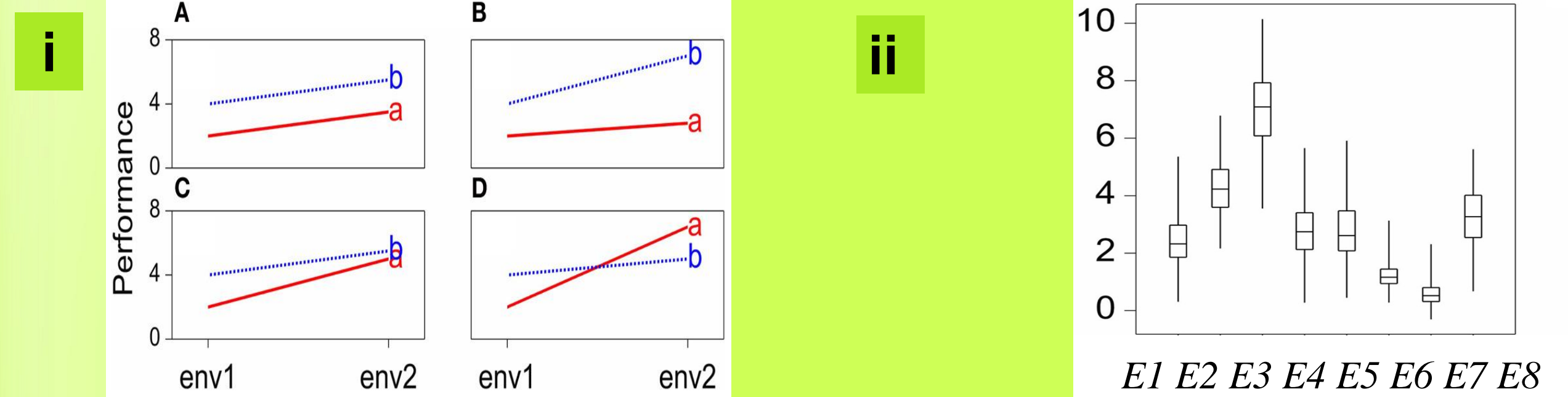




## Background

➤ **Genotype-by-Environment Interaction (GEI)** exists whenever the relative phenotypic performance of genotypes depends on the environment, therefore, GEI is very important in plant breeding.

➤ **GEI can be introduced in two different ways (i and ii).**



GEI in terms of the relative difference between genotype means (i) and heterogeneity of genetic variance and covariance (ii). In (i), A shows the case where this is no GEI; B, C and D shows the divergence, convergence and crossover interaction respectively (Griffiths et al, 1996). Boxplot (ii) shows that GEI not only occurs on mean performance but also on the genetic variance across environments (shown by the length of bars).

➤ **Common bean (*Phaseolus vulgaris*)** is one of the most important legumes in the world for a source of protein, especially in Latin America and Africa.

➤ **Node addition is important for plant growth and thus final yield.**

Here, we are analyzing the GEI for node addition rate in the common bean.

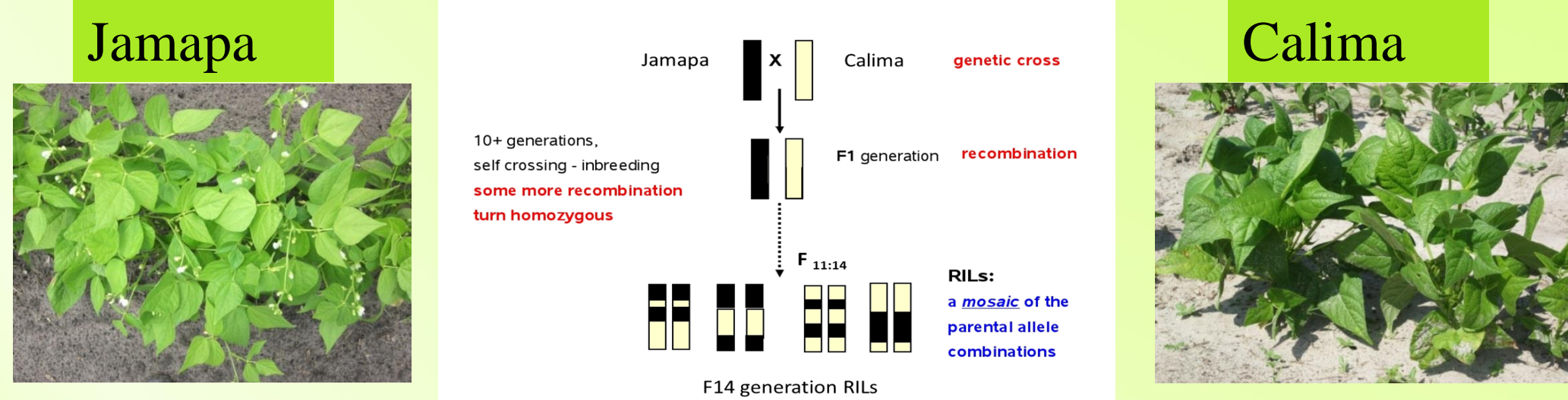
## Motivation

1. What type(s) of GEI does the node addition rate data have?
2. What model should we select to represent the data for GEI?
3. Can we model the GEI and its genetic basis through quantitative trait loci (QTL) analysis?
4. If there is GEI, what environment covariates are responsible for the QTL by environment interaction (QEI)?
5. Can we predict node addition rate according to the model?

## Experiment

### Genotyping

- Plant materials:  
~180 Recombinant Inbred lines (RILs) from two contrast parents



- High density linkage map (genotyping by sequencing)

### Phenotyping

- Field locations (CT, PA, PO, PR, ND, 2011-2012):



Temp: Temperature  
MASL: Meters above sea level  
DL: Day length

- Node Addition Rate (NAR)

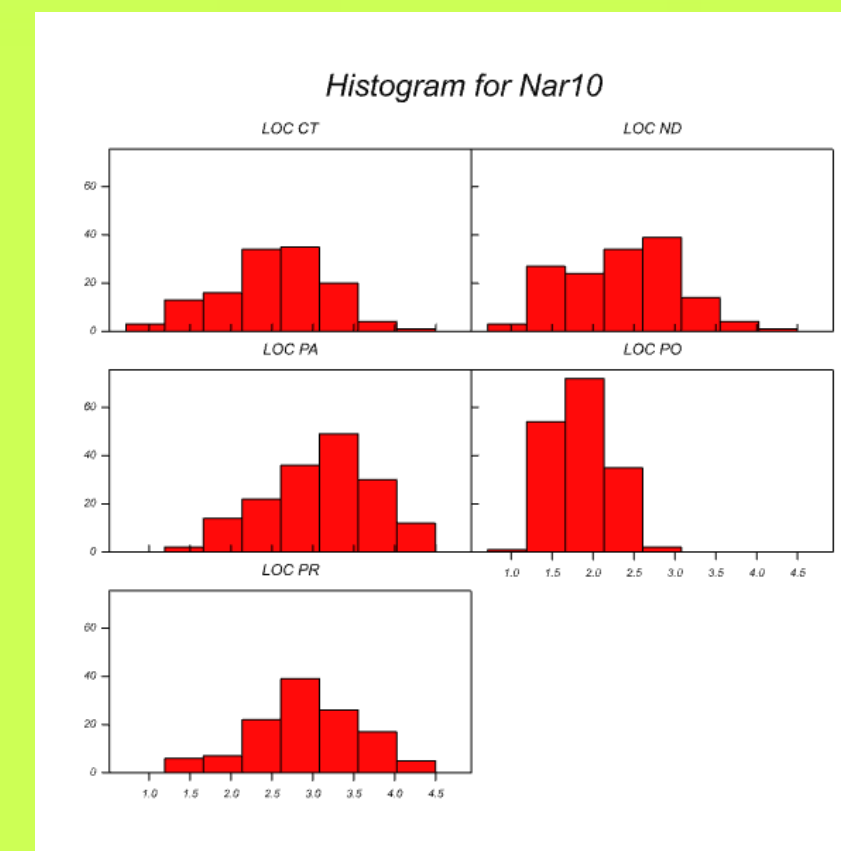
NAR (node/day) was calculated by taking regression of nodes on main stem vs. calendar days for the first three or five harvests for determinate and indeterminate genotypes, respectively, for each RIL at each field location.

### Working Environment

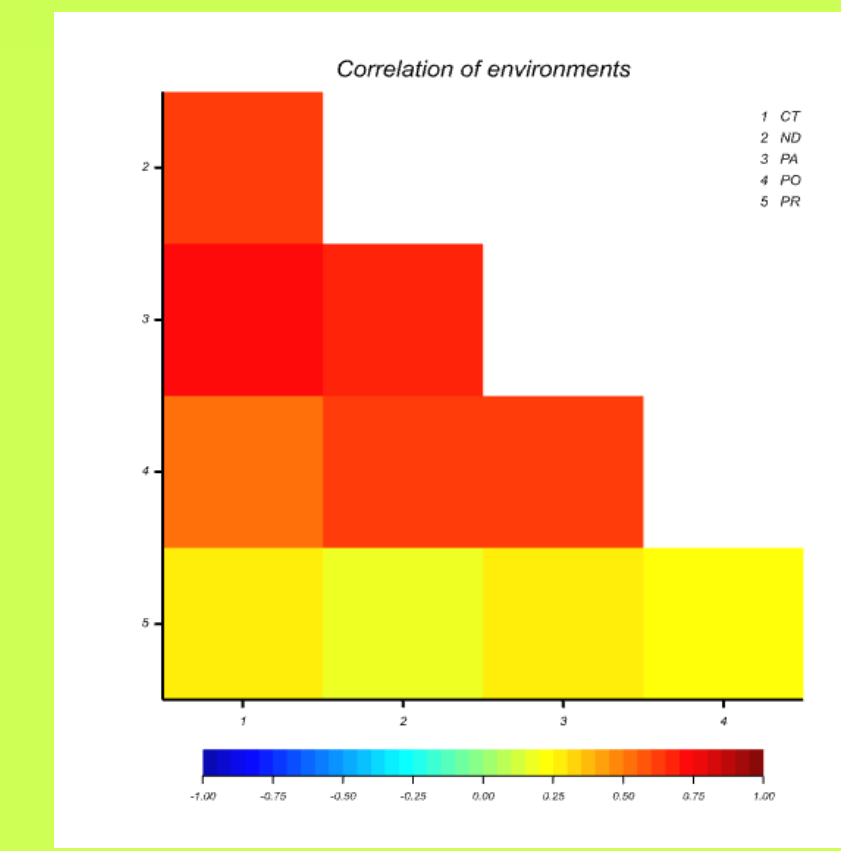
- R programming
- GenStat (VSN international, 2012)

## Results and Discussion

### Phenotypic Analysis



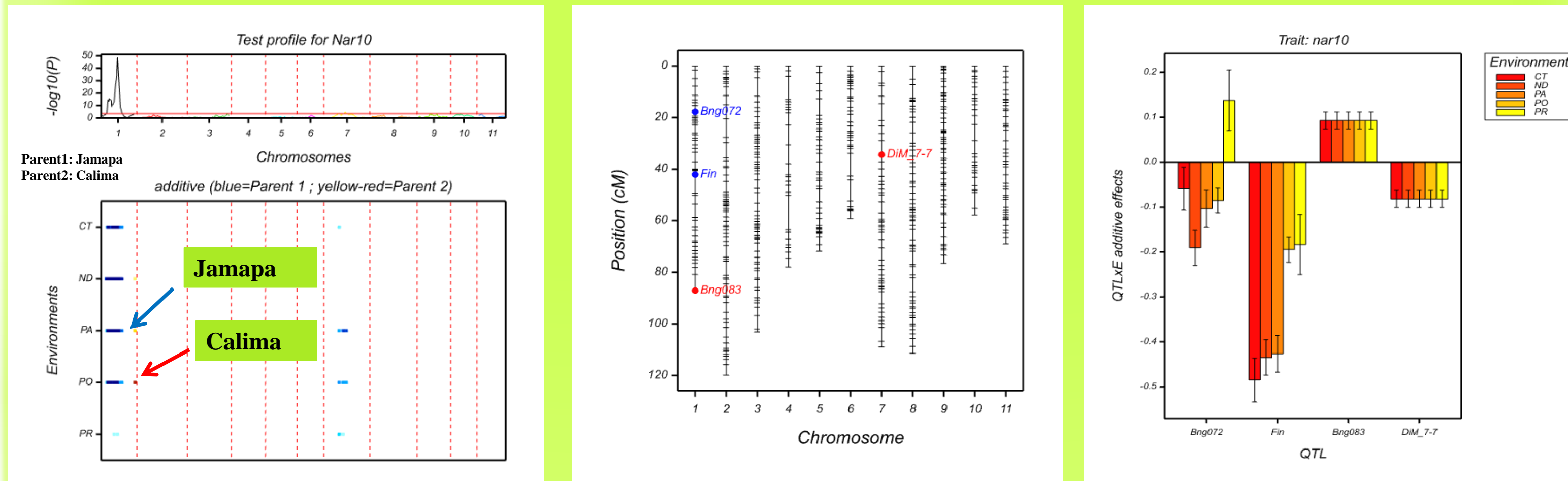
NAR (X10) for all the RILs at each site. This shows different phenotypic performance that depends on environment.



Correlation of environments. CT, ND and PA shows high correlations while this is little correlation between Popayan and Puerto Rico.

### QTL Analysis

- **Model selection:** UNSTRUCTURED Variance-covariance model was selected.
- Model GEI:



Four QTLs were detected after: 1) the initial simple interval mapping (SIM), 2) 3~4 times of composite interval mapping (CIM), and 3) the backward selection of final QTLs. The relative intensity of the color shows the effect of each QTL at each field site.

The positions of the four QTLs on the chromosome. QTLs with blue color indicates the increase of NAR when a given genotype has Jamapa allele, while QTLs in red indicates increase of NAR when having a Calima allele.

*Bng072* and *FIN* are showing GEI while *Bng083* and *DiM\_7-7* are not, since there is no difference of QTL additive effect among different field site. Therefore, QEI were detected for two QTLs.

- QEI model (LOC: field site; QTLs were coded according to their positions; Q10=*Bng072*; Q28=*fin*; Q47=*Bng083*; Q285=*DiM\_7-7*)

$$NAR = f(LOC + LOCXQ10 + LOCXQ28 + Q47 + Q285)$$

### Environment Covariates Analysis

- Environmental covariates: temperature (Temp), day length (DL), solar radiation (SRAD)
- Model development and test

Fixed term	Wald statistic
Temp X Q28	35.98
Q10 X DL	13.57
Q285	19.87
Q47	23.78
Q28	175.71
Q10	18.20
SRAD	106.21
DL	16.51
Temp	1555.51

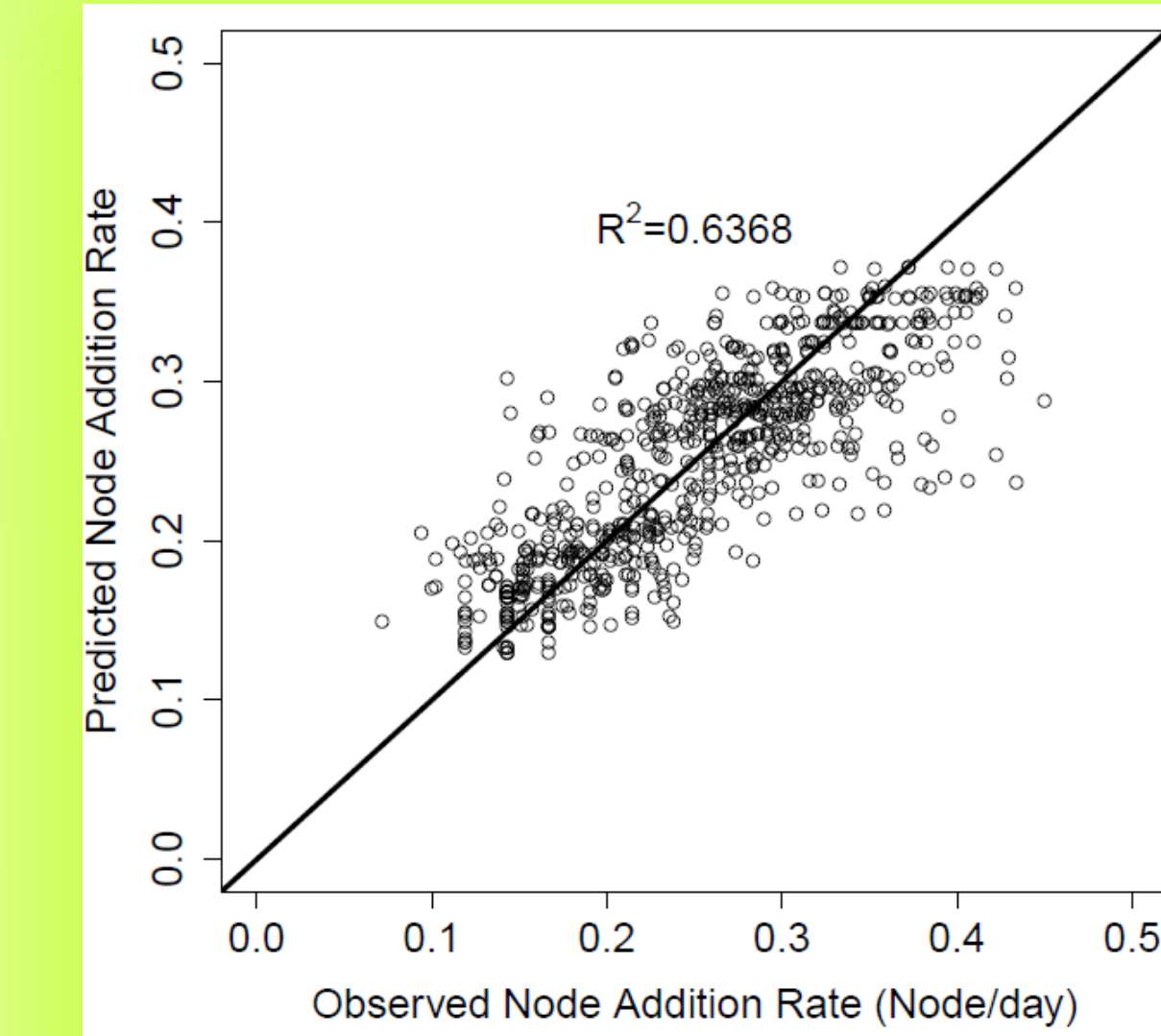
- ❖ Wald's test is the modified F-test assuming the degree freedom of error is infinity.
- ❖ All the fixed terms shown in the table were tested significant with  $df = 1$ ,  $p\text{-value} = 0.001$ ;
- ❖ Temperature is the main environmental factor affecting node addition rate (NAR), while Q28 (*FIN* gene) has the largest additive QTL effect on NAR, which is not surprising, since *FIN* is also responsible for the determinacy in beans.

### Final Predictive Model

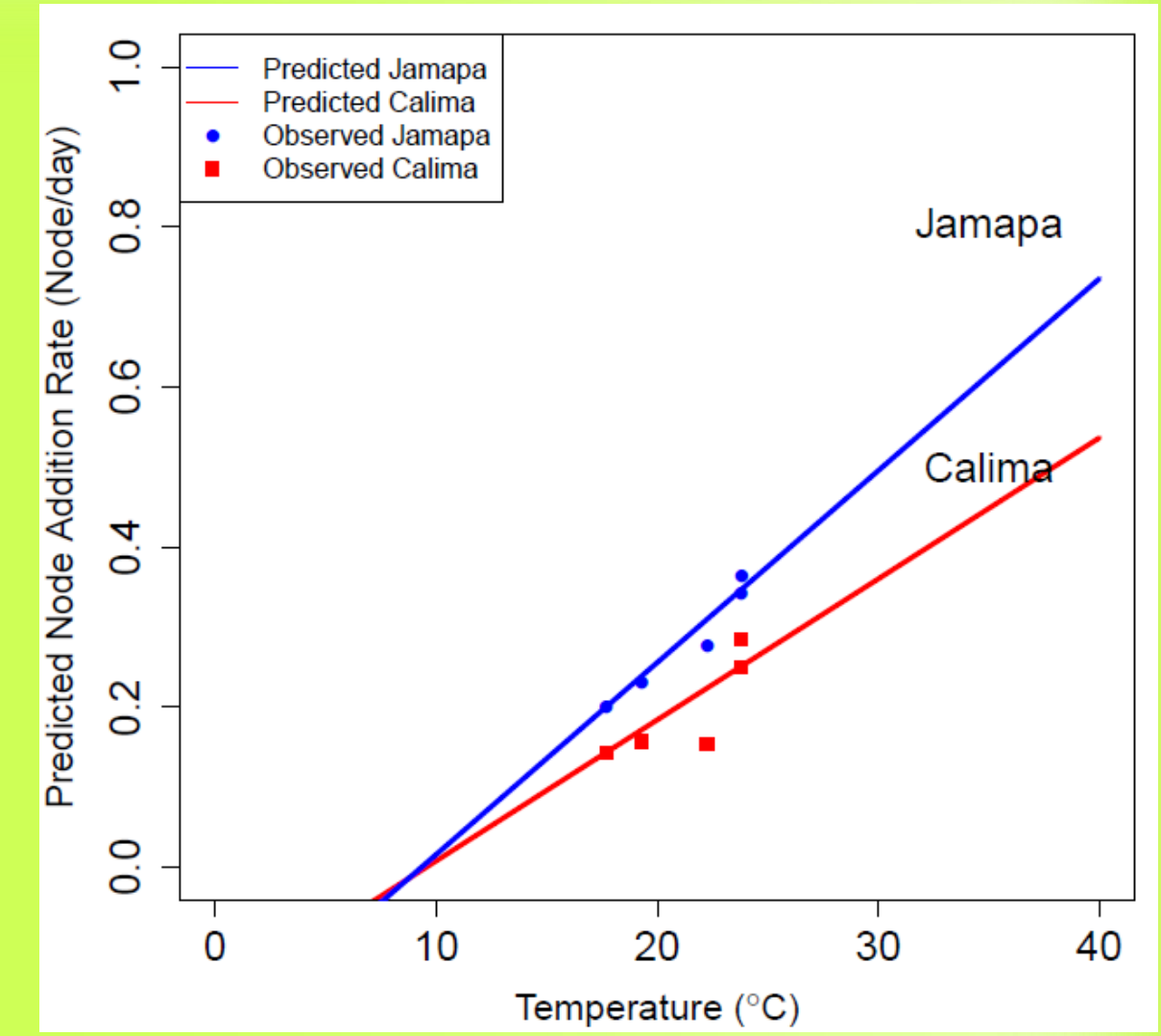
$$NAR = \text{constant} + \text{Temp} + \text{DL} + \text{SRAD} + \text{Q10} + \text{Q28} + \text{Q47} + \text{Q285} + \text{DLXQ10} + \text{TempXQ28}$$

## Results and Discussion (continued)

### Final Model Evaluation



The GEI model explained 64% of the variation of NAR for this population. The unexplained percentage may be accounted by water, nitrogen etc., which we lacked information of. Also, the nature of the data (nodes on main stem vs. day after planting) may cause the error because nodes can only be counted as a few integers.



The predicted NAR (node/day) from the final predictive model showed good prediction for the two parental lines (Jamapa and Calima) grown at the five locations where average temperatures were obtained and used. For a given genotype, the NAR can be predicted under any temperatures.

## Conclusions

- Genotype-by-environment interaction in terms of relative mean difference and also genetic variance was found for node addition rate.
- **Unstructured variance-covariance model** was selected to model GEI, and **four QTLs** were identified, with *FIN* gene which is responsible for determinacy, interacting with environment.
- **Temperature** was identified as the main environment covariate affecting node addition rate even though day length and solar radiation have some effect too.
- The final GEI predictive model explained **64%** of the variation for node addition rate (Node/day) in this population, and it showed good prediction for the two parental lines.
- Given a genotype under any environmental conditions, node addition rate can be predicted according to the genetic information and environmental input.

## References

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- **Griffiths, A.J.F., Miller, J.H., Suzuki, D.T., Lewontin, R.C., and Gelbart, W.M.** 1996. An Introduction to Genetic Analysis. New York, NY: WH Freeman and Company.

## Contact Information

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