Genotype × Environment Interactions of Mean Genetic Components for Days to Silking and Grain-filling Period in Maize

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INTRODUCTION

The mean genetic components estimates for quantitative traits, m+a (contribution of homozygous loci – additive effects) and d (contribution of heterozygous loci – dominance effects) are strongly influenced by genotype x environment interactions (GE), especially in tropical conditions. The effect of the interaction is particularly significant for traits such as the number of days to flowering (NDF) and the number of days to reach maximum dry matter accumulation in the grains (NDMG).





Figure 1 Maize earshoot at silking stage when NDF was measured.

Acknowledgements:



Figure 2 Maize grain showing black layer at NDMG.

RESULTS

 \succ NDF: dominance tended to decrease the expression of the trait, though the m + a effect was more significant.

To verify the GE effect on m + a and d estimates for NDF and NDMG traits with F1 and F2 generations of nine commercial maize (Zea mays L.) hybrids.

MATERIALS AND METHODS

- Germplasm: Nine commercial maize hybrids from different seed companies differing in NDF and NDMG, F1 and F2 generations. F₂ was made by self-pollinated.
- Environments: Three environments with sowing date in October 2014, January 2015 and October 2015 in Lavras, MG, Brazil.
- **Design:** split-plot design main plots were the hybrids and the subplots were the two generations, with four replications.
- Data collection: NDF was calculated as number of days from planting/ emergence to when 50%+1 of the plants were at the

- > The NDMG results were consistent with those for NDF, except for some hybrids in which dominance increased expression of the trait.
- ✓ Number of days to flowering (NDF) had R² estimates of 27% with homozygous loci (m + a) and 33% for heterozygous loci (d)
- ✓ Number of days to maximum dry matter accumulation in grain (NDMG) had similar R² values of 78% with either homozygous loci.

Table 1: Summary of analyses of variance for obtained in the evaluation of m+a and d considering NDF and NDMG.

df	MS (NDF)		MS (NDMG)	
	m+a	d	m+a	d
8	114.86**	116.315**	172.53**	255.58**
2	357.06**	257.37**	40.9*	158.78**
16	37.65**	44.745**	331.44**	512.49**
72	8.25	11.318	12.61	14.56
_	8 2 16	dfm+a8114.86**2357.06**1637.65**	dfm+ad8114.86**116.315**2357.06**257.37**1637.65**44.745**	dfm+adm+a8114.86**116.315**172.53**2357.06**257.37**40.9*1637.65**44.745**331.44**

silking stage (Figure 1). NDMG was calculated as number of days from silking stage to 50% Black layer in the center of the ear of plots (Figure 2).

Data Analysis: $m + a = 2 F_{2i} - F_1$ $d = 2 (F_{2i} - F_{1i})$ R Software was used to analise the data.

* *i* refers to each hybrid

CONCLUSIONS

 \checkmark Genotype × environment interactions contributed a large portion of the total variation.

✓ Both number of days to flowering and to maximum dry matter were highly influenced by genotype x environment interactions.

FAPEMIG

(RCNPg

