Modeling Genetic Traits of five Common Bean (*Phaseolus vulgaris*) Genotypes in Multi-location Trials

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1. Modeling growth of the common bean

- The common bean is **the most important grain legume for direct human consumption**, providing up to 33% of the daily protein in developing nations.
- Modeling efforts using the DSSAT-CROPGRO model have provided acceptable predictions of common bean growth and development under contrasting management conditions. However, a **lack of reliable characterizations of contrasting cultivars, and a scarcity of experiments from contrasting environments** has hindered modeling efforts.
- We studied the differences in phenological and growth traits for five common bean genotypes grown in contrasting environments using the CROPGRO-BEAN model, assessing the genetic variability in solved Genotype-Specific Parameters (GSPs) and the model's predictive capacity.

2. The experiments: genotypes, sites and data collection

- Genotypes were parental lines Calima (Andean, large-seeded determinate) and Jamapa (Mesoamerican, indeterminate small-seeded) and a subset of 3 indeterminate genotypes (RIJC135, RIJC141 and RIJC142) of the Jamapa×Calima ($F_{11:14}$, n=186) recombinant inbred (RIL) population with contrasting reproductive growth and development.
- Plants were grown at five sites with contrasting environmental conditions under a row-column design with three repetitions, and standard agronomic practices (Table 1).

Table 1. Planting information and relevant weather characteristics of study sites

Site location	Soil type	Planting	Irrigation	Plant density (plants m^{-2})	Mean solar radiation (MJ m^{-2} d^{-1})	Average temperature Min - Max (°C)	Daylength (h)
Palmira, Colombia (PAL)	Mollisol	11 Nov 2011	Furrow	3.0	14.7	19.5 - 28.8	11.8
Popayan, Colombia (POP)	Inceptisol	23 Mar 2012	Rain fed	4.3	15.6	13.7 - 25.5	12.1
Isabela, Puerto Rico (PR)	Oxisol	6 Feb 2012	Drip	3.9	22.4	20.5 - 29.2	12.2
Prosper, N. Dakota, USA (ND)	Mollisol	10 May 2012	Rain fed	3.3	21.4	12.9 - 27.8	15.0
Citra, Florida, USA (CIT)	Ultisol	24 Mar 2011	Pivot	4.3	20.5	17.6 - 31.7	13.3

- Six plants per plot were phenotyped every 2-3 days for the onset of reproductive stages. Weekly single-plant samples were taken from each plot for destructive growth measurements.

3. CROPGRO stepwise GSP parameter calibration procedure

- Genotype Specific Parameters were calibrated for each common bean genotype within the CROPGRO-DSSAT V4.5 model following the sequence of life cycle events of the crop.
- Parameter estimates were obtained iteratively, by minimizing the root mean squared error (RMSE) of the prediction vs. observed values and maximizing the d-statistic, a measure of model agreement to the data (Table 2).

Table 2. CROPGRO parameter calibration sequence and target variables

Sequence	Name	Genotype Specific Parameter Description	Target field measurements
1	PL-EM	[a]T-Time between planting and emergence (VE)	VE
2	EM-V1	T-Time from VE to first true leaf (V1)	V1
3	EM-FL	[b]PT-Time from VE to 1st flower (R1), w/o ND	R1
4	PPSEN	Slope of R1 relative response to photoperiod	R1
5	EM-FL	PT-Time from VE to R1	R1
6	RWDTH	Canopy width (m)	Canopy height
7	RHGHT	Canopy height (m)	Canopy width
8	FL-SH	PT-Time from R1 to first pod (R3)	R3
9	FL-SD	PT-Time from R1 to first seed (R5)	R5
10	SD-PM	PT- Time from R5 to physiological maturity (R7)	R5-R7
11	R7-R8	PT-Time from R7 to harvest maturity (R8)	R7 and R8
12	SLPF	Soil fertility factor per site	Slope of above-ground biomass
13	TRIFL	Rate of main stem leaf appearance	Node number on main stem
14	FL-VS	PT-Time from R1 to last leaf on main stem (LLMS)	Last leaf appearing on main stem
15	SDPDV	Number of seeds per pod	Seeds per pod at final harvest
16	WTPSD	Single seed weight	Single seed weight at final harvest
17	THRSH	Percentage seed in pod (%)	% seed at maturity
18	SLAVR	Specific leaf area (SLA, cm^2 g^{-1})	SLA over time
19	SIZLF	Leaf area of fully expanded leaf (cm^2)	Leaf area over time before R1
20	LFMAX	Light-saturated leaf photosynthesis rate	Total crop weight over time
21	FL-LF	PT-Time from R1 to end of leaf expansion on plant	Last leaf on plant (days)
22	PODUR	PT-Time required to reach final pod load	R3 and time to last pod added
23	FL-SD	PT-Time from R1 to R5	R1 and R5
24	SD-PM	PT-Time from R5 to R7	R5 and R7

[a] T-Time refers to thermal time, calculated using base and optimum temperatures of 9 and 23 °C, respectively.
[b] PT-Time refers to photothermal time, which includes the delay on anthesis due to increased photoperiods above 12.5 hours.

4. Solved GSPs reflect differences between genotypes

Table 3. Parameter calibration results

Parameter	Unit	Genotype CAL	JAM	RIJC135	RIJC141	RIJC142
PPSEN	Slope of flowering response to photoperiod	0.110	0.022	0.022	0.022	0.035
EM-FL	PD	24.1	30.2	31.9	30.2	34.5
FL-SH	PD	3.5	5.3	4.9	4.9	5.9
FL-SD	PD	10.0	11.5	14.0	11.9	12.0
SD-PM	PD	20.9	20.7	19.0	20.0	19.0
FL-LF	PD	17	25	21	21	21
LFMAX	mg CO_2 m^{-2} s^{-1}	0.94	1.02	0.76	0.82	0.81
SLAVR	cm^2·g^{-1}	147	215	210	172	226
SIZLF	cm^2	300	210	210	240	200
WTPSD	g·seed^{-1}	0.45	0.23	0.32	0.30	0.21
SDPDV	seed·pod^{-1}	4.00	6.00	4.25	4.60	5.20
PODUR	PD	5	10	10	8	10
THRSH	%	75	75	76	70	77
FL-VS	PD	0	10	10	8	9
TRIFL	leaf·TD^{-1}	0.25	0.37	0.30	0.34	0.31

- All indeterminate genotypes took a longer time to flower than photoperiod-sensitive Calima. RIJC142 was ~15% later than Jamapa.

- Leaf-level GSPs: LFMAX, SLA and SIZLF showed large variation between parents and RI lines.

- Despite varying seed weights and numbers of seeds per pod, cultivars maintained similar threshing (%)

5. Calibrated parameters give good predictions of plant growth and development across sites and genotypes
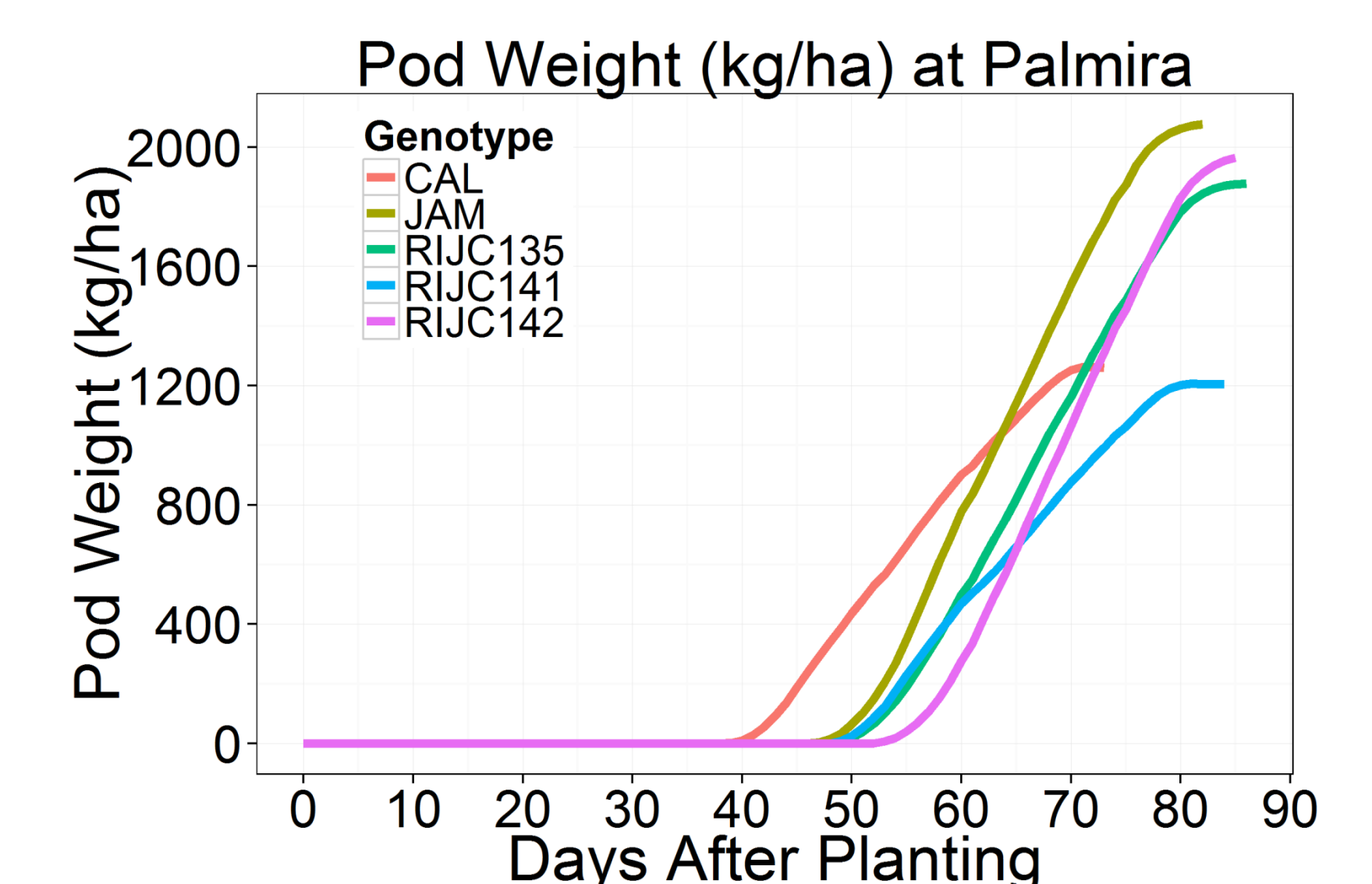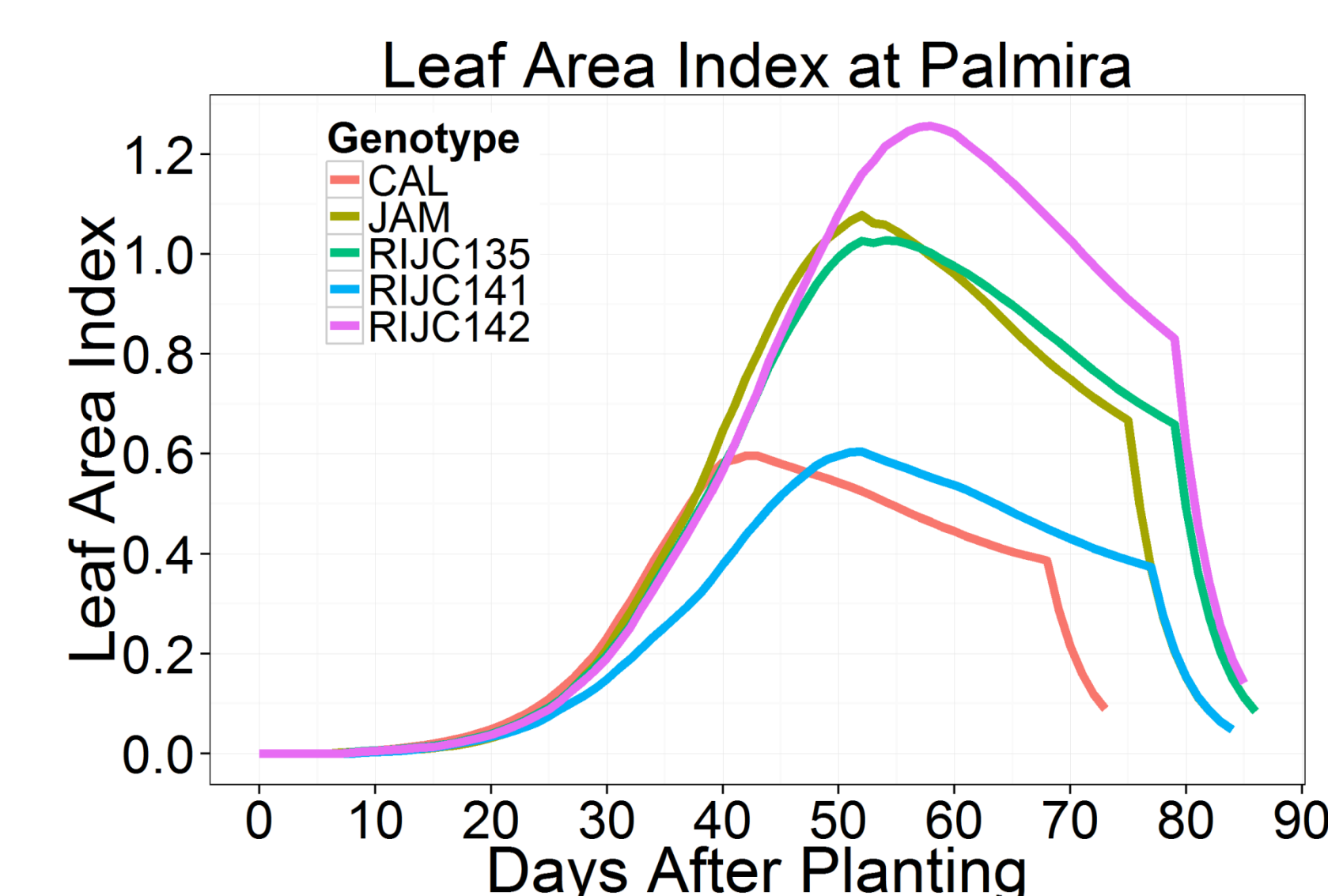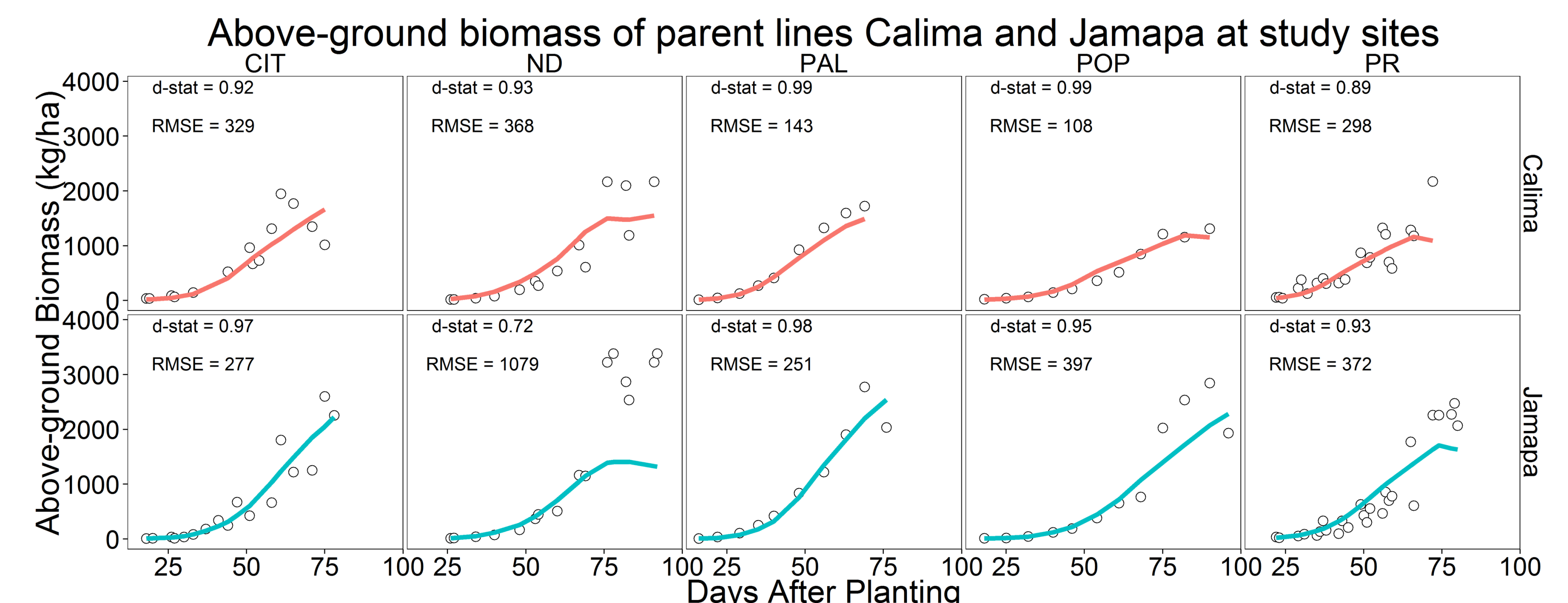
Table 4. Goodness-of-fit of phenology predictions

Variable	RMSE (days)[a]	RMSE (CV%)[b]	d-stat
Emergence Day (VE)	2.2	23.0	0.62
Anthesis Day (R1)	2.0	4.4	0.98
First Pod Day (R3)	2.8	5.4	0.97
First Seed Day (R5)	4.3	7.2	0.94
Harvest Maturity (R8)	4.5	5.3	0.95

[a] RMSE refers to the root mean squared error
[b] refers to the coefficient of variation of the RMSE

- Calibrated parameters resulted in low RMSE and high d-stat for phenology stages, averaging 3.2 days and 0.89, respectively.

- Growth predictions provided good fits, although harvests after 50 dap were predicted with less accuracy.

Above-ground biomass of parent lines Calima and Jamapa at study sites

Leaf Area Index at Palmira

Pod Weight (kg/ha) at Palmira

- The solved GSPs gave contrasting growth dynamics between genotypes. In some cases, genotypes reached similar end-point phenotypes but with different growth trajectories.

6. Conclusions and future directions

- Overall, the calibrated genetic parameters provided good predictions of phenology and growth of diverse genotypes from contrasting environments, and a reference for future bean modeling efforts using novel statistical calibration procedures.
- Future work will include modeling the remainder of the Jamapa × Calima RI population with the goal of connecting calibrated model GSPs to quantitative QTL traits for genetic mapping.