Linking Genes to Node Development in Common Bean (*Phaseolus vulgaris*)

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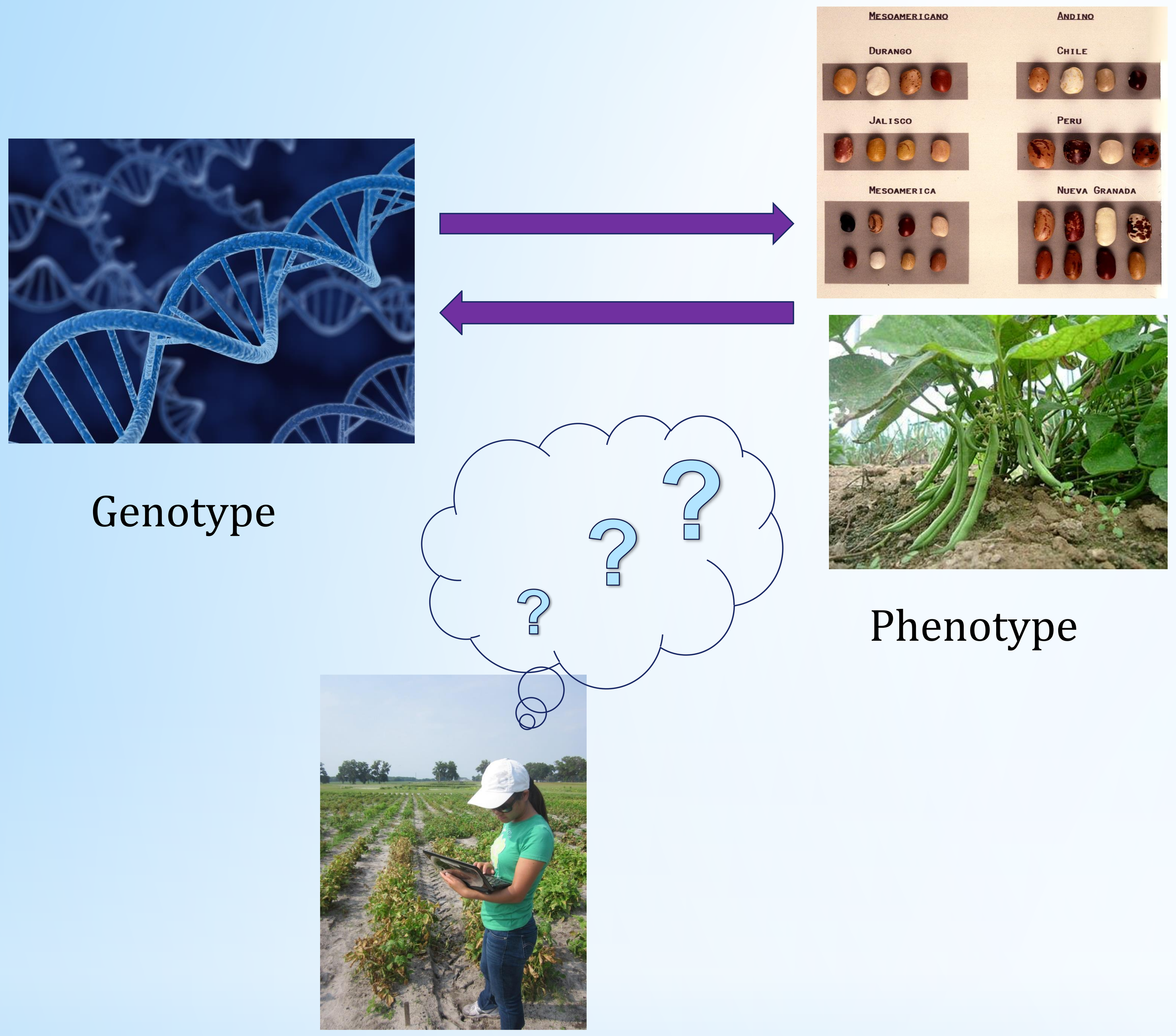
Background and Challenge



Goal

To identify Quantitative Trait Loci (QTL) controlling node development under a range of environments, and to incorporate this genetic information for node development.

Hypothesis and Model Description

Hypothesis : node development during the vegetative phase is only a function of temperature (Jones et al., 1999)

Model:

$$dN/dt = Nm \bullet f(T)$$

dN/dt, node addition/appearance rate (node per physiological day (**PD**));
Nm, maximum node appearance rate under optimum condition (node PD^{-1});
PD, Physiological Day, normalized form of thermal time accumulated per calendar day, *PD = f(T) × f(PP), f(PP)* is photoperiod function and equal to 1 in our model based on our hypothesis, therefore, daily *PD = f(T);*
f(T), cardinal temperature function used in most crop model (see **Results**):

T_H, hourly temperature;
T_{base}, base temperature below which no growth occurs;
T_{opt1}, 1st optimum temperature above which growth reaches maximum.

Reference

Jones, J., Kenig, A., & Vallejos, C. (1999). Reduced state-variable tomato growth model. Transactions of the ASAE-American Society of Agricultural Engineers, 42(1), 255-266.

Wang S., C.J. Basten, and Z.B. Zeng. 2012. Windows QTL Cartographer 2.5. Department of Statistics, North Carolina State University, Raleigh, NC. (http://statgen.ncsu.edu/qtlcart/WQTLCart.htm)

Wu, R. L., and Lin, M. (2006). Functional mapping-how to map and study the genetic architecture of dynamic complex traits. *Nat. Rev. Genet. 7*, 229-237.

Materials and Methods

Field Experiments

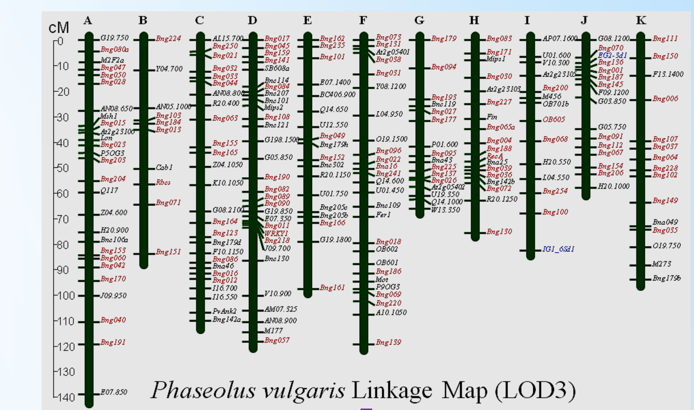
	Experiment 1	Experiment 2	Experiment 3	Experiment 4	Experiment 5
Location	Citra, Florida, USA (CT) †	Palmira, Colombia (PA) †	Isabella, Puerto Rico (PR) †	Popayan, Colombia (PO) †	Prosper, North Dakota, USA (ND) †
Latitude, Longitude	29° 39' N, 82° 06' W	03° 29' N, 76° 81' W	18° 28' N, 61° 02' W	02° 25' N, 76° 62' W	47° 00' N, 96° 47' W
Growing season	Mar, 2011-Jun, 2011	Nov, 2011-Jan, 2012	Feb, 2012-May, 2012	Mar, 2012-Jun, 2012	May, 2012-Aug, 2012
Previous culture	Fallow	Beans	Beans	Fallow	Wheat
Soil texture	Sand	Clay	Clayey Kaolinite	Medium Loam	Silt Clay Loam
Fertilization ($kg\ ha^{-1}$)	136 (N); 60 (P);112 (K)	40 (Urea)	NA	96 (P); 129 (N); 80.3 (K);	No fertilizer
Irrigation	Central Pivot Sprinkler System	Rain fed	Drip	Rain fed	Rain fed
Plant density ($plants/m^2$)	4.3	3.0	3.9	4.3	3.3
Row spacing (cm)	90	120	100	90	NA
# of replicates/harvest	3	3	3	3	3
Total # of genotypes‡	188	174	128	178	176
Frequency of Measurement	weekly	weekly	weekly	weekly	weekly

Parameter Estimation

- According to the hypothesis that temperature is the only factor affecting node addition, node appearance rate for a specific genotype should be the same or similar across locations if calendar days are adjusted to physiological day by choosing proper T_{base} and T_{opt1}.
- The default cardinal temperature function (T_{base}= 5° C, T_{opt1}=27° C) during vegetative phase in CROPGRO-Dry Bean model embedded in DSSAT software package were tested.
- A new set of T_{base}, T_{opt1}, and *Nm* were estimated based on the model using Levenberg-Marquardt nonlinear least square (*nls.lm*) function from minpack.lm package in R (version 2.14.2).
- Levenberg-Marqurdt optimization algorithm searches for the best fits of T_{base} and T_{opt1}, and *Nm* across locations for a specific genotype by minimizing the sum square of the estimates with the observations from each location.

Genotypic Analysis

High Density Maker Map (2013)



Phenotypic data: Nodes on Main Stem

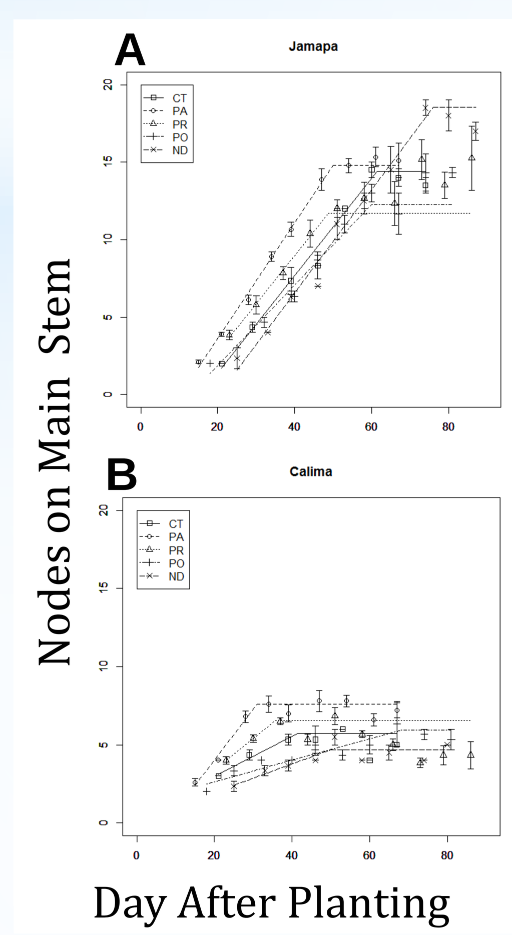
Traditional QTL Mapping

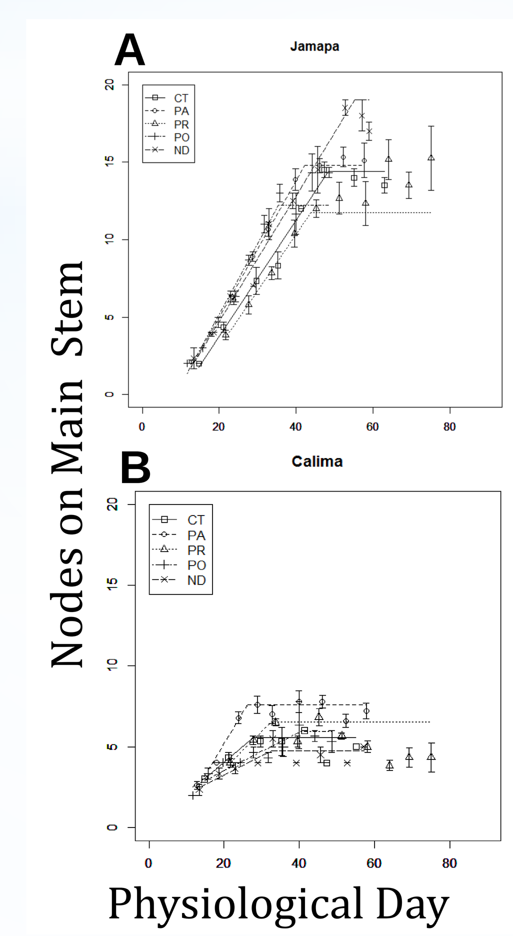
- Composite Interval Mapping (CIM);
- Multiple Interval Mapping (MIM);
- Deal with end-point traits

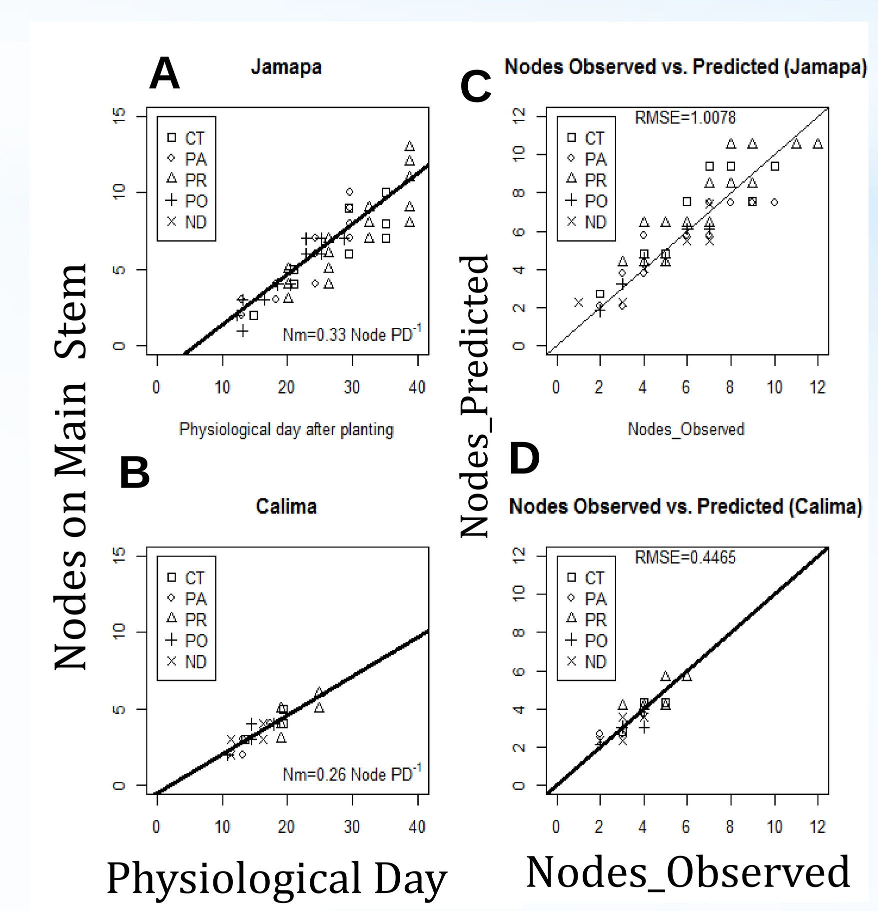
Functional Mapping

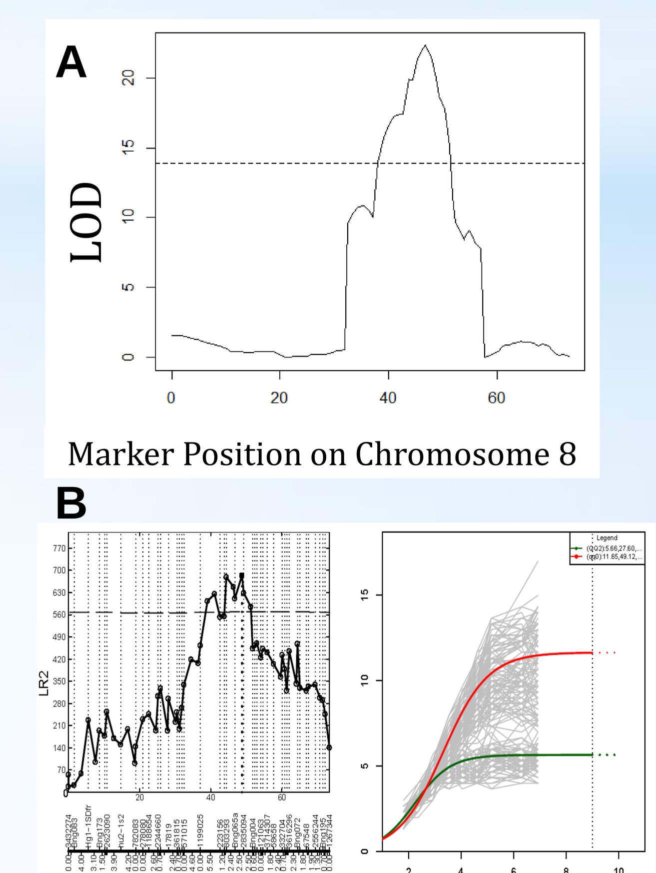
- Statistical mapping framework;
- Deal with dynamic traits

Results









Gene-based model

$$dN/dt = [Nm\_Det + (Nm\_Indet - Nm\_Det) * fin] \bullet f(T)$$

$$fin = \begin{cases} 0, & \text{if a given genotype is determinate;} \\ 1, & \text{if a given genotype is indeterminate;} \end{cases}$$

$$f(T) = \begin{cases} 0, & \text{if } T_H < Tbase \\ \sum_{H=1}^{24} \frac{T_H - Tbase}{24 * (Topt1 - Tbase)}, & \text{if } Tbase <= T_H < Topt1 \\ 1/24, & \text{if } T_H >= Topt1 \end{cases}$$

T_{base} = 9.3 ° C
T_{opt1} = 22.2 ° C

Step 1:

- Nodes on Main Stem vs. **Calendar day**;
- Significant difference among some locations($P < 0.05$) for most of genotypes ;
- Temperature plays an important role in node development.

Step 2:

- Nodes on Main Stem vs. **Physiological Day** (PD) using default T_{base} **(5° C)** and T_{opt1} **(27° C)** from CROPGRO-Bean;
- Significant difference among some locations for most of genotypes;
- T_{base} and T_{opt1} need to be estimated for our population.

Step 3:

- **Parameter estimation** using nls.lm function;
- Using newly estimated T_{base} and T_{opt1} for each genotype, nodes on main stem vs. **PD** from different locations can be lined-up with the same node appearance rate (Nm);
- The average T_{base} and T_{opt1} are **9.3** and **22.2° C** respectively for our population.

Step 4:

- Traditional QTL mapping (**CIM & MIM**) peak (above) for Nm;
- Functional Mapping (**FM**) peak (below) for nodes on main stem (N_m & N_{max});
- The same QTL region on **chromosome 8** where ***fin*** gene is occupied was identified.
- Gene ***fin*** is responsible for **node development.**

Step 5:

- ***Nm_Det*** and ***Nm_Indet*** represent maximum node appearance rate (node PD^{-1}) under optimum condition for indeterminate and determinate genotypes respectively;
- The average *Nm_Det* and *Nm_Indet* are **0.32** and **0.25** node PD^{-1} in our population.

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