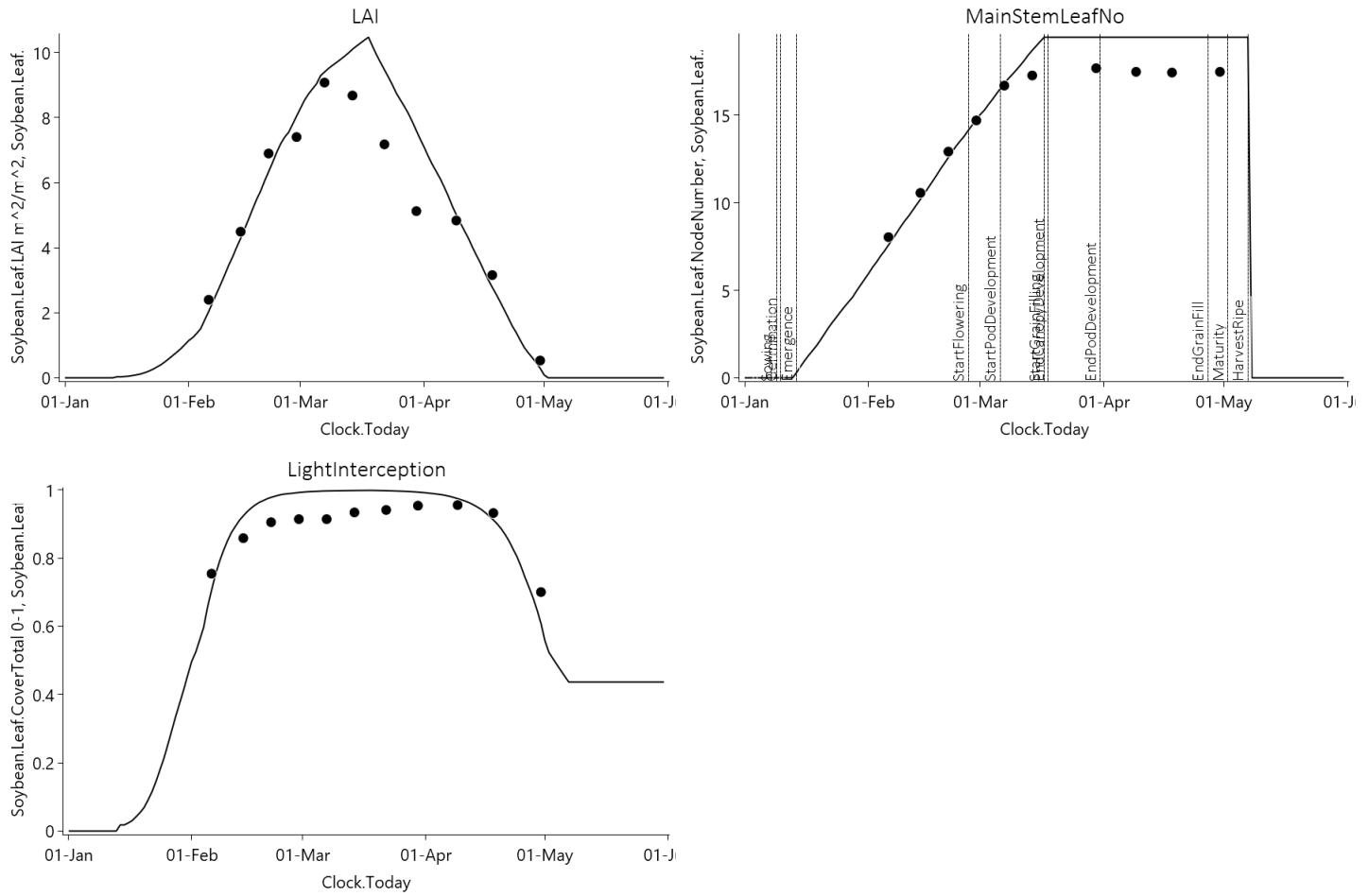
Experiment Name	Design (Number of Treatments)
Gatton	Sow (1)

#### 4.3.2.1 Graphs

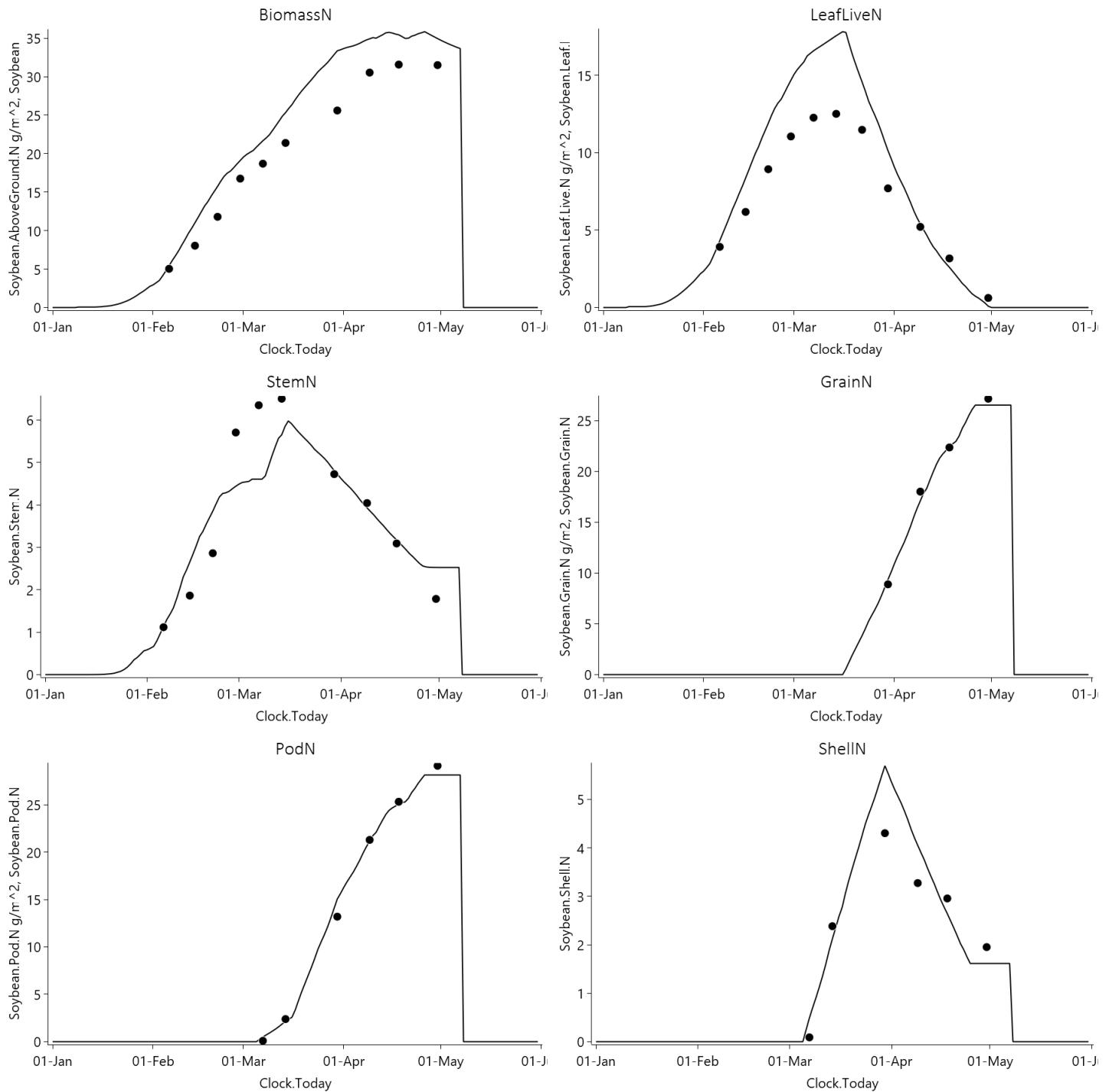
##### 4.3.2.1.1 Biomass



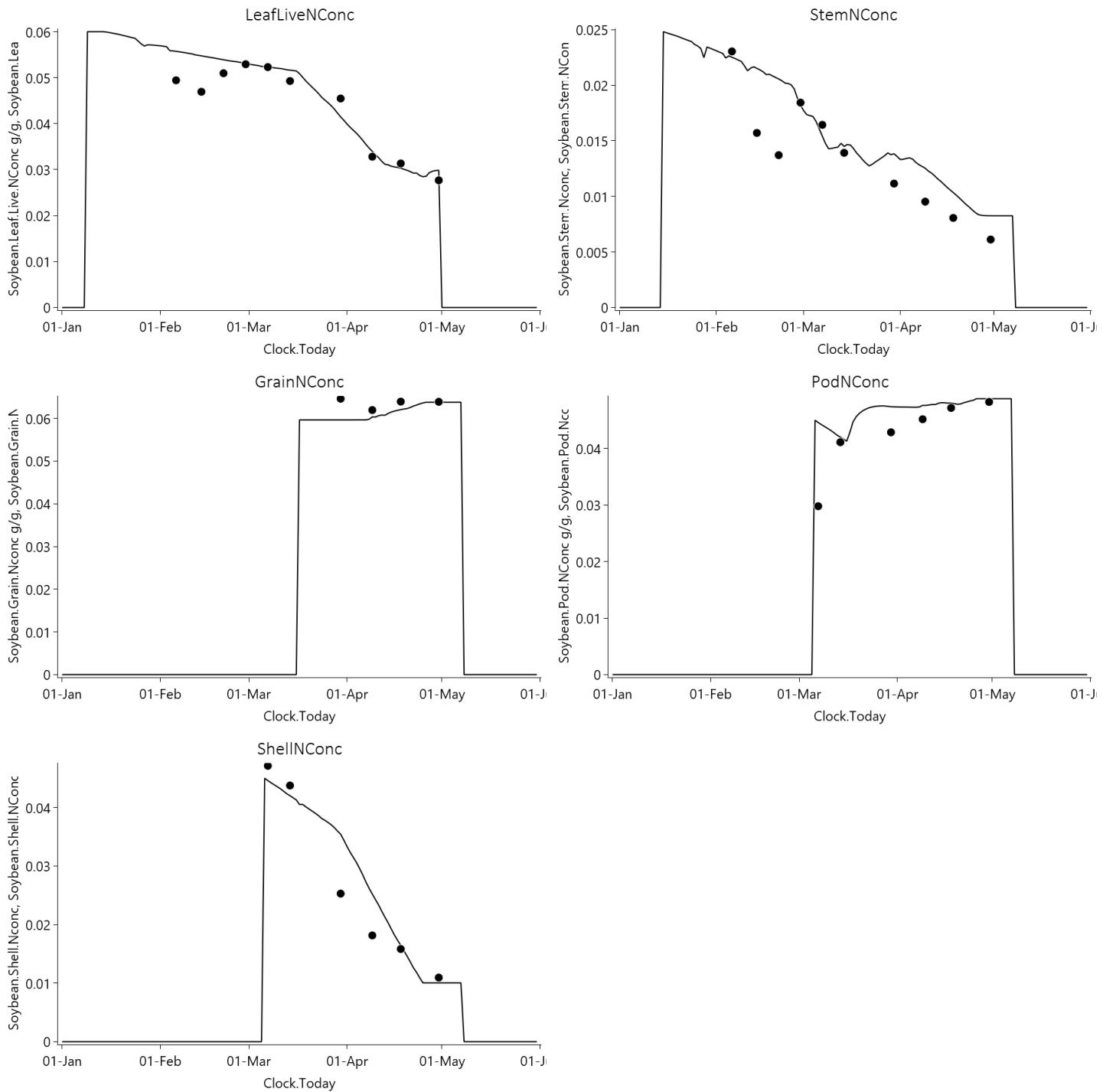
#### 4.3.2.1.2 Canopy



#### 4.3.2.1.3 Nitrogen



#### 4.3.2.1.4 Nitrogen Concentration



#### 4.3.3 Griffith

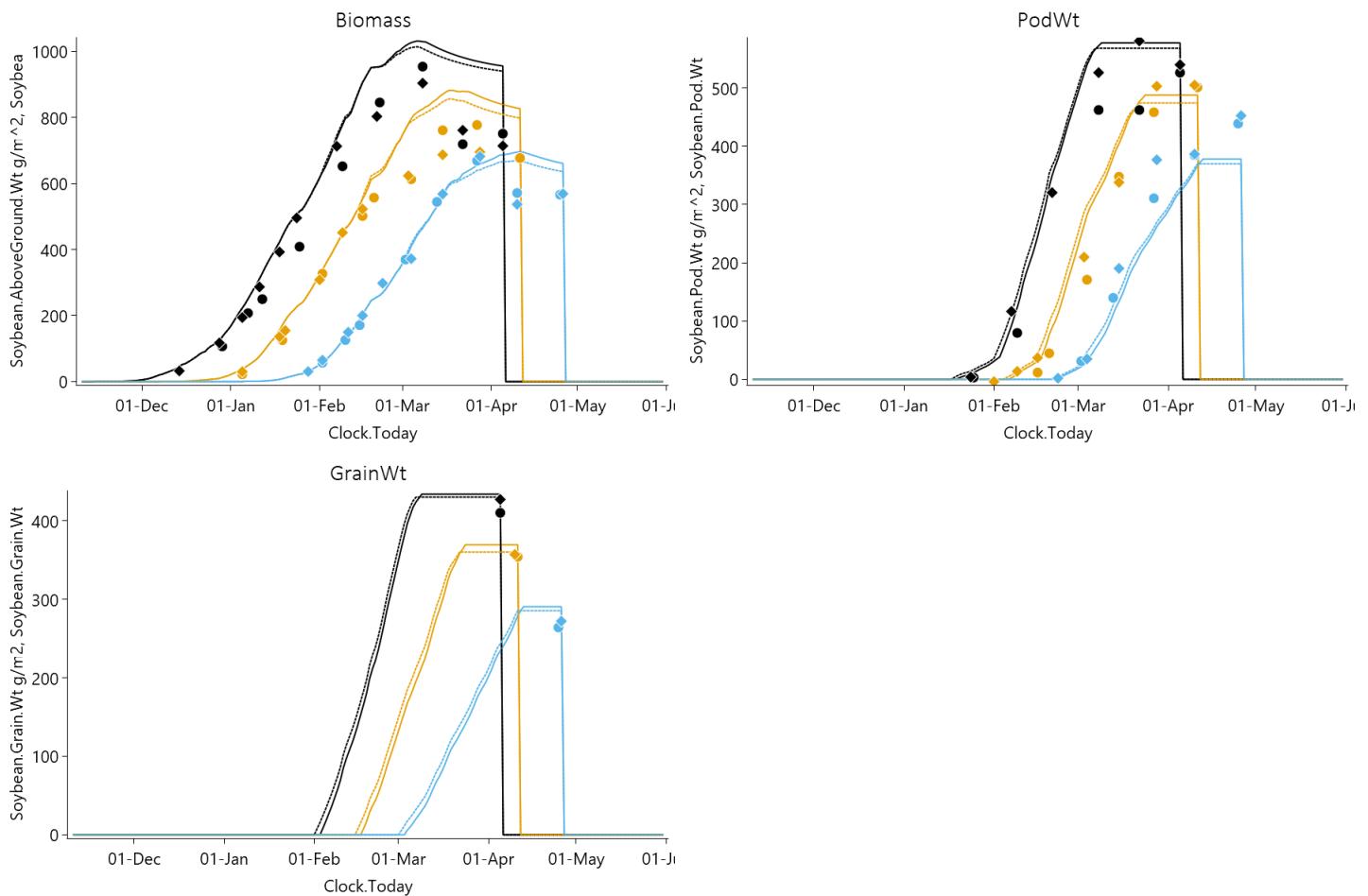
These data [Timsina et al., 2007](#) were obtained from a field experiment conducted in 1999–2000 on a Hanwood loam soil at CSIRO Land and Water, Griffith, Australia. Two indeterminate soybean cultivars (Hooper and Stephens belonging to late maturity group [MG] 3 or early MG 4) were on 15 November, 8 December, and 6 January.

#### List of experiments.

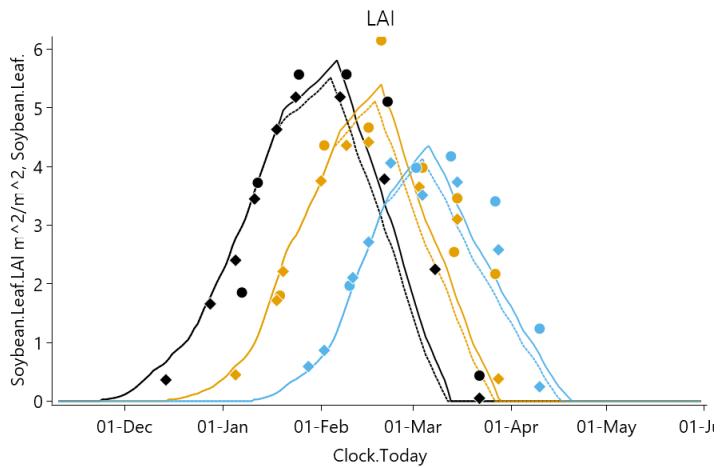
Experiment Name	Design (Number of Treatments)
Griffith	(6)

### 4.3.3.1 Griffith

#### 4.3.3.1.1 Biomass



#### 4.3.3.1.2 Canopy



### 4.3.4 Katherine

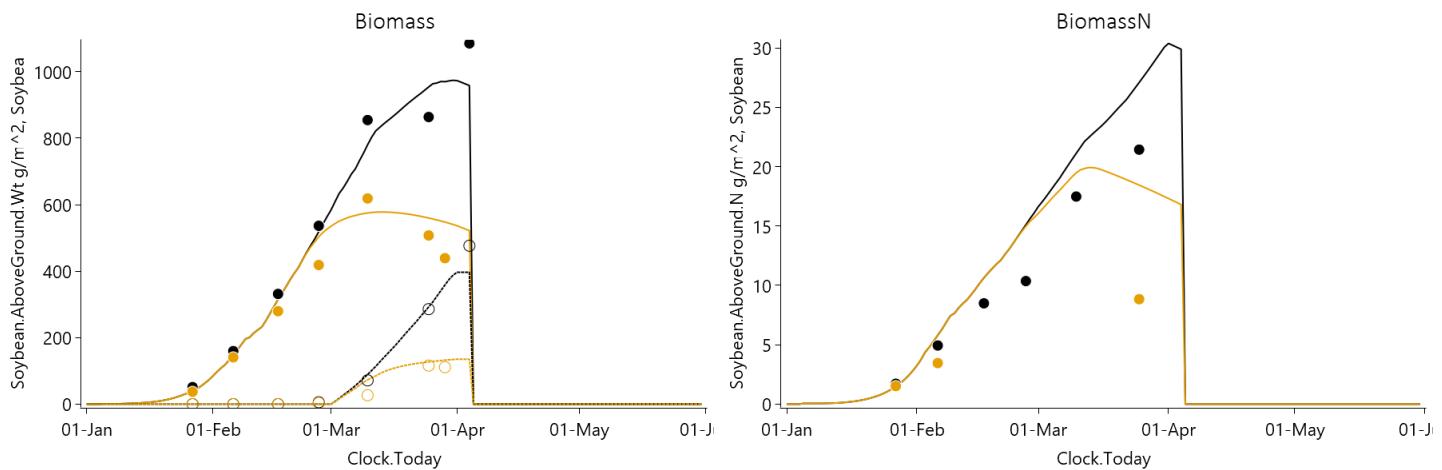
This dataset ([Muchow et al., 1993](#)) includes the cultvar "Buchanan" grown under a range of conditions in a tropical environment at the Katherine Research Station in the Northern Territory, Australia. This includes two irrigated conditions in 1988 and two planting dates in 1989.

#### List of experiments.

Experiment Name	Design (Number of Treatments)
Katherine1988	Water (2)
Katherine1989	Sow (2)

#### 4.3.4.1 Katherine1988

##### 4.3.4.1.1 Biomass



#### 4.3.5 Kununurra

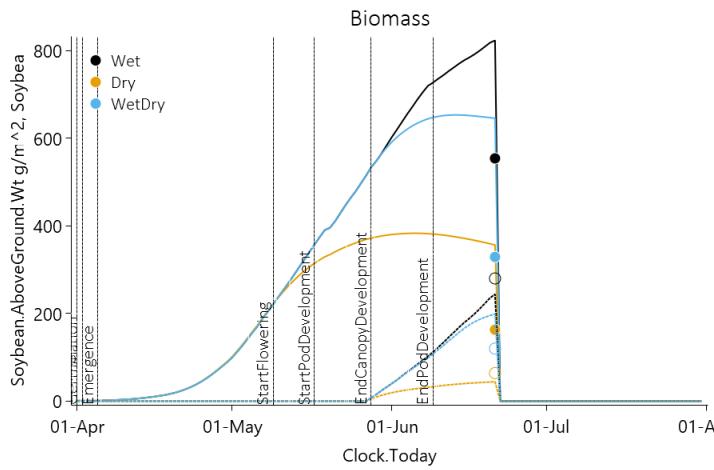
This dataset [Muchow et al., 1986](#) includes a short-season and a long-season cultivar grown on two different soil types under both irrigated and water-limited conditions in a semi-arid tropical environment at the Kimberley Research Station ( $15^{\circ} 38' S$ ,  $128^{\circ} 43' E$ ) in northern Western Australia. Crops were grown over the winter months because of the tropical location.

##### List of experiments.

Experiment Name	Design (Number of Treatments)
Kununurra1980	Water (3)
Kununurra1979	Water (3)

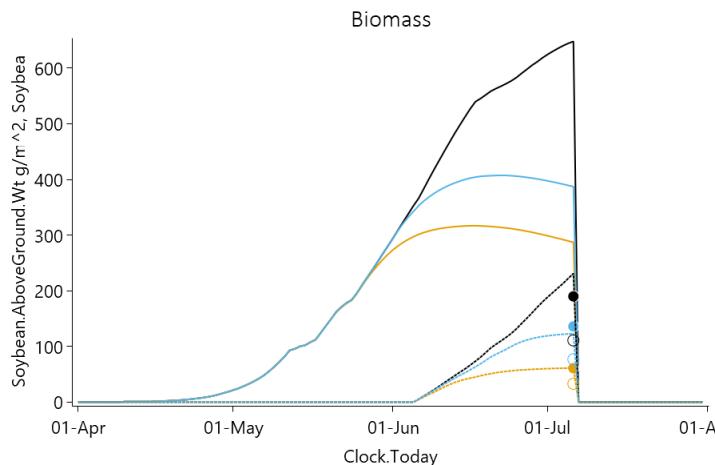
#### 4.3.5.1 Kununurra1980

##### 4.3.5.1.1 Biomass



## 4.3.5.2 Kununurra1979

### 4.3.5.2.1 Biomass

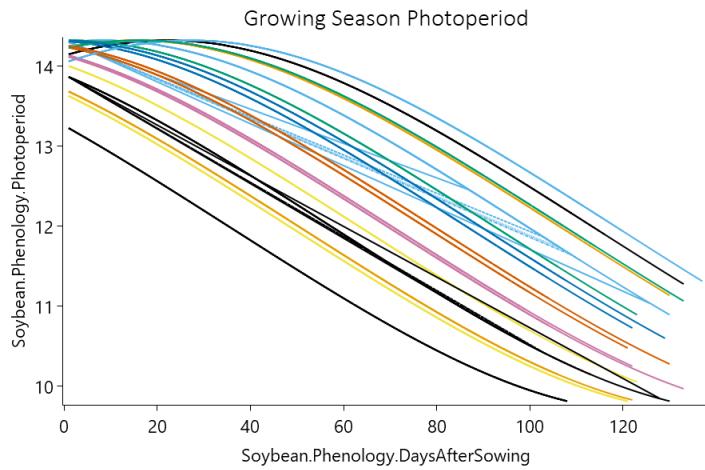


## 4.3.6 Leeton

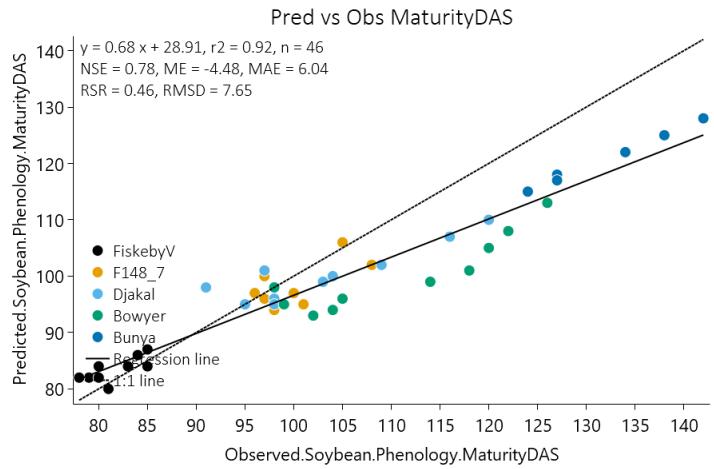
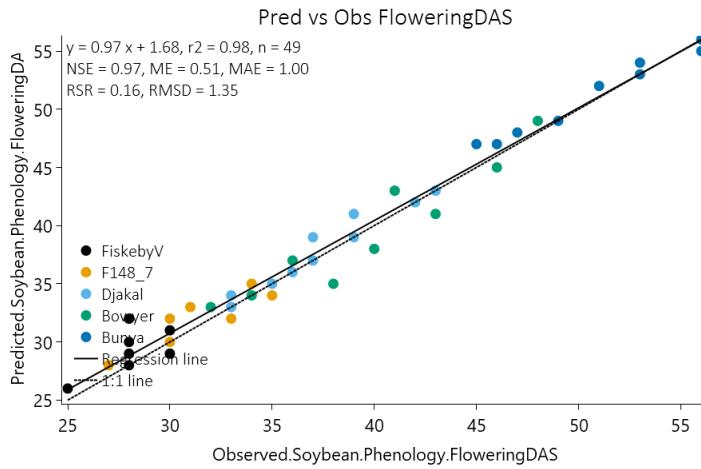
This dataset [Gaynor et al., 2011](#) is derived from a small-plot serial sowing date study were conducted over the summers of 2006–07 and 2007–08, at the NSW Department of Primary Industries' Leeton Field Station, New South Wales, Australia (348280S, 1468250E). The soil was a grey self-mulching clay, described as a Vertosol under the Australian Soil Classification. Ten diverse soybean genotypes ranging from very early to very late maturity were grown with 10 sowing dates in the first season and 9 in the second.

### List of experiments.

Experiment Name	Design (Number of Treatments)
Leeton2006	(50)
Leeton2007	(45)

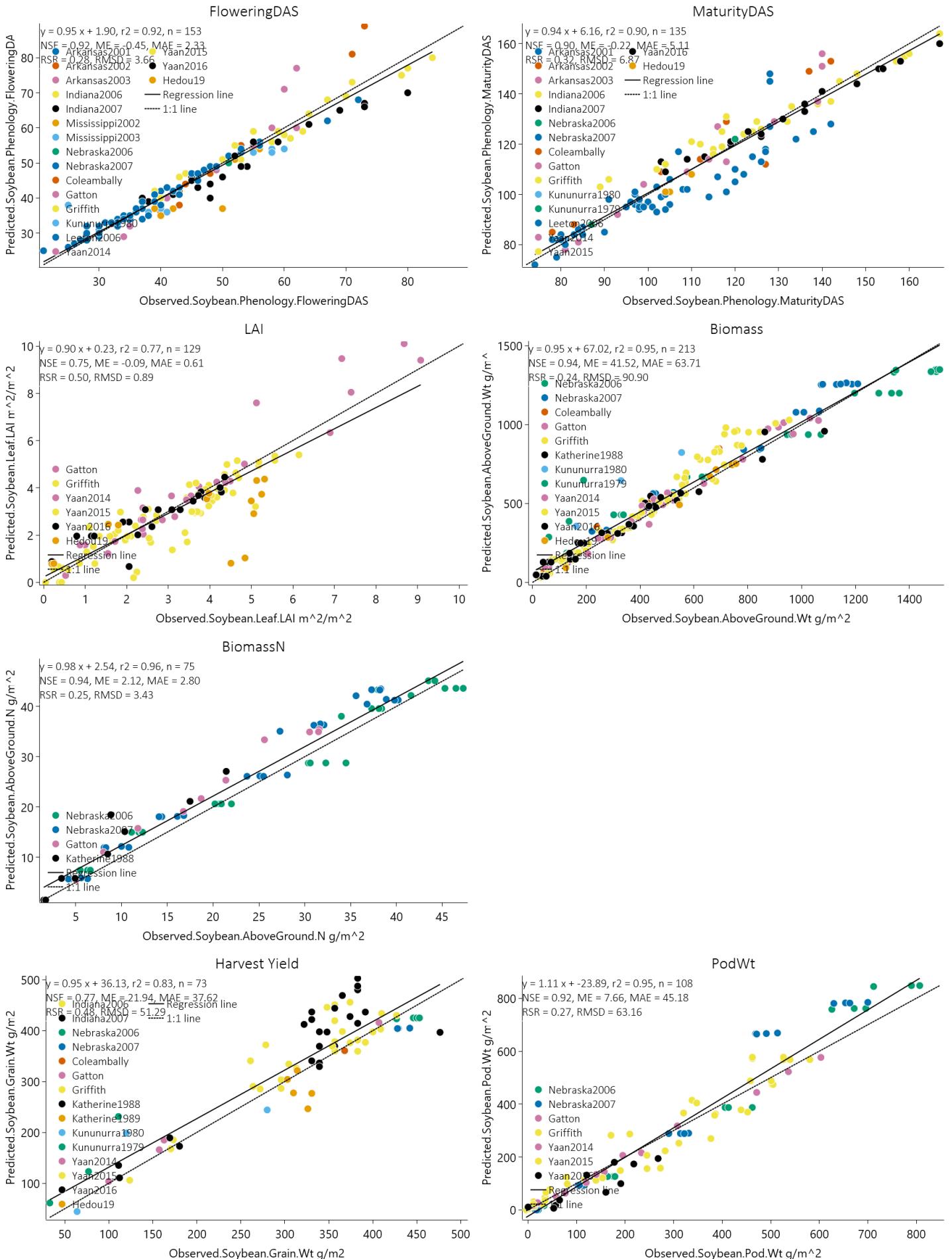


#### 4.3.6.1 Phenology



#### 4.4 Combined Results

Simulation results for the combined datasets from the various countries are shown in the following graphs. The model is able to adequately capture the influence of growing conditions (soil, climate) and management (population, Nitrogen, irrigation, sowing date).



## 4.5 China

### 4.5.1 Yaan

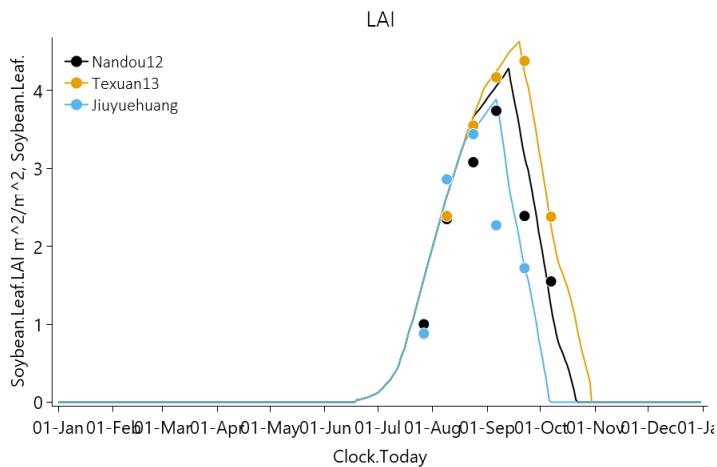
These data [Wu2019] were obtained from a field experiment conducted in 2014–2016 on a Purple clay loam(XI-Luvic Xerosols, FAO classification) at Sichuan Agricultural University, Yaan, China. Three soybean cultivars (Jiuyuehuang,Nandou12, and Texuan13 belonging to maturity group [MG] 5-7 ) were sown on 15 Jun 2014, 18 Jun 2015, and 18 Jun 2016.

#### List of experiments.

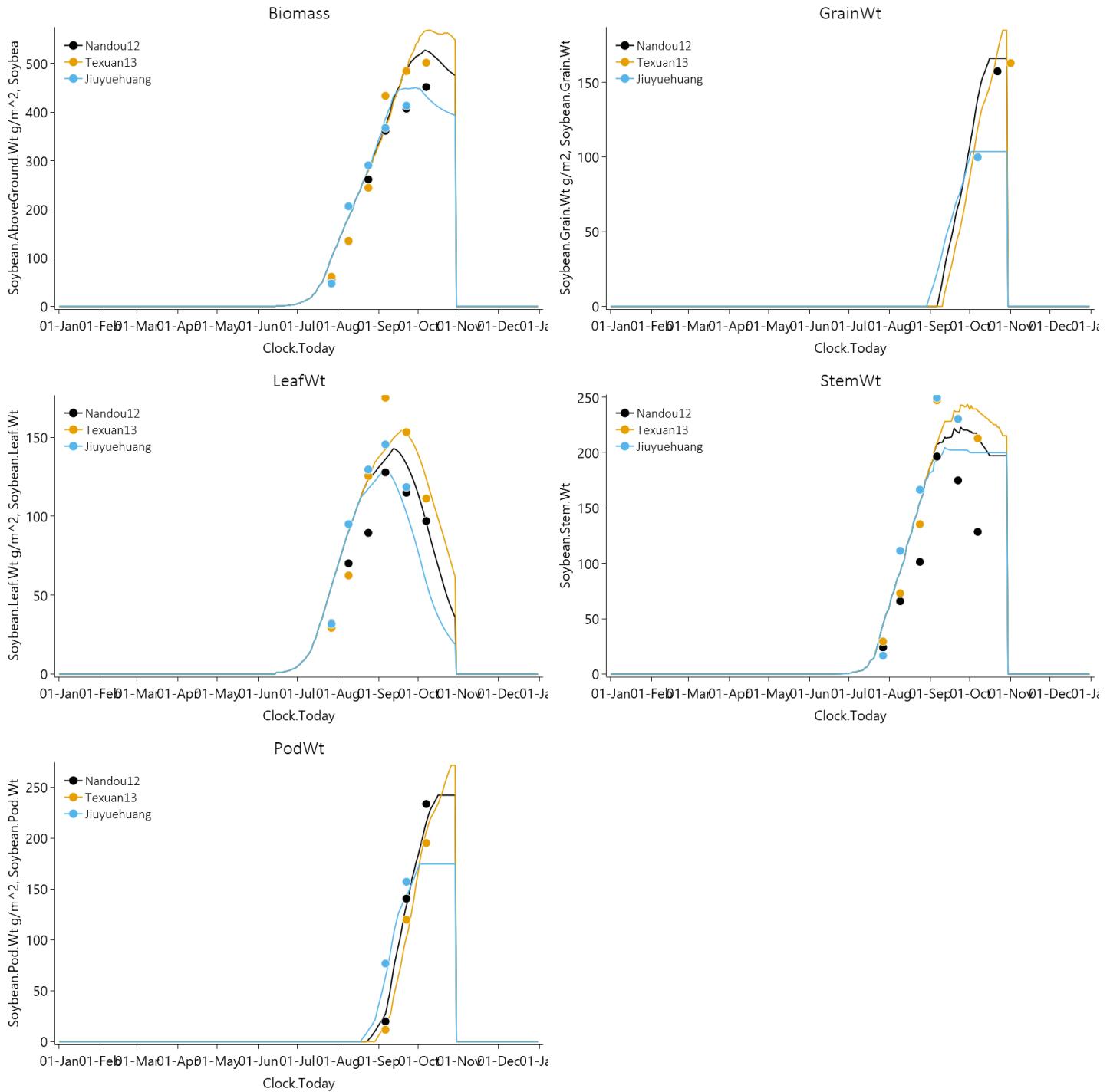
Experiment Name	Design (Number of Treatments)
Yaan2014	Cv (3)
Yaan2015	Cv (3)
Yaan2016	Cv (3)

#### 4.5.1.1 Yaan2014

##### 4.5.1.1.1 Canopy

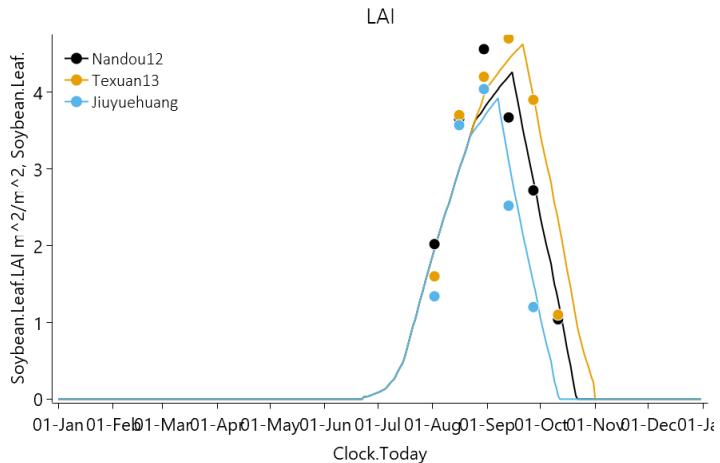


#### 4.5.1.1.2 Biomass

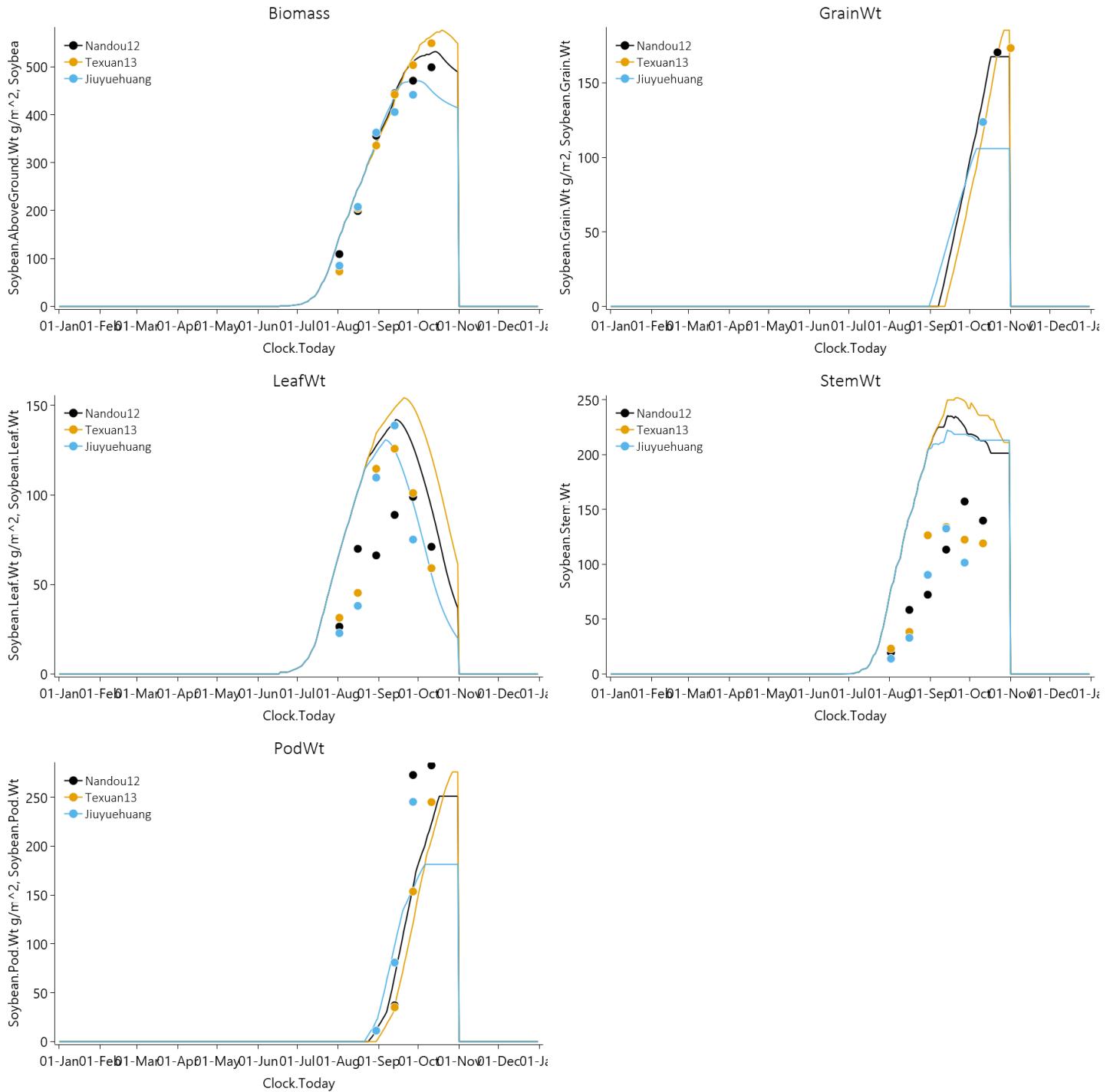


#### 4.5.1.2 Yaan2015

##### 4.5.1.2.1 Canopy

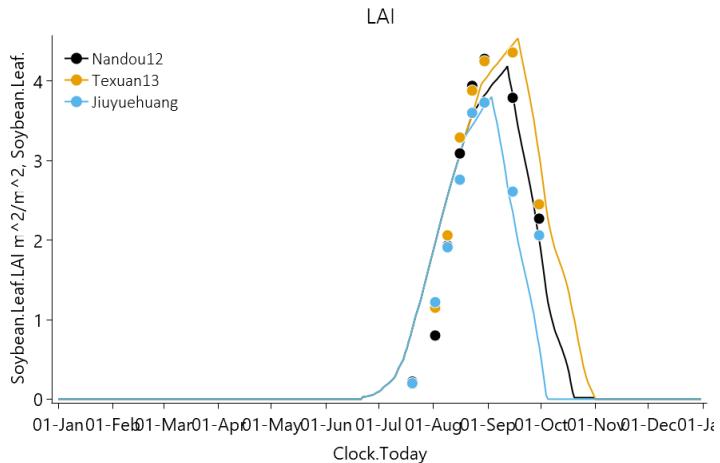


#### 4.5.1.2.2 Biomass

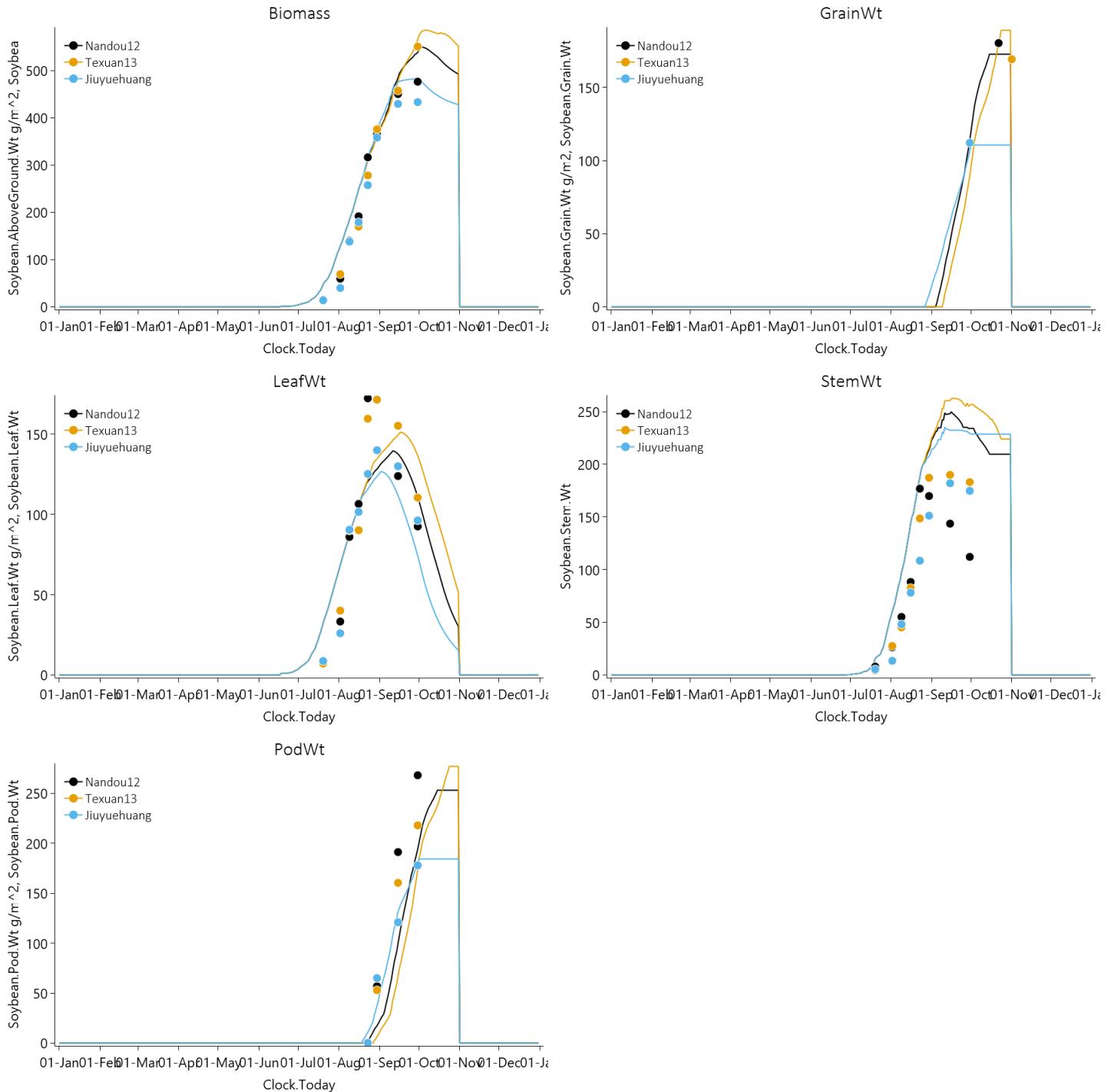


#### 4.5.1.3 Yaan2016

##### 4.5.1.3.1 Canopy

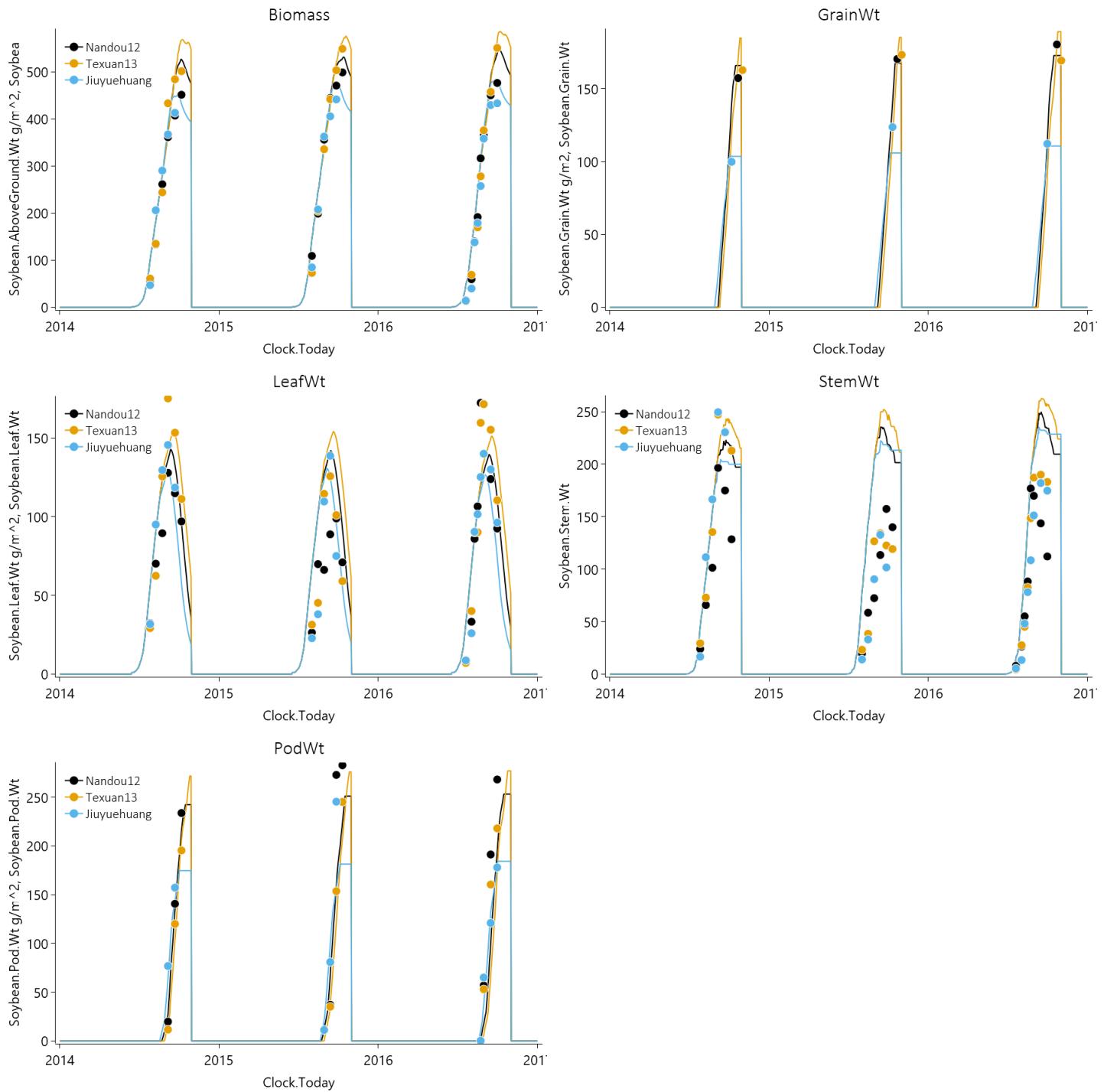


#### 4.5.1.3.2 Biomass

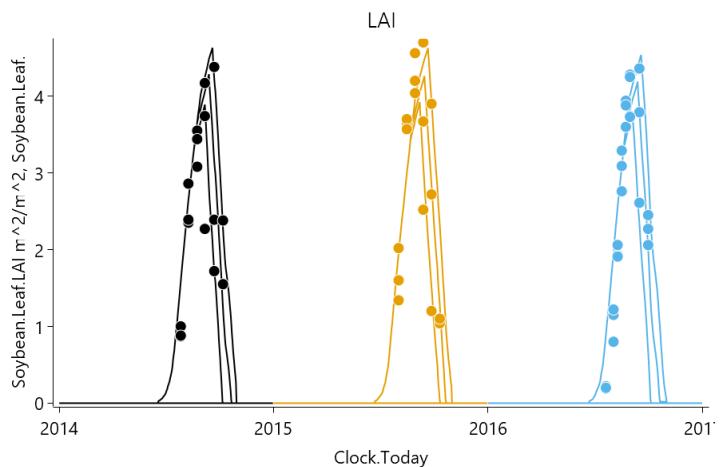


## 4.5.1.4 Graphs

### 4.5.1.4.1 Biomass



### 4.5.1.4.2 Canopy



## 4.5.2 Heze

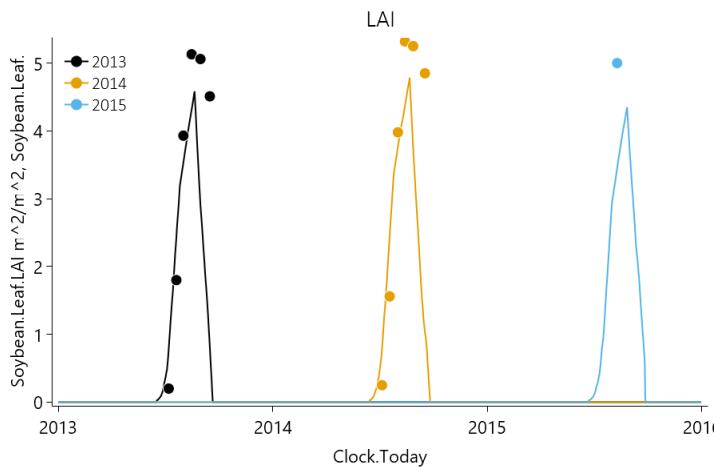
These data [Wu2019] were obtained from a field experiment conducted in 2013–2015 on sandy loam (J-Fluvisols, FAO classification) in the surface 0.5 m, changing to loam at depth with a deep soil profile (> 2 m) in Heze city, China. One soybean cultivar (Hedou19 belonging to maturity group [MG]3) were sown on 15 Jun 2014, 18 Jun 2015, and 18 Jun 2016.

### List of experiments.

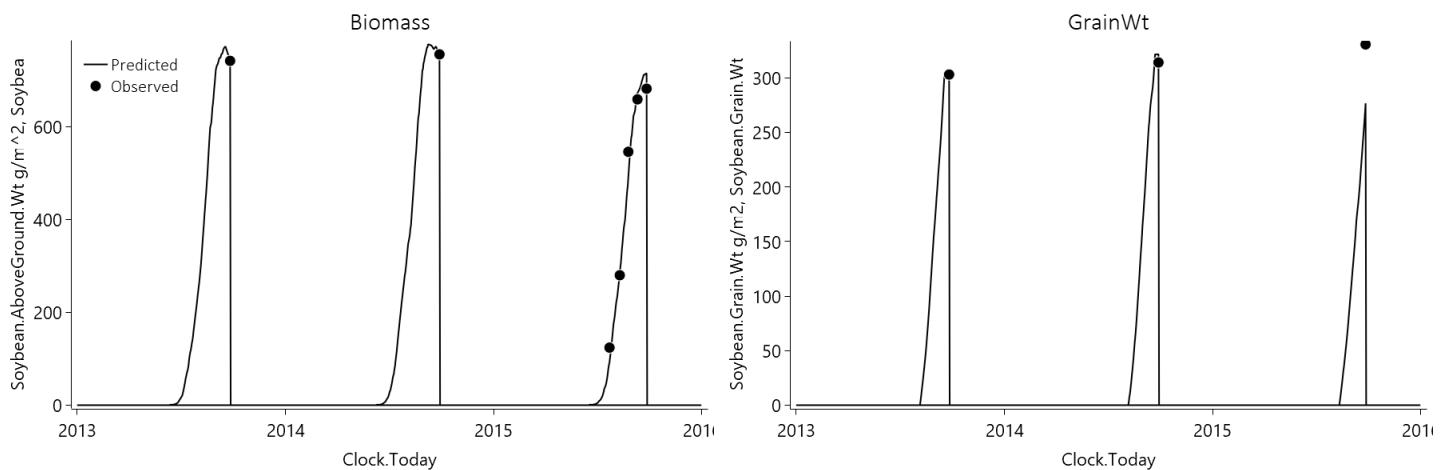
Experiment Name	Design (Number of Treatments)
Hedou19	Sow (3)

### 4.5.2.1 Hedou19

#### 4.5.2.1.1 Canopy

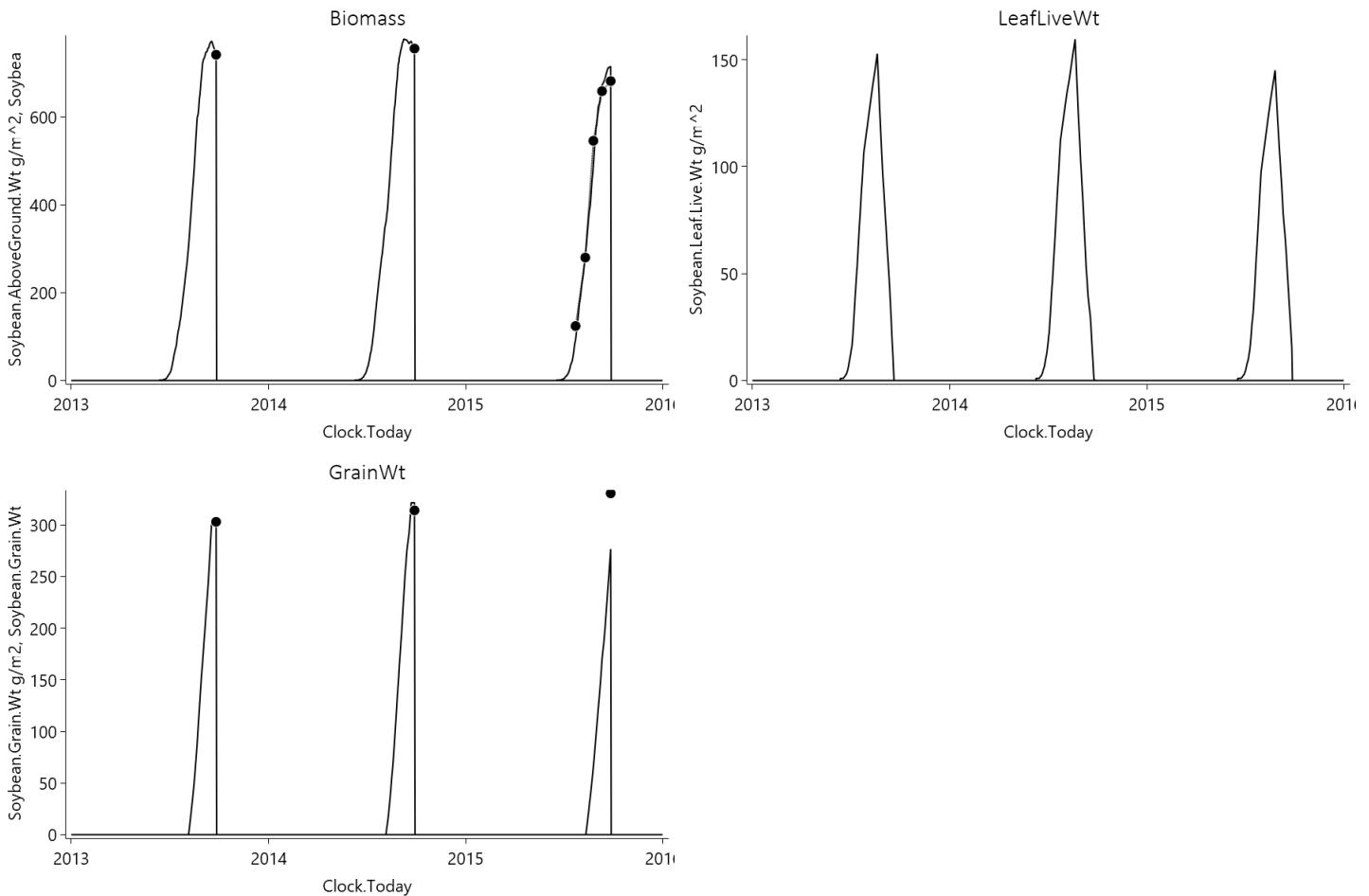


#### 4.5.2.1.2 Biomass

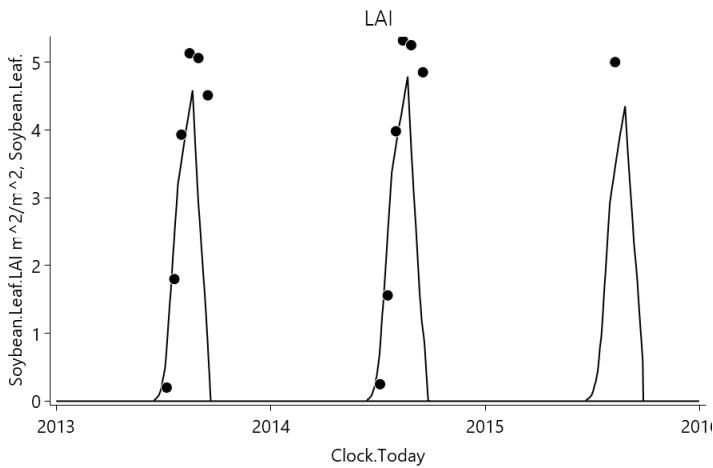


## 4.5.2.2 Graphs

### 4.5.2.2.1 Biomass



### 4.5.2.2.2 Canopy



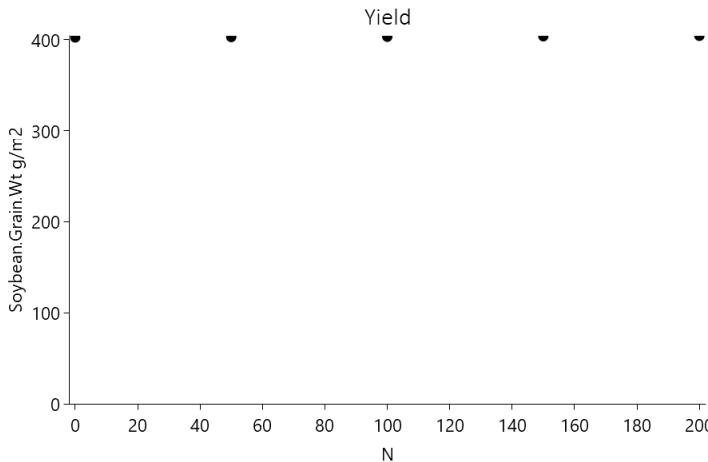
## 5 Sensibility

### 5.1 FertiliserResponse

This sensibility test checks that Soybean yield response to N fertiliser is modest under normal field conditions. A simulation experiment has been constructed to simulate yield in Nebraska for different rates of N applied at sowing. Yield variation in response to this should be low.

#### List of experiments.

Experiment Name	Design (Number of Treatments)
FertiliserResponse	N (5)

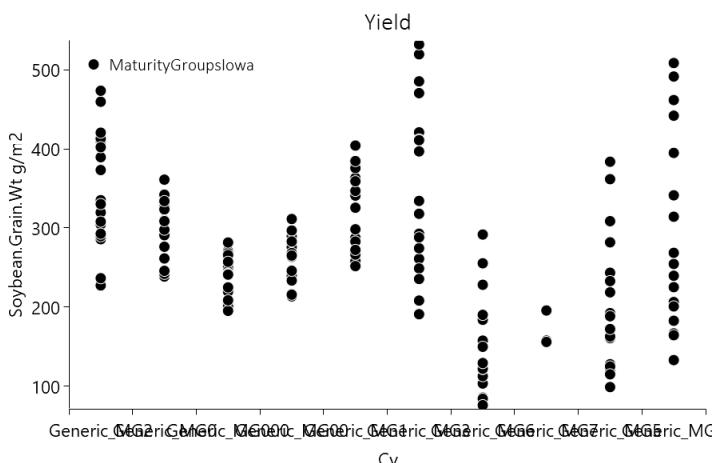


## 5.2 MaturityGroups

The optimum maturity class for soybean in Iowa should be approximately 2 to 3. Simulations are provided for the entire range of generic cultivars for several years at Ames, Iowa.

## List of experiments.

Experiment Name	Design (Number of Treatments)
MaturityGroupsIowa	Cv (13)

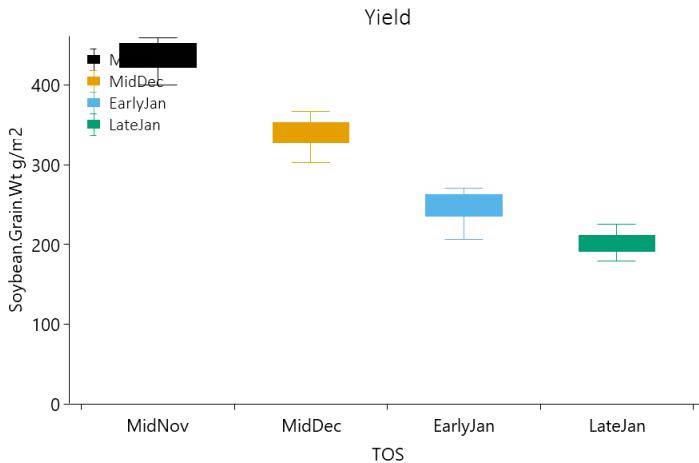


### 5.3 TimeOfSowing

The data of [Gaynor et al., 2011](#) show that Soybean yield should be approximately 4t/ha for early sown soybean (Mid November) in the Australian Riverina region and decrease across the growing season to lower values (1.5-2t/ha) by late January.

## List of experiments.

Experiment Name	Design (Number of Treatments)
TimeOfSowingGriffith	TOS (4)



## 6 References

- Brown, Hamish E., Huth, Neil I., Holzworth, Dean P., Teixeira, Edmar I., Zyskowski, Rob F., Hargreaves, John N. G., Moot, Derrick J., 2014. Plant Modelling Framework: Software for building and running crop models on the APSIM platform. *Environmental Modelling and Software* 62, 385-398.
- Edwards, J.T., Purcell, L.C., 2005. Soybean yield and biomass responses to increasing plant population among diverse maturity groups: I. Agronomic characteristics. *Crop Science* 45, 1770-1777.
- Gaynor, L.G., Lawn, R.J., James, A.T., 2011. Agronomic studies on irrigated soybean in southern New South Wales. I. Phenological adaptation of genotypes to sowing date. *Crop & Pasture Science* 62, 1056-1066.
- Holzworth, Dean P., Huth, Neil I., deVoil, Peter G., Zurcher, Eric J., Herrmann, Neville I., McLean, Greg, Chenu, Karine, van Oosterom, Erik J., Snow, Val, Murphy, Chris, Moore, Andrew D., Brown, Hamish, Whish, Jeremy P. M., Verrall, Shaun, Fainges, Justin, Bell, Lindsay W., Peake, Allan S., Poulton, Perry L., Hochman, Zvi, Thorburn, Peter J., Gaydon, Donald S., Dalgliesh, Neal P., Rodriguez, Daniel, Cox, Howard, Chapman, Scott, Doherty, Alastair, Teixeira, Edmar, Sharp, Joanna, Cichota, Rogerio, Vogeler, Iris, Li, Frank Y., Wang, Enli, Hammer, Graeme L., Robertson, Michael J., Dimes, John P., Whitbread, Anthony M., Hunt, James, van Rees, Harm, McClelland, Tim, Carberry, Peter S., Hargreaves, John N. G., MacLeod, Neil, McDonald, Cam, Harsdorf, Justin, Wedgwood, Sara, Keating, Brian A., 2014. APSIM – Evolution towards a new generation of agricultural systems simulation. *Environmental Modelling and Software* 62, 327-350.
- 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. *European Journal of Agronomy* 18 (3-4), 267-288.
- McCown, R. L., Hammer, G. L., Hargreaves, J. N. G., Holzworth, D., Huth, N. I., 1995. APSIM: an agricultural production system simulation model for operational research. *Mathematics and Computers in Simulation* 39 (3-4), 225-231.
- McCown, R. L., Hammer, G. L., Hargreaves, J. N. G., Holzworth, D. P., Freebairn, D. M., 1996. APSIM: a Novel Software System for Model Development, Model Testing and Simulation in Agricultural Systems Research. *Agricultural Systems* 50 (3), 255-271.
- Monteith, J. L., Moss, C. J., 1977. Climate and the Efficiency of Crop Production in Britain [and Discussion]. *Philosophical Transactions of the Royal Society of London. Series B, Biological Sciences* 281 (980), 277-294.
- Muchow, R.C., Sinclair, T.R., 1986. Agronomic studies on irrigated soybean in southern New South Wales. I. Phenological adaptation of genotypes to sowing date. *Field Crops Research* 15, 143-156.
- Muchow, R.C., Robertson, M.J., Pengelly, B.C., 1993. Accumulation and partitioning of biomass and nitrogen by soybean, mungbean and cowpea under contrasting environmental conditions. *Field Crop Research* 33, 13-36.
- Reyenga, P.J., Howden, S. M., Meinke, H., McKeon, G.M., 1999. Modelling global change impacts on wheat cropping in south-east Queensland, Australia. *Environmental Modelling & Software* 14, 297-306.
- Robinson, A.P., Conley, S.P., Volenec, J.J., Santini, J.B., 2009. Analysis of high yielding, early-planted soybean in Indiana. *Agronomy Journal* 101, 131-139.

Salvagiotti, F., Specht, J.E., Cassman, K.G., Walters, D.T., Weis, A., Dobermann, A., 2009. Growth and N fixation in high yielding soybean: impact if N fertilization. *Agronomy Journal* 101, 958-970.

Timsina,J., Boote,K.J., Duffield,S., 2007. Evaluating the CROPGRO Soybean Model for Predicting Impacts of Insect Defoliation and Depodding. *Agronomy Journal* 99, 148-157.

Zhang, L., Zhang, J., Kyei-Boahen, S., 2004. Developing phenological prediction tables for soybean.. *Crop Management*.