Preliminary models for a developing tomato plants and trusses

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Keygene

- Founded about 20 years ago by plant breeding companies
- Currently 120 employees
- What we do: develop and provide, technologies, to help plant breeders
  - Molecular markers (AFLP, SNP's, …)
  - Whole genome sequencing,
  - Whole genome profiling
  - lead discovery,
  - genetic analysis,
  - phenotyping (image analysis),
  - software development,
  - Targeted mutagenesis
  - …

Why modelling

- To get an insight in the processes relevant during the development of tomato plant and truss.
- This will lead to way to design experiments.

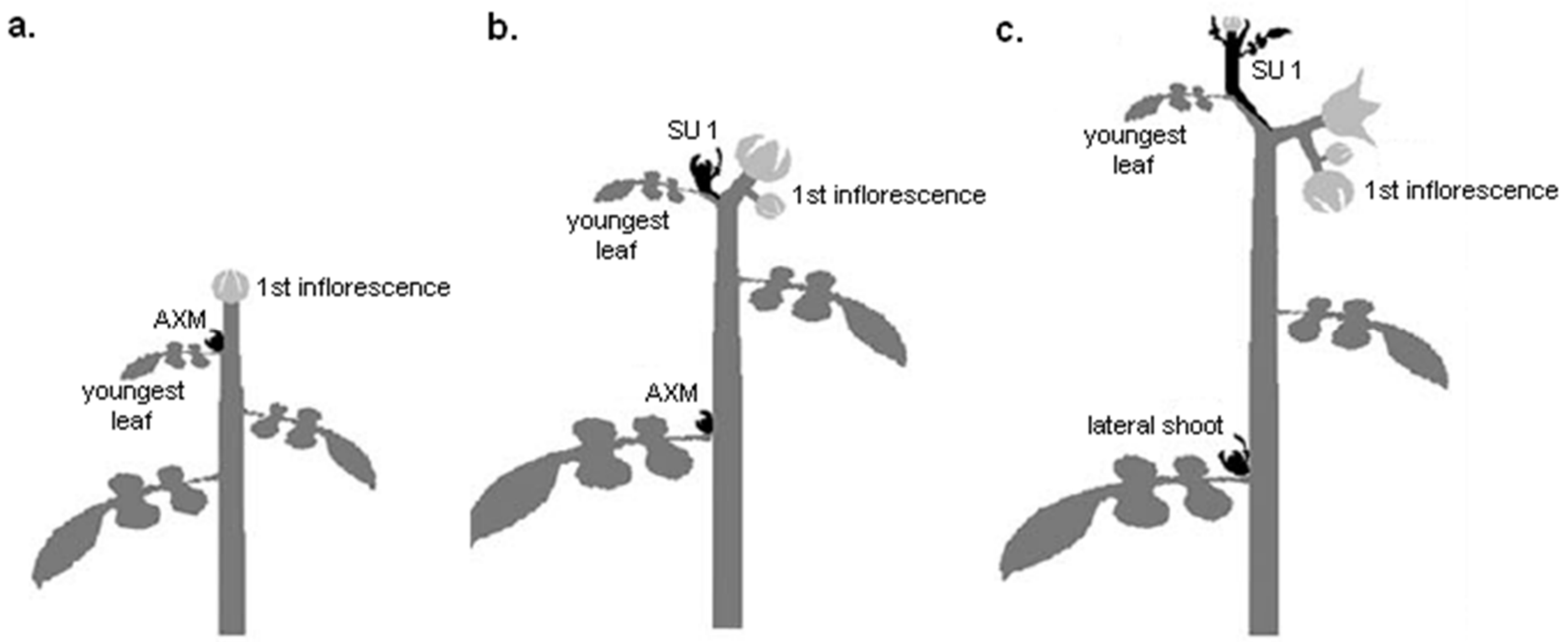
- In turn → better insights → explore scenario's →better models → better insights → better models etc.

- ➔ Identify breedable / interesting genes.

- Also: optimize control of environment (light: (type, amount, ..), water uptake, but also pruning, etc.).

Tomato development

-



- Tomato truss
  - Growth strategy:?
  - very varied in shape

Tomato trusses

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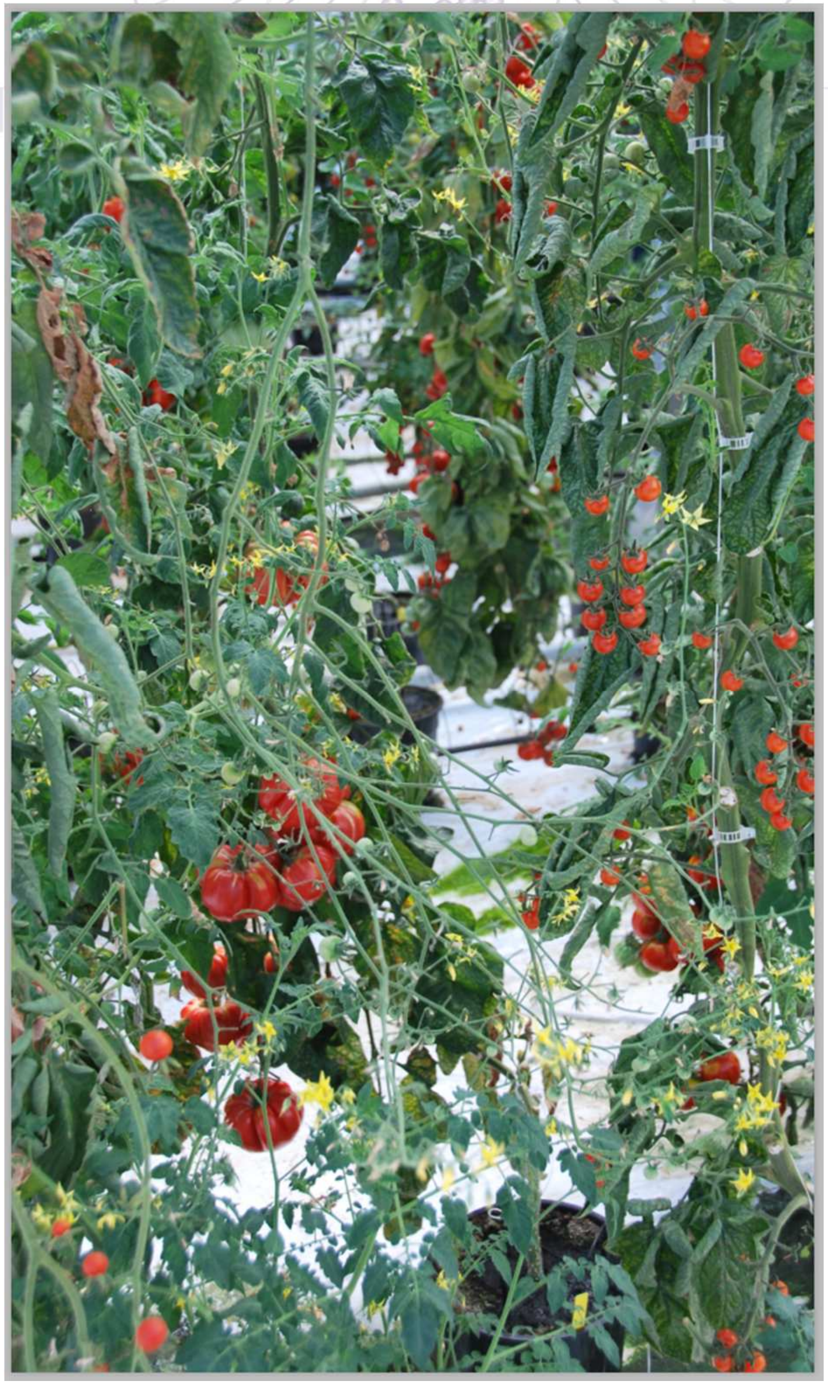


Tomato trusses

Tomato trusses

Tomato trusses

Tomato trusses

Genes involved in flowering and truss shapes

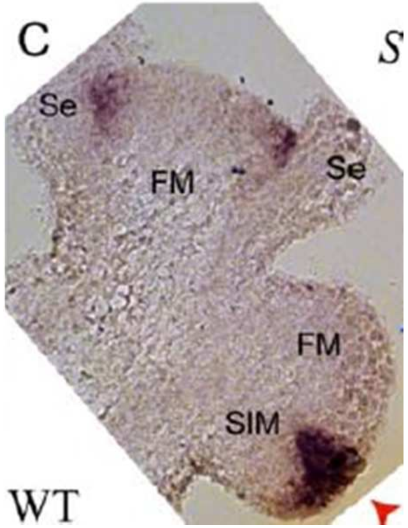
- Involved genes:

SFT -	florigen, makes it flowering
S-mutants	heavily branched trusses
FA-mutants	flower → leaves
J-mutants	no pedicel, latered truss
SP-mutants	growth terminats early
AN-mutants	cauliflower like truss
F-mutants	branching trusses
UF-mutants	small number flowers
…	

  - If and how interacting: ???

Gene expression data

- Very limited
- Data such as:



Goal – of model

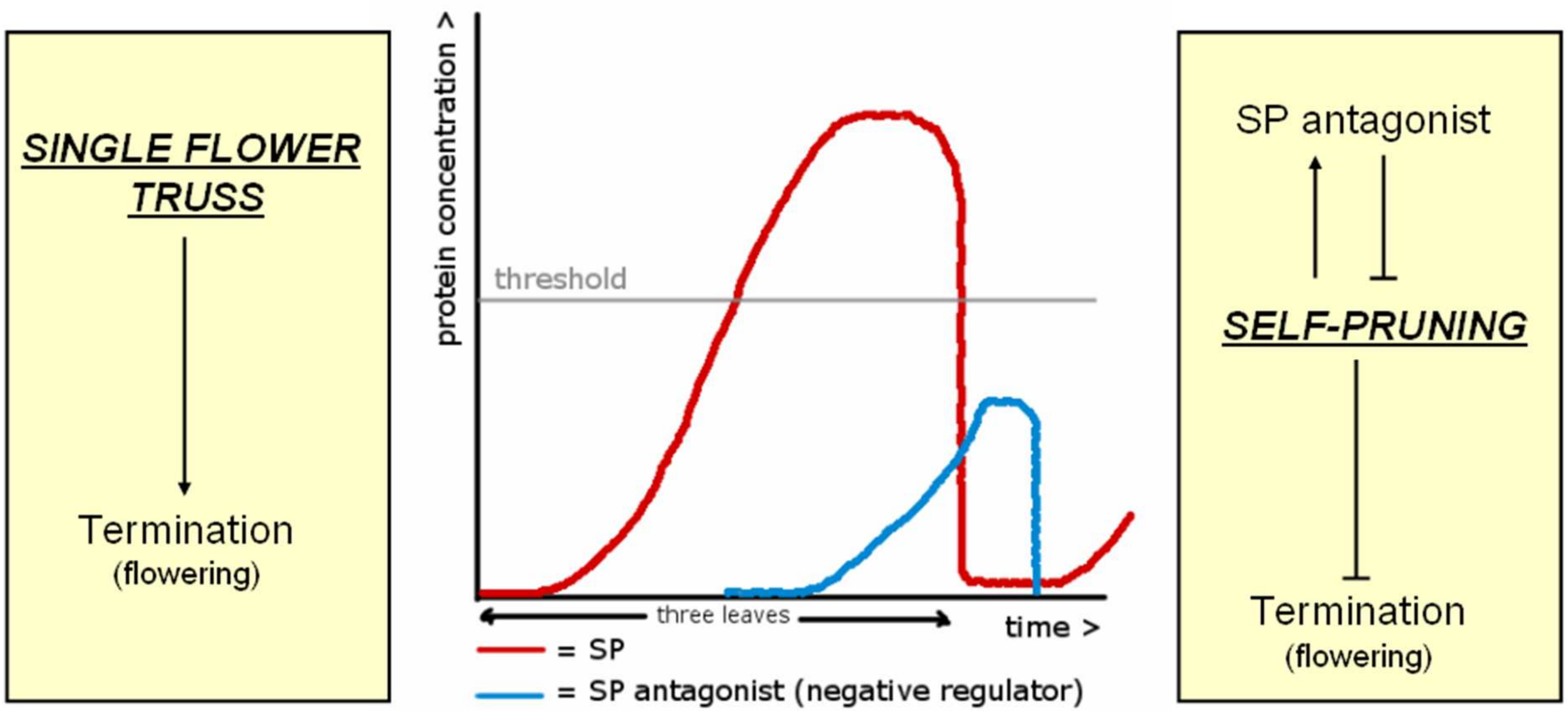
- Gaining insight in the developments during and leading up to flowering, by combining the genetic data with gene expression data en morphological observation.

- At the moment is a lot of trial and error.

- Models are very much “work in progress”.

Modeling – tomato plant

- Focus on switch to flowering



SINGLE FLOWER TRUSS

Termination
(flowering)

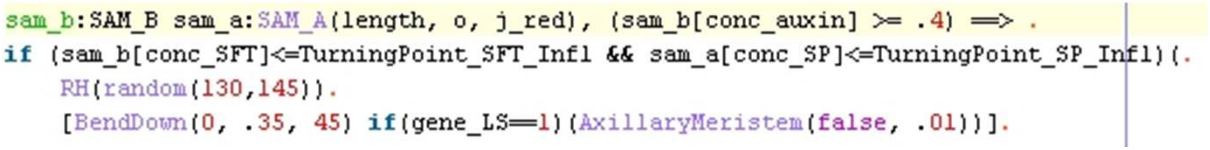
SP antagonist

SELF-PRUNING

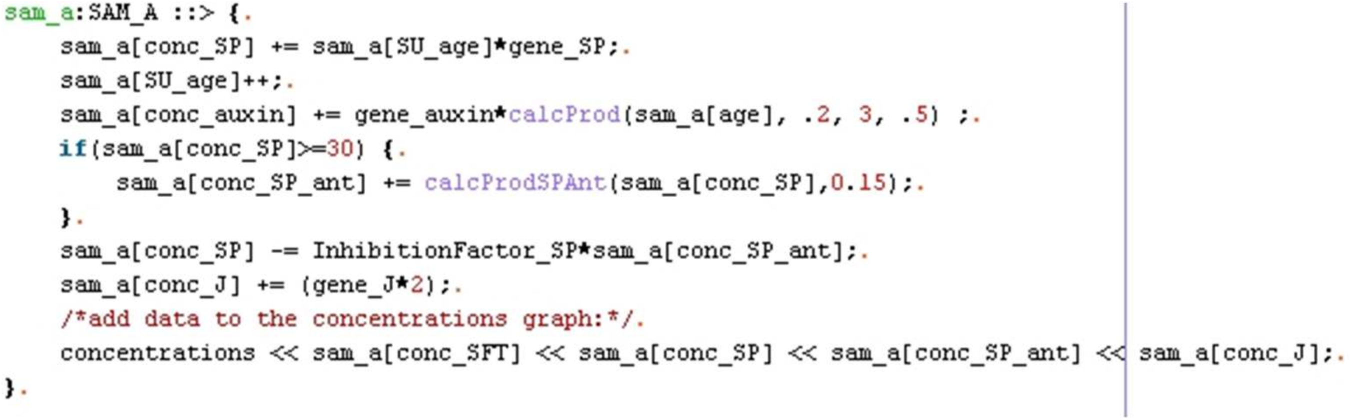
Termination
(flowering)

Modeling – tomato plant

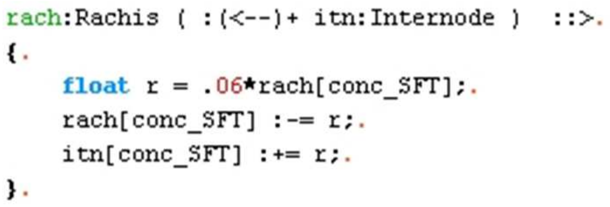
- GroIMP code



```
sam_b:SAM_B sam_a:SAM_A(length, o, j_red), (sam_b[conc_auxin] >= .4) ==> 
if (sam_b[conc_SFT]<=TurningPoint_SFT_Infl && sam_a[conc_SP]<=TurningPoint_SP_Infl)(
    RH(random(130,145))
    [BendDown(0, .35, 45) if(gene_LS==1)(AxillaryMeristem(false, .01))]
```



```
sam_a:SAM_A ::> {
    sam_a[conc_SP] += sam_a[SU_age]*gene_SP;
    sam_a[SU_age]++;
    sam_a[conc_auxin] += gene_auxin*calcProd(sam_a[age], .2, 3, .5) ;
    if(sam_a[conc_SP]>=30) {
        sam_a[conc_SP_ant] += calcProdSPAnt(sam_a[conc_SP],0.15);
    }
    sam_a[conc_SP] -= InhibitionFactor_SP*sam_a[conc_SP_ant];
    sam_a[conc_J] += (gene_J*2);
    /*add data to the concentrations graph:*/
    concentrations << sam_a[conc_SFT] << sam_a[conc_SP] << sam_a[conc_SP_ant] << sam_a[conc_J];
}
```



```
rach:Rachis ( :(<--)+ itn:Internode )  ::>
{
    float r = .06*rach[conc_SFT];
    rach[conc_SFT] :-= r;
    itn[conc_SFT] :+= r;
}
```

Modeling – tomato p

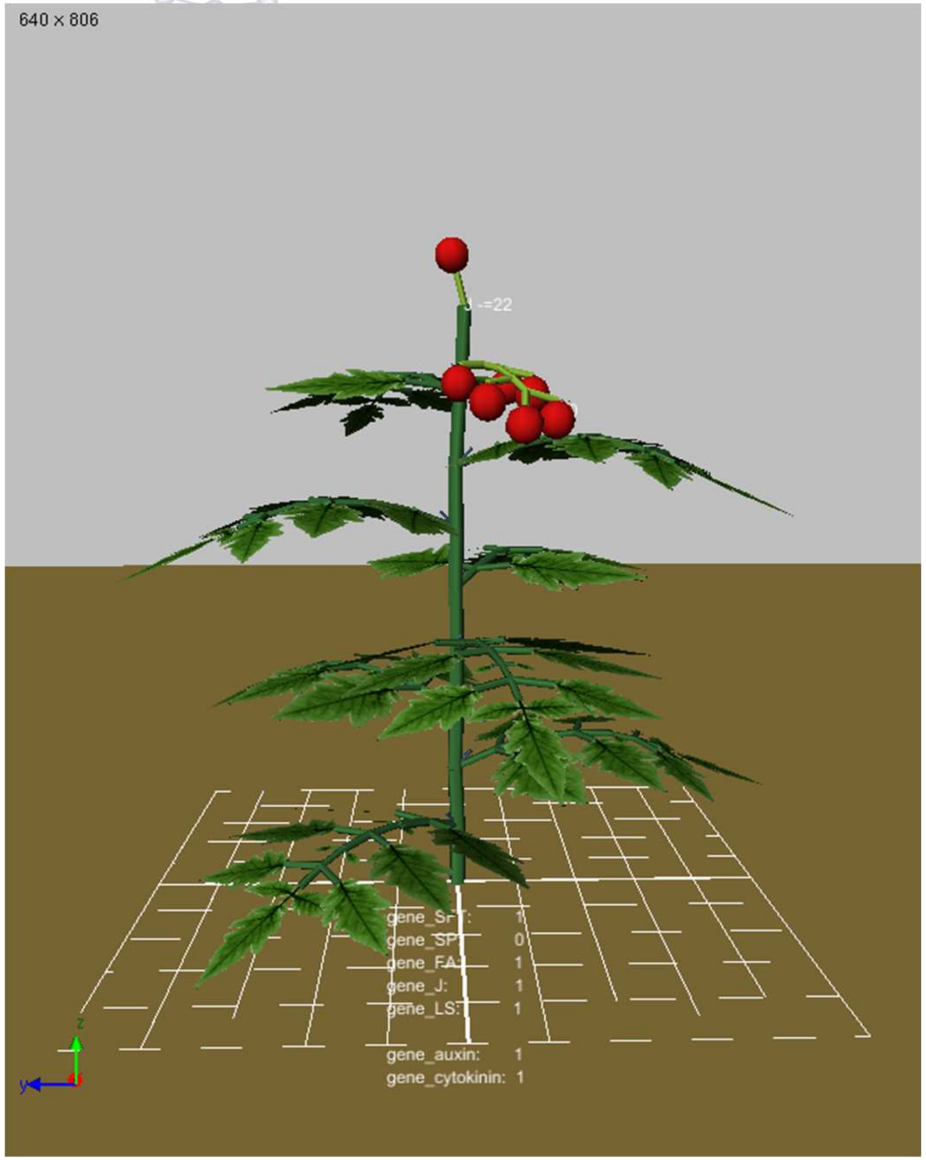
- Wild type

```
gene_SFT:       1
gene_SP:        1
gene_FA:        1
gene_J:         1
gene_LS:        1

gene_auxin:     1
gene_cytokinin: 1
```

Modeling – tomato plant

- SP mutant

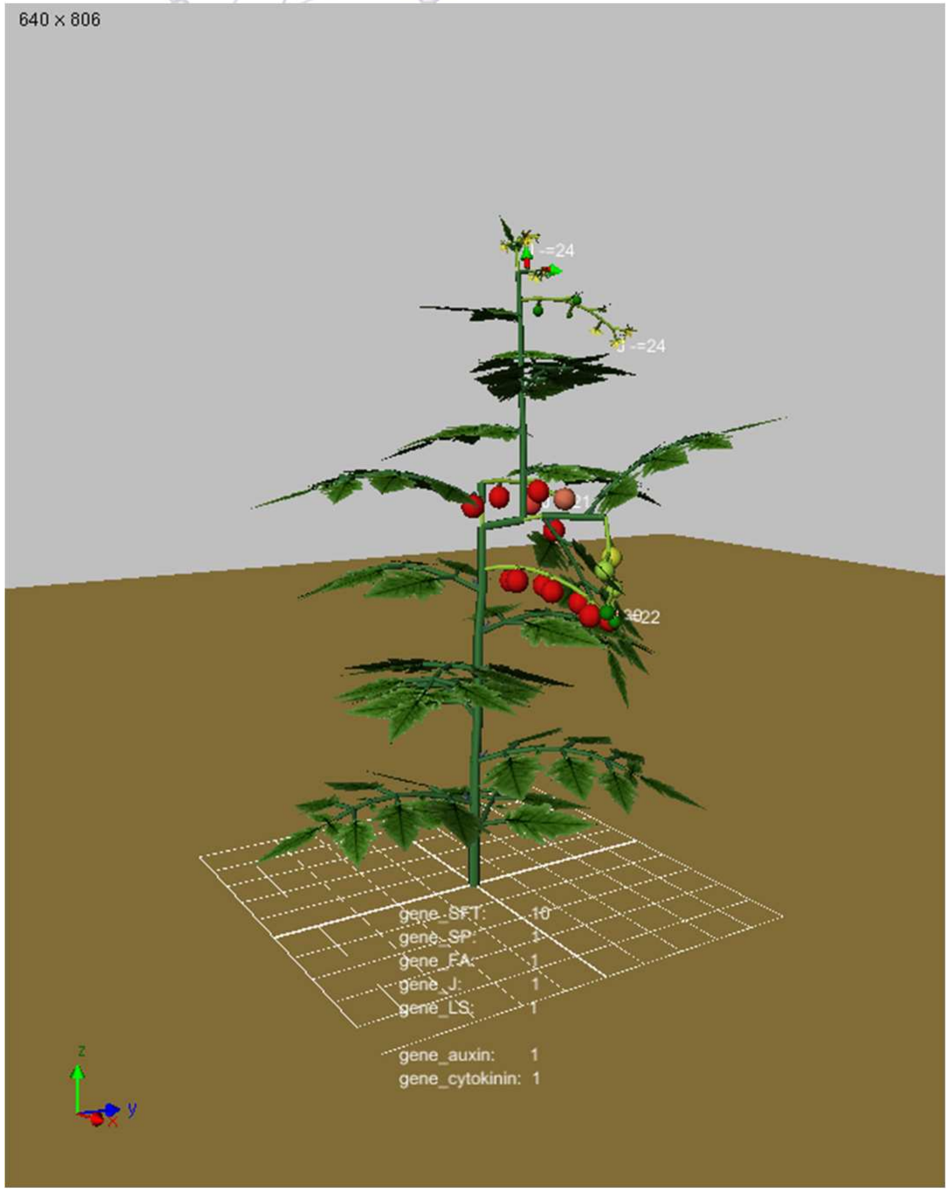


gene_SFT: 1
gene_SP: 0
gene_FA: 1
gene_J: 1
gene_LS: 1

gene_auxin: 1
gene_cytokinin: 1

Modeling – tomato plant

- SFT overexpression



```
gene_SFT:        10
gene_SP:         1
gene_FA:         1
gene_J:          1
gene_LS:         1

gene_auxin:      1
gene_cytokinin:  1
```

Modeling – tomato plant

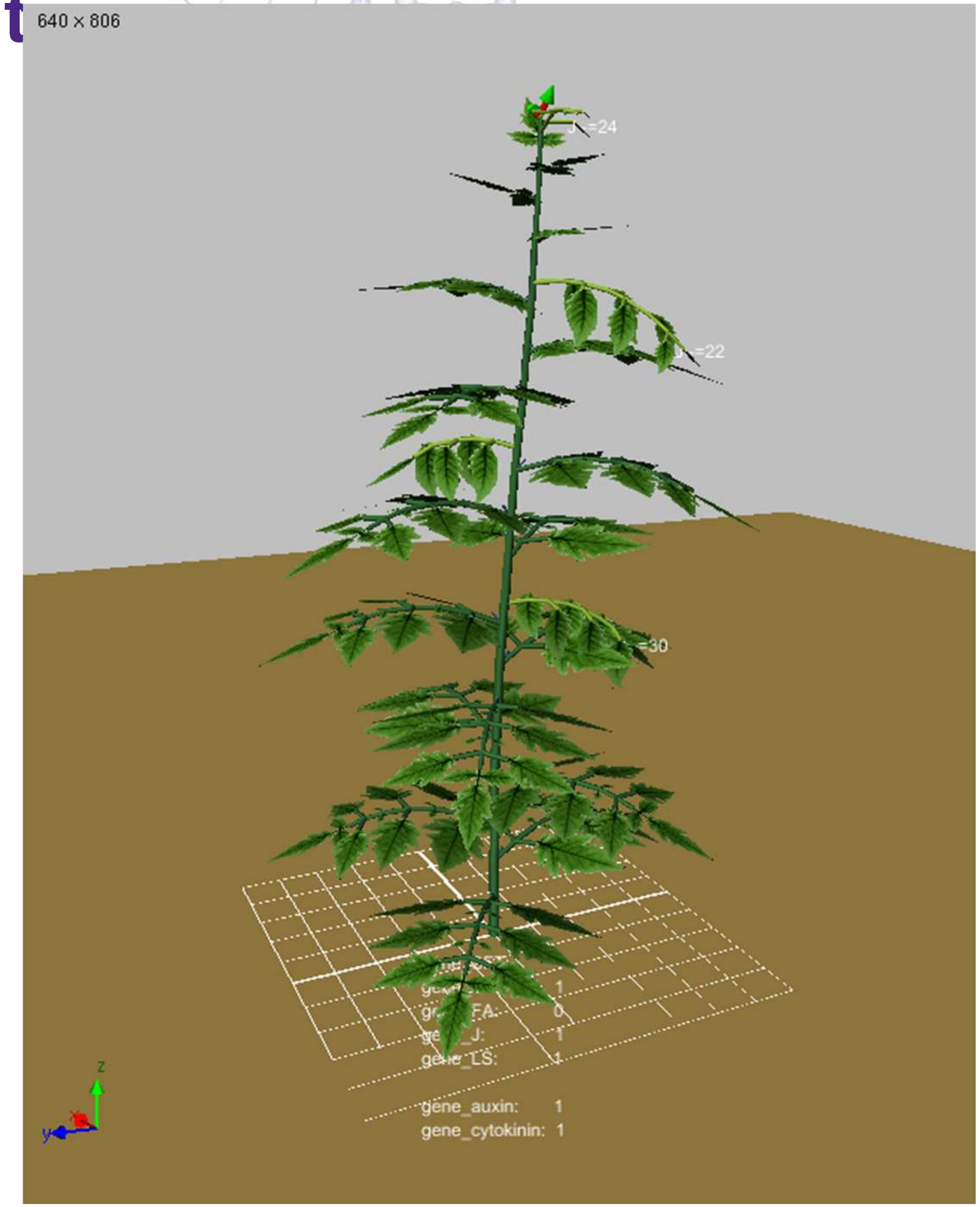
- SFT mutant

gene_SF 0
gene_SP: 1
gene_FA: 1
gene_J: 1
gene_LS: 1

gene_auxin: 1
gene_cytokinin: 1

Modeling – tomato plant

- FA mutant



Modeling – tomato plant

- Deviating inflorescence

Modeling – tomato truss

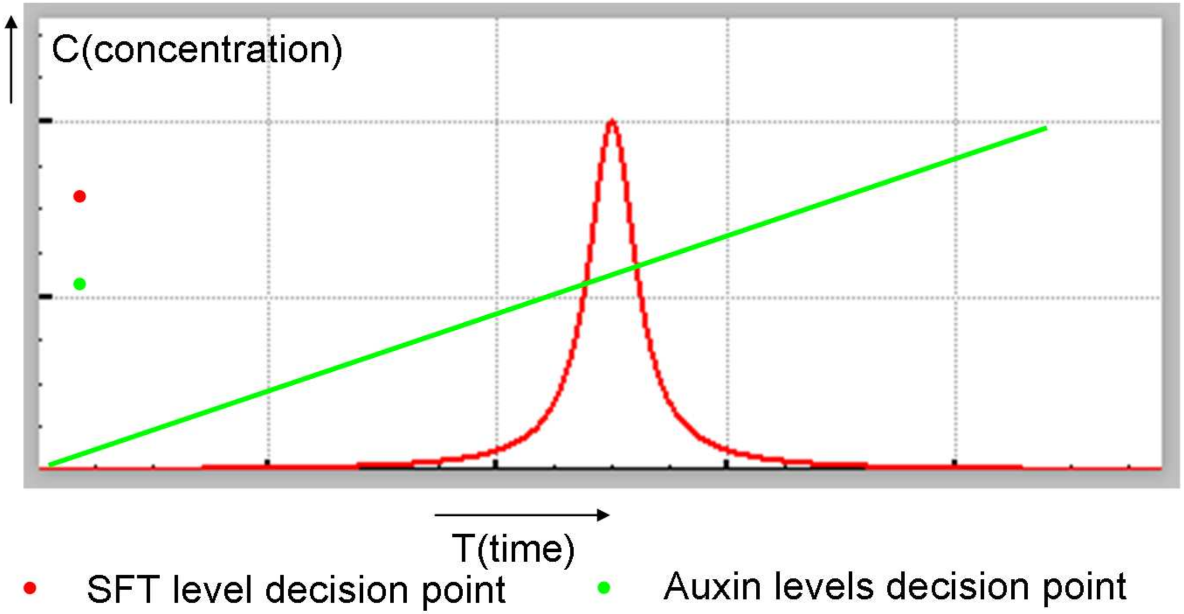
- Tomato truss
  - Meristem (SAM)
    - → flower
    - → primordium
      - → flower
      - → meristem
        - → flower
        - → meristem
        - (→ leaf, → “new plant”)
- Primordia formed at specific intervals
- Shift to flower at specific level of SFT

Tomato truss model – biological assumptions

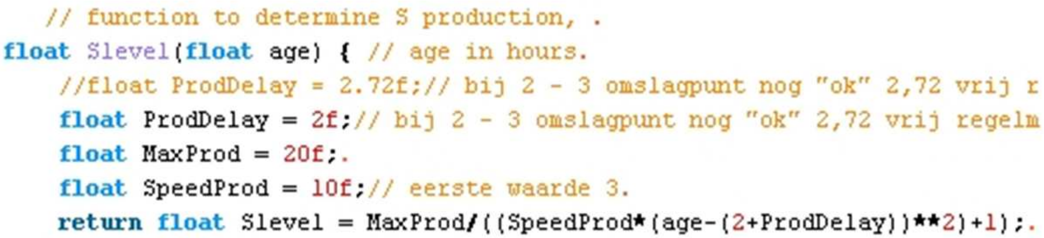
- Two factors modeled:
  - (Speed of) Formation of primordia based on auxin level. Auxin is “produced” in SAM at constant rate and reset after primordium formation
  - Switch to flowering based on level SFT, which is imported actively into the meristem by S, which has a short peak of expression. Above a threshold → SAM ➔ Flower

Tomato truss model – biological assumptions

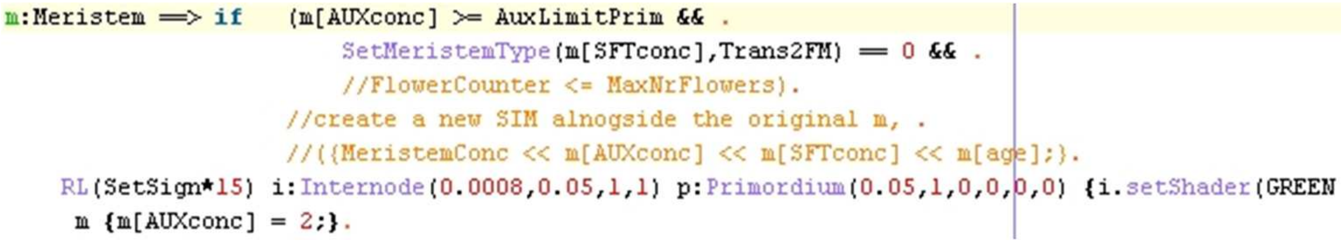
- Level of factors:



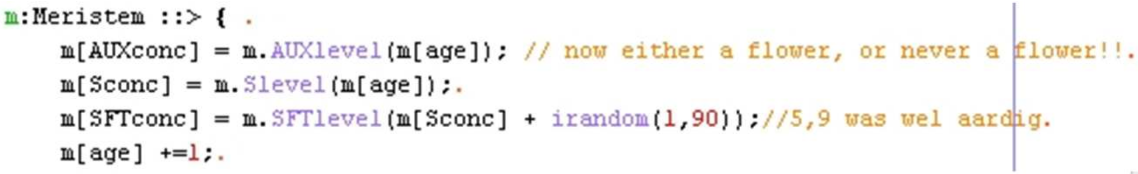
Tomato truss model – code



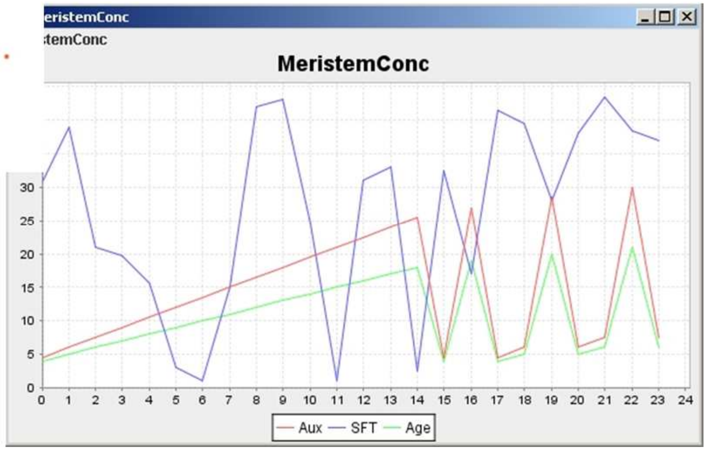
```
   // function to determine S production, .
float Slevel(float age) { // age in hours.
    //float ProdDelay = 2.72f;// bij 2 - 3 omslagpunt nog "ok" 2,72 vrij r
    float ProdDelay = 2f;// bij 2 - 3 omslagpunt nog "ok" 2,72 vrij regelm
    float MaxProd = 20f;.
    float SpeedProd = 10f;// eerste waarde 3.
    return float Slevel = MaxProd/((SpeedProd*(age-(2+ProdDelay))**2)+1);.
```



```
m:Meristem ==> if    (m[AUXconc] >= AuxLimitPrim && .
                         SetMeristemType(m[SFTconc],Trans2FM) == 0 && .
                         //FlowerCounter <= MaxNrFlowers).
                     //create a new SIM alnogside the original m, .
                     //({MeristemConc << m[AUXconc] << m[SFTconc] << m[age];}).
    RL(SetSign*15) i:Internode(0.0008,0.05,1,1) p:Primordium(0.05,1,0,0,0,0) {i.setShader(GREEN
     m {m[AUXconc] = 2;}.
```

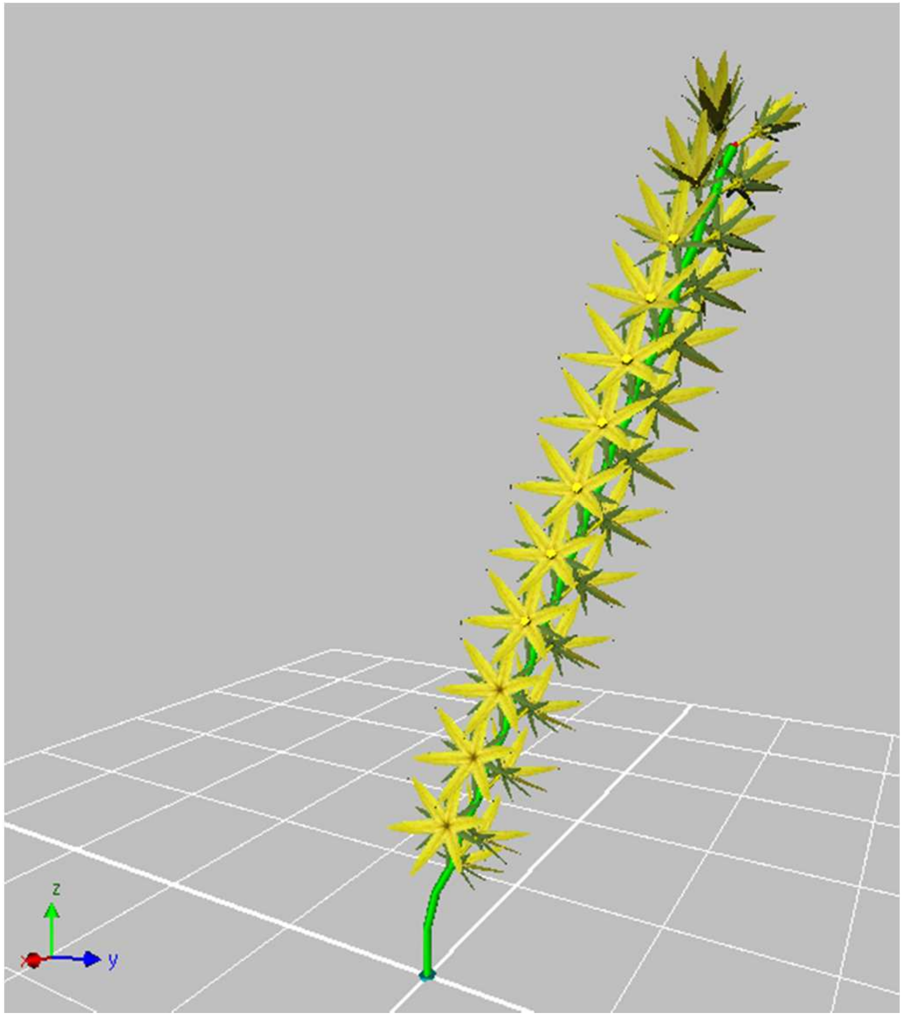


```
m:Meristem ::> { .
    m[AUXconc] = m.AUXlevel(m[age]); // now either a flower, or never a flower!!.
    m[Sconc] = m.Slevel(m[age]);.
    m[SFTconc] = m.SFTlevel(m[Sconc] + irandom(1,90));//5,9 was wel aardig.
    m[age] +=1;.
```



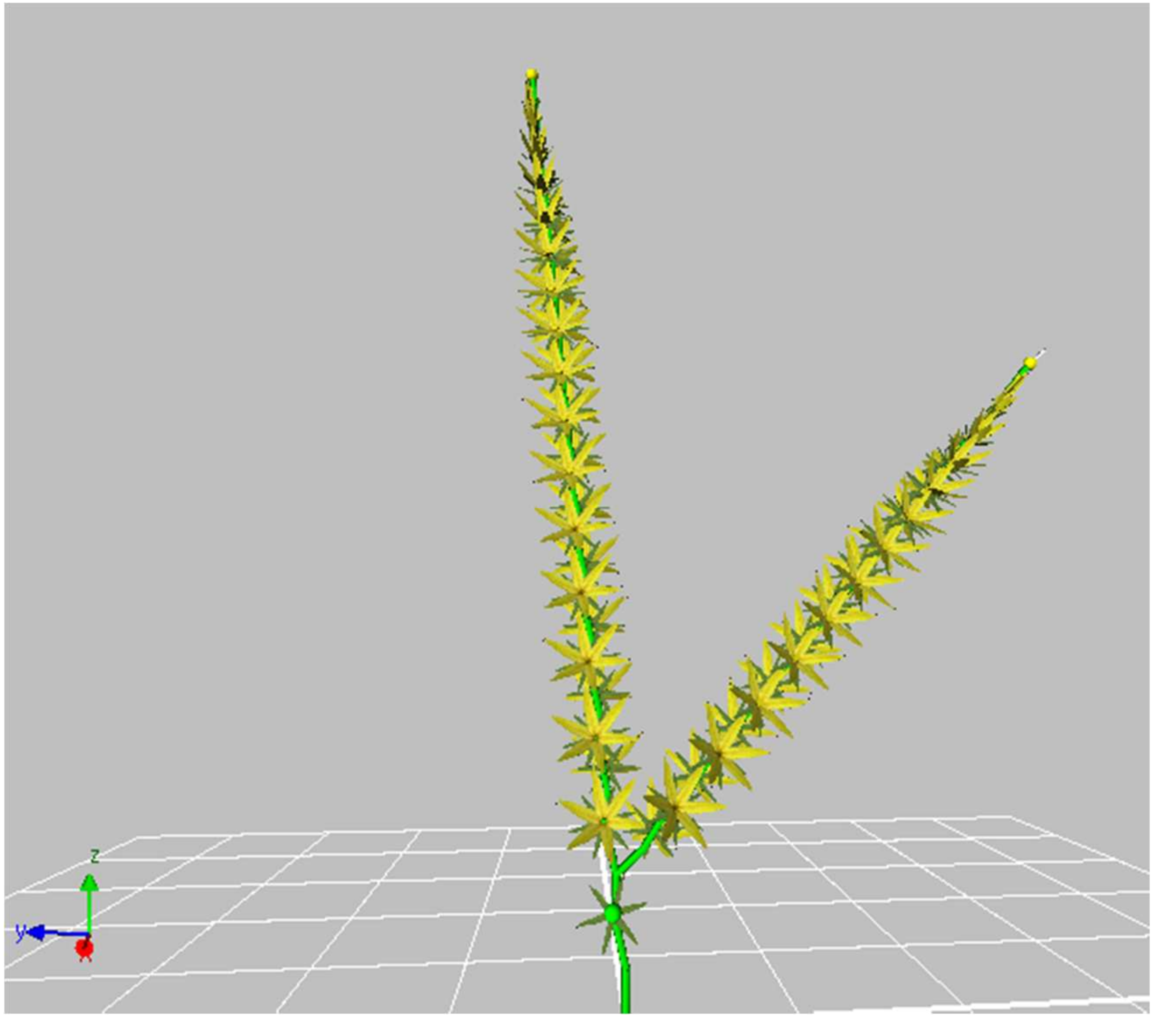
Tomato truss model – diversity

- Regular truss:



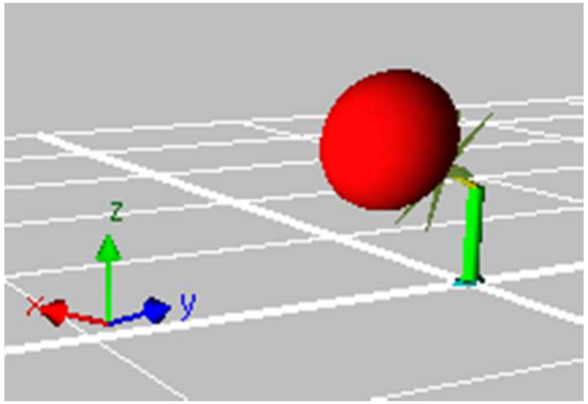
Tomato truss model – diversity

- Split truss:



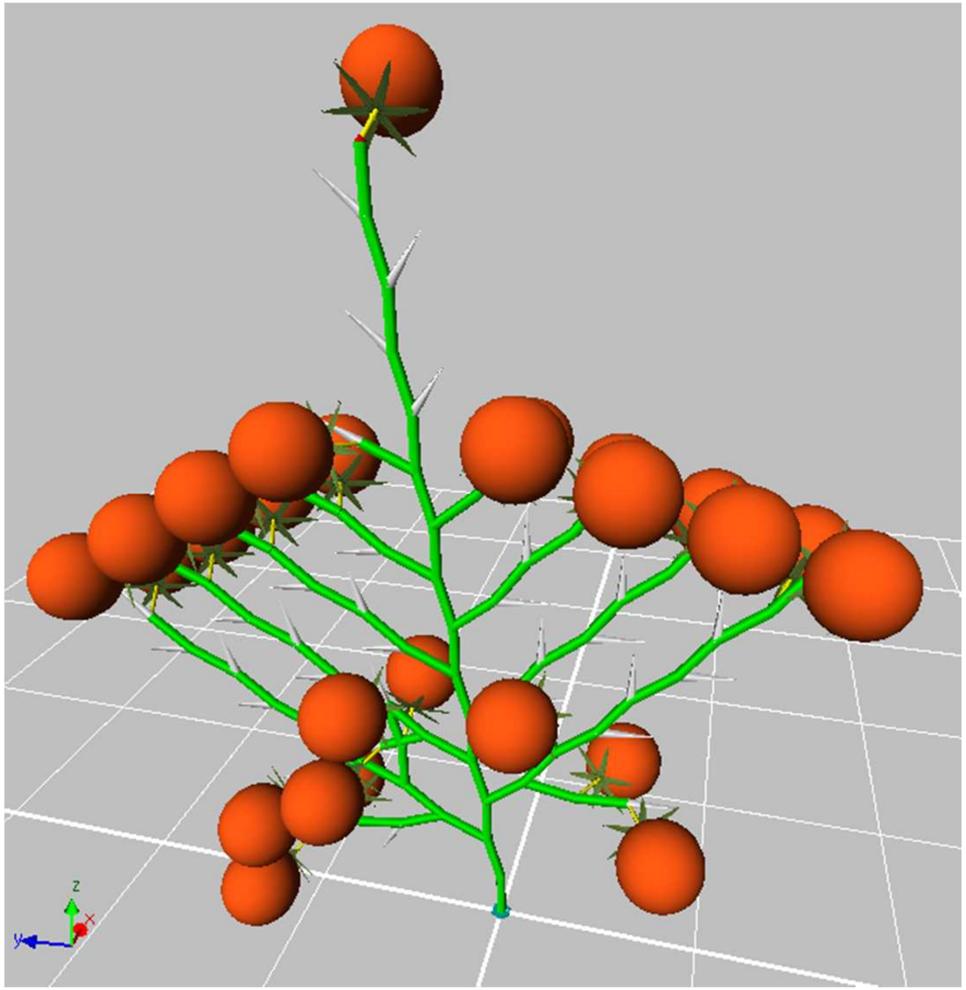
Tomato truss model – diversity

- One flower truss (UF like):



Tomato truss model – diversity

- Miscellaneous



Current state

- At this moment something to go on.
- Meristem is one module, needs to be extended to 3 (to represent different zones), or at cellular level??.
- More genes need to be incorporated.
- Extend to reversion to vegetative growth.
- The sympodial growth of truss: is it true? Is abandoned.
- …

Acknowledgements

- Peter van Dam
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