

Introduction

Common bean (Phaseolus vulgaris L.) is one of t cultivated legumes and economically important worldwide.

During the last two decades common bean has be significant economic crop in North Dakota, which is the US producer.

Early monitoring of vegetative growth can help in identifying a second secon quality and diseases in order to ensure high seed yields.

The relationship of the bean life cycle and seed yield can to develop an economic growth rate.

Crop models help enhance agricultural research. Prev weight simulations in common bean (Adikua et al. 2001) su good predictions under water stress conditions.

Knowledge of the phenological stages influencing comm growth and development is crucial to obtain reliable yield e and help optimizing management and production practices.

Objectives

This study aims to predict the growing rates and ph stages of 164 common bean recombinant inbred lines (R the parents ('Negro Jamapa' and 'ICA-Calima') at five The results from North Dakota are reported.



Figure 1. Field view of flagged plants at Prosper Research Site in 20⁻







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Early Vegetative Growth Simulation in a Common Bean RIL F

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	Materials and Metho
the most	The experiment was conducted at the Pro- located ~ 30 km NW of Fargo, North Dakota. F was 157.0 mm and the average temperature was growing season.
S leading	Phenological data were collected twice a we plants over 164 plots replicated three times i column design.
n be used	 Dry weight of the main stem (DWMS), hypot primary leaves (DWU) were used to pred vegetative stages.
vious dry uggested	• Growth rates were determined by using the equation: $W=W_0 e^{r(t-t0)}$ W = biomass (g) $W_0 = initial biomass at t_0 (g)$ $r = growth rate (g day^{-1})$
non bean estimates	t = time (days) e = natural logaritm (Ln)
	 Data were analyzed (ANOVA) using the PRC (SAS Institute, 2008).
nenologic RILs) and locations.	 Predictions were evaluated by using the square error [RMSE (Willmott, 1985)]: (P= predicted and O=observed)
	Calima Calima Calima Calima Co Calima Co Co Co Co Co Co Co Co Co Co Co Co Co
	0.5 - 0.4 - Calima · · · · · · · · · · · · · · · · · · ·
	Figure 2. Predicted (PDWU) and observed (ODWU) of
	leaves.
12.	0.30 - 0 0.25 - Calima Jamapa 0.20 - 0

Figure 3. Predicted and observed dry weight of hypocotyl.

0.2

0.3

000000000000

0.10

0.05

0.0

0000 400000

0.1

NDS

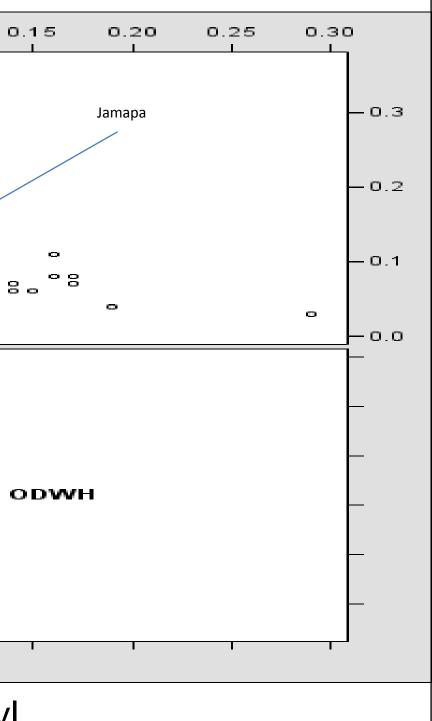
ds sper Research Site ainfall for the period PDWMS as 20.0 °C during the 0.5 0.4 eek from six flagged in a resolvable row-0.1 -0.6 cotyl (DWH), and the ict bean growth at ne Blackman (1919) and DWMS (0.24). accurately. C MIXED procedure are root mean square vegetative growth. $\sum_{i=1}^{n} (P_{i-}O_{i})^{2}$ =n in breeding program. 0.3 0.4 - 0.4 0.2 -0.0 ODWU dry weight (g) of primary 0.15 0.20 0.25 0.30 Acknowledg — 0.3

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Referen

Adikua, S.G.K., M. Rengerb, G. Wessolekb, M. Facklamb, and C. Hecht-Bucholtzc. 2001. Simulation of the dry matter production and seed yield of common beans under varying soil water and salinity conditions. Agric. Water Management 47:55-68.

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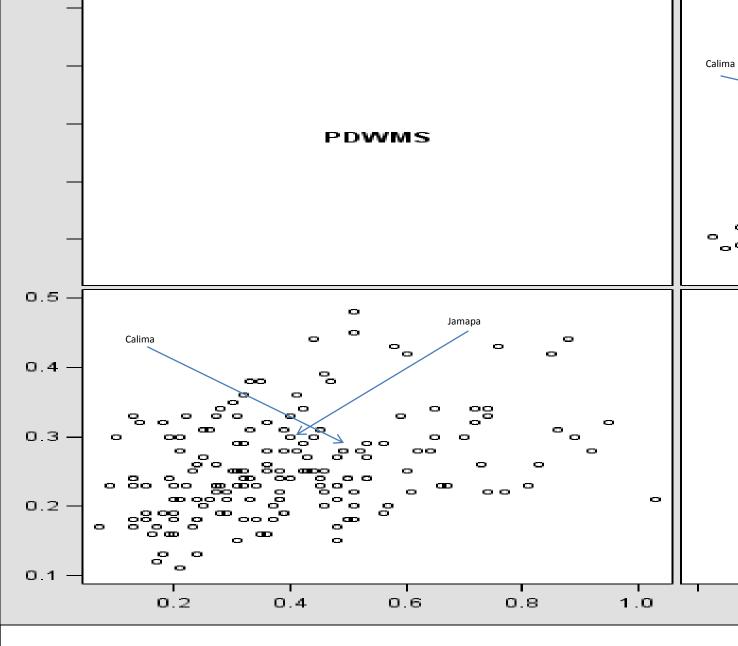


Figure 4. Predicted and observed dry weigh

- RMSE values close to 0 indicate go
- DWH was predicted better with R
- Early vigor of the selected traits
- DWH of Jamapa was predicted bet

Summary and F

The evaluation indicates good pred

Primary leaves, hypocotyl and ma associated with grain yield and thus

DWH can be used as direct sel following by DWU and DWMS.

These preliminary results will be us data set can be adjusted and match gene-based crop model including all

Results across locations in North and two locations in Colombia will be by environment interaction.

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0.2 0.3 0.4 0.5 1.0 0.8 0.8 0.6 0.4 0.2 0.2		
t of the main stem.		
ood predictions.		
RMSE (0.06) than DWU (0.11)		
was predicted more or less		
tter than Calima.		
uture Work		
dictions for common bean early		
ain stem dry weight are traits can be good selection criteria		
lection criteria for early vigor		
seful in the near future and the ned with QTL for developing a locations.		
Dakota, Florida, Puerto Rico e a good evidence of genotype		
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