CHARACTERIZATION OF EARLY GENOTYPES OF COMMON BEAN

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INTRODUCTION: The use of early cycle cultivars of common bean (*Phaseolus vulgaris* L.) that allow achieving high grain yields in the shortest time thus providing irrigation water and power savings and hence the cost of production is an old desire of farmers. In this sense, Embrapa Rice and Beans developed earlier cycle genotypes to meet this demand. However, these elite lines have to be characterized in more detail in order to develop a management system that allows fully exploit their genetic potential. Growth analysis is a technique which details the allocation of photosynthate partition as a function of the age of the plant. Determination of dry matter (plant and its parts: stems, leaves, pods and seeds) is the most suitable for the growth analysis (Taiz & Zeiger, 2004). The information generated can be used to verify the adaptation of the crop to new environments, interspecific competition and management systems effects (Andrade et al., 2009). The aim of this study was to was to characterize the agronomic performance of three elite genotypes of common bean with early cycle by growth analysis technique.

MATERIAL AND METHODS: The irrigated field experiment was performed on autumn/ winter (May to July) in 2014 at the Capivara farm from Embrapa Rice and Beans in Santo Antônio de Goiás, GO, Brazil. An irrigated field experiment with a randomized block experimental design with eight replications was conducted in Brazil during the 2014 growing seasons. The treatments consisted of common bean genotypes with early maturity, CNFC 15873, CNFC 15874 and CNFC 15875. Sowing of common bean was mechanically held on May 20, 2014, spaced 0.50 m between rows and with 15 viable seeds per meter. Fertilization in sowing furrows in all treatments was 45 kg ha^{-1} of N as urea, 50 kg ha^{-1} of K as potassium chloride 26 kg ha^{-1} of P as triple superphosphate. In the V_4 vegetative stage of the common bean (four trifoliate leaves), a topdressing fertilization of 45 kg ha^{-1} of N as urea was performed for all plots. Other cultural practices were performed according to the recommendations of the crops to keep the area free of weeds, disease and insects. It was collected plants weekly in a linear meter in each plot for the realization of the growth analysis. Plants were separated into stems, leaves, pods and seeds. We made the mass accumulation graphs of dry matter of each plant structure and total. At harvest time it was made the evaluation of the yield and yield components of each genotype. Data were subjected to an analysis of variance, and the means were compared by Tukey's test at $p<0.05$.

RESULTS AND DISCUSSION: The CNFC 15874 genotype showed the highest dry matter mass of seeds (119.32 g m-1) and total (236.96 g m-1) in relation to genotypes CNFC 15873 (89.78 g m-1 and 200.30 g m-1, respectively) and CNFC 15875 (93.29 g m-1 and 178.24 g m-1, respectively) at 72 days after sowing (Figure 1). This further development of CNFC 15874 also allowed the highest grain yield (3615 kg ha-1), which differed significantly from genotypes CNFC 15873 (2660 kg ha-1) and CNFC 15875 (2677 kg ha-1), which did not differ each other (Table 1). The highest accumulation values for seed and total dry matter of CNFC 15874 are related to the genotype potential. It was observed that untill 60 days after sowing, CNFC 15873 genotypes (29.98 g m-1) and CNFC 15875 (32.78 g m-1) accumulated the maximum mass of dry matter in leaves. After this period, leaves dry matter started to decline indicating that there was translocation of their photoassimilates to the seeds. On the other hand, the CNFC 15874 genotype accumulated dry matter in the leaves up to 66 days (46.23 g m-1). This longer period of CNFC 15874 accumulating mass of dry matter in the leaves seems to be crucial to provide the higher yield of this genotype. According to Wien et al. (1976) in the formation and filling of seeds phases about 45% of photoassimilates in the leaves and stems are translocated into the seeds. From the results it can be seen that the growth analysis technique was effective to explain the higher yield of CNFC 15874 genotype in relation to the others tested genotypes.

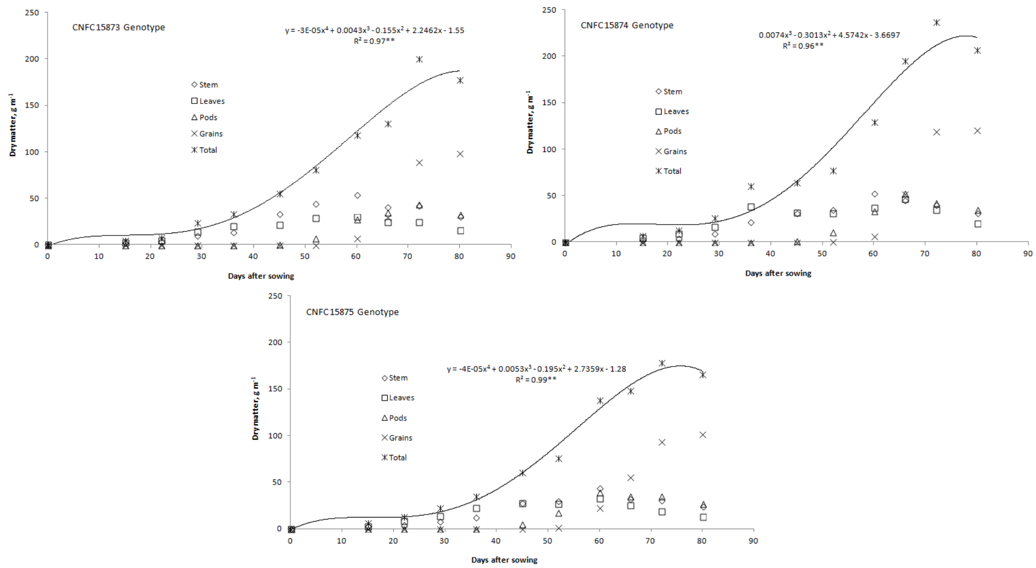

Figure 1. Growth analysis of three common beans genotypes (CNFC 15873, CNFC 15874 and CNFC 15875) cultivated in Santo Antônio de Goiás, Goiás State, Brazil in the growing season 2014.

Table 1 – Number of pods per plant (NPP), number of seeds per pods (NSP), mass of 100 seeds (MASS) and yield of early genotypes of common beans. Santo Antônio de Goiás, Brazil, growing season 2014.

Genotypes	NPP	NSP	MASS	YIELD
	unit	unit	grams	Kg ha^{-1}
CNFC 15873	14b*	5a	22a	2660b
CNFC 15874	18a	4a	24a	3615a
CNFC 15875	15ab	4a	23a	2677b
Factor		ANOVA (F probability)		
Genotype	<0.047	0.6325	0.8545	<0.001
Coefficient of variation (%)	14.07	11.12	3.43	13.76

*means followed by the same letter vertically are not significantly different at p<0.05 according to Tukeys's test.

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