

## Growth analysis of the grain filling process in sunflower

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**ABSTRACT** The main object of this study was to investigate the process of dry matter accumulation (DMA) in achene during the grain filling period of diverse sunflower genotypes. Forty-eight hybrids were planted and six characteristics of the growth curves of DMA (fittY<sub>MAX</sub> – maximum value of dry matter content, AGR<sub>AVG</sub> - average increase in DMA during the sampling period, AGR<sub>MAX</sub> - maximal increase in DMA, X<sub>AGRMAX</sub> - time of maximal speed of growth, RGR<sub>AVG</sub> – average increase in relative DMA, b<sub>RGR</sub> – incline of curve RGR<sub>AVG</sub>.) were compared. The calculations of the characteristics were based on relevant equations. The dynamics of DMA was modelled by the formula:  $\ln Y = P_0 + P_1 X + P_2 X^2$ , where X denotes the period (in 7-day units) passed since the end of flowering and Y denotes the DMA value (g/1000achene) at time X. Analysis of variance (ANOVA) showed considerable differences among DMA of genotypes. The Hunt-formula was suitable to fit to experimental data. Prime association between fittY<sub>MAX</sub> and AGR<sub>MAX</sub> ( $r = 0,889^{***}$ ) were demonstrated by testing of correlation. It indicates that AGR<sub>MAX</sub> determined almost 80 percent the dynamics of DMA. Verifying this, we have analysed AGR<sub>MAX</sub> data by ANOVA. Based on LSD(0,05) values, we classified the hybrids into three groups of showing low level (7,67-11,03 grams/week), medium level (11,04-12,97 grams/week), and high level (13,0-15,43 grams/week) of AGR<sub>MAX</sub> values. The results suggest that sunflowers possess large variance in the speed of the grain filling process determined by the genotype. This indicates a strong genetic control, which could be utilized in hybrid development.

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The grain filling of an annual plant species as sunflower is a fundamental process for the reproduction and survival of the species. The primary value of fitness for plants is to procreate grains as the base of the new generation. In optimal conditions the redundant energy of plant is drained to the growth of achene. But optimal environmental conditions for plant production could hardly be achieved. The interaction between the environment and the genetic background may have a forceful influence on the grain filling process. The question arose whether the grain filling process has enough variability to take a part effectively in achene production. On the other hand, we could find a definite proof of the genetic control of this character.

### Materials and Methods

The experiment was carried out at the Bicsérd Experimental Station of the Iregszemcse Research Institute for Forage Crops of the Kaposvár University, in the year of 2000. Forty-eight hybrids were planted in randomised blocks with four replications without any fertilization. Plot sizes were of 25 m<sup>2</sup>, plant density were 50000 plant\*ha<sup>-1</sup>, soil type is brown forest soil. During the vegetation period the plots were protected against pathogens and pests by tree times fungicide and insecticide treatments.

After the flowering period samples of 3 heads per plot were taken from all plots in ten times at 7-day intervals. After hand threshing of the samples the dry matter content of 1000 achene (ADMC) was determined. In the first step, data were

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### KEY WORDS

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analysed by ANOVA. Then growth curves were estimated on the basis of the formula  $\ln Y(X) = P_0 + P_1 X + P_2 X^2$  according to Hunt and Parsons (1974) and Hunt (1982), where X denotes the time (in 7-days units) since the end of the flowering and Y(X) denotes the DMA (g/1000 achene) at the time X. This method has earlier been adapted successfully for sunflower (Csikász 1998; Csikász and Józsa 1998). By using the Hunt-formula the genotype-specific parameters of DMA equations ( $P_0$ ,  $P_1$  and  $P_2$ ) were obtained for both the average of the replications and also for single replications (during this process it was possible to employ ANOVA in estimating the influence of genotype on the characteristics). The accuracy of fitting was determined by orthogonal polynomials as in Sváb (1981). The curves of absolute growth rate (AGR) and relative growth rate (RGR) were derived from the DMA equations by differentiation, after which the three characteristics were computed using the following formulas:

- average increase in DMA during the sampling period (in dry matter/week):

$$AGR_{avg} = (1/6)\{Y(6) - Y(0)\} = (1/6)\{\exp(P_0 + 6P_1 + 36P_2) - \exp(P_0)\},$$

- maximal increase in DMA (in dry matter/week):

$$AGR_{max} = \sqrt{-2P_2} \exp(P_0 - P_1^2/4P_2 - 0.5),$$

- time of maximal speed of growth (in 7-day units after the end of flowering):

$$X_{AGRmax} = (P_1 - \sqrt{-2P_2}) / (-2P_2).$$

(Where the sqrt stands for square root.)

Besides these, the values of fittY<sub>MAX</sub> (maximum values of DMA curves), RGR<sub>AVG</sub> (average values of relative DMA curves), b<sub>RGR</sub> (incline values of curves RGR<sub>AVG</sub>) were also estimated. For describing associations of characteristics the

**Table 1.** Correlation coefficients 'r' between characteristics of sunflower hybrids.

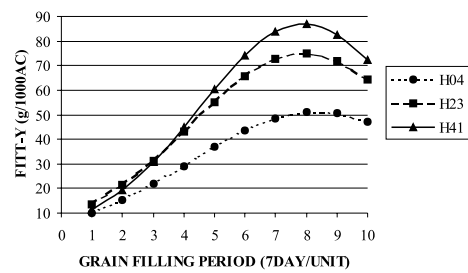
	$fitt-Y_{MAX}$	$AGR_{AVG}$	$AGR_{MAX}$	$X_{AGRMAX}$	$RGR_{AVG}$	$b_{RGR}$
$fitt-Y_{MAX}$	1					
$AGR_{AVG}$	0,820	1				
$AGR_{MAX}$	0,889	0,709	1			
$X_{AGRMAX}$	-0,421	0,084	-0,172	1		
$RGR_{AVG}$	-0,384	0,044	-0,060	0,972	1	
$b_{RGR}$	0,212	0,225	-0,255	-0,509	-0,678	1

$r_{crit, p<0,01} = 0,342$

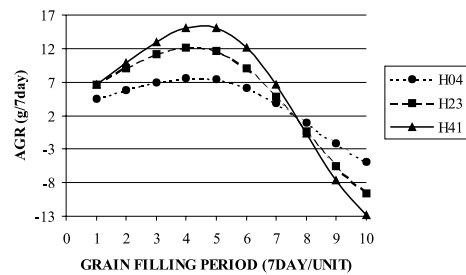
**Table 2.** The  $AGR_{MAX}$  values and classification of sunflower hybrids.

Hybrid	Line A	Line R	$AGR_{MAX}$	Level of $AGR_{MAX}$
FP41	LCMS18	LR5	15,433	high
FP21	LCMS8	LR2	14,405	high
FP13	LCMS6	LR2	14,091	high
FP45	LCMS8	LR8	13,893	high
FP12	LCMS10	LR2	13,603	high
FP40	LCMS8	LR4	13,589	high
FP9	LCMS9	LR2	13,210	high
FP24	LCMS3	LR3	13,191	high
FP16	LCMS7	LR2	13,125	high
FP18	LCMS14	LR2	13,024	high
FP47	LCMS8	LR9	13,000	high
FP15	LCMS12	LR2	12,974	medium
FP35	LCMS8	LR3	12,951	medium
FP17	LCMS13	LR2	12,881	medium
FP11	LCMS3	LR2	12,821	medium
FP48	LCMS18	LR9	12,811	medium
FP43	LCMS8	LR6	12,799	medium
FP27	LCMS5	LR3	12,790	medium
FP31	LCMS13	LR3	12,747	medium
FP46	LCMS19	LR9	12,382	medium
FP14	LCMS11	LR2	12,313	medium
FP30	LCMS7	LR3	12,310	medium
FP34	LCMS16	LR3	12,271	medium
FP19	LCMS15	LR2	12,197	medium
FP23	LCMS1	LR3	12,184	medium
FP28	LCMS6	LR3	12,069	medium
FP10	LCMS1	LR2	11,794	medium
FP33	LCMS15	LR3	11,780	medium
FP32	LCMS14	LR3	11,768	medium
FP44	LCMS19	LR7	11,706	medium
FP39	LCMS7	LR4	11,577	medium
FP42	LCMS5	LR6	11,517	medium
FP29	LCMS11	LR3	11,455	medium
FP25	LCMS4	LR3	11,405	medium
FP50	LCMS19	LR11	11,034	low
FP8	LCMS8	LR1	10,959	low
FP3	LCMS3	LR1	10,896	low
FP26	LCMS17	LR3	10,894	low
FP36	LCMS4	LR4	10,843	low
FP22	LCMS9	LR3	10,742	low
FP38	LCMS5	LR4	10,715	low
FP6	LCMS6	LR1	10,623	low
FP37	LCMS17	LR4	10,408	low
FP5	LCMS5	LR1	9,941	low
FP1	LCMS1	LR1	9,229	low
FP7	LCMS7	LR1	8,895	low
FP2	LCMS2	LR1	8,706	low
FP4	LCMS4	LR1	7,669	low
Mean		12,1		
LSD0,05		1,79		

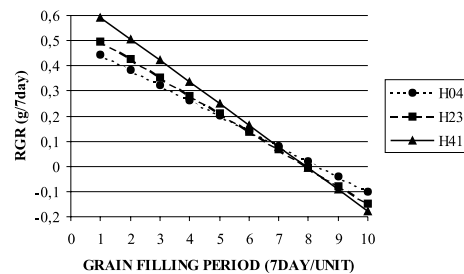
**FIG. 1** DMA OF H04, 023 AND H41



**FIG. 2** AGR OF H04, H23 AND H41



**FIG. 3** RGR OF H04, H23 AND H41



**Figure 1,2 and 3.** Demonstrate the variations of the grain filling processes determined by the genotypes.

Pearson product-moment correlation 'r' was applied. Finally, the data of the characteristics were subjected to ANOVA.

## Results and Discussion

The ANOVA of data set showed a strong significant difference ( $P < 0,001$ ) among the DMA of the genotypes and the interaction too. The  $R^2$  values of fitted Y curves were higher than 0,93 in all cases and the quadratic influence were significant; consequently the Hunt-formula described the DMA process very well.

As an example, results of the hybrids number H04, H23 and H41 are shown below. The grain filling process of these genotypes are described by following equations:

$$\text{H04; } \ln Y = 1,844 + 0,504X - 0,0303X^2; \quad R^2 = 0,96^{***}$$

$$\text{H23; } \ln Y = 2,063 + 0,569X - 0,0359X^2; \quad R^2 = 0,96^{***}$$

$$\text{H41; } \ln Y = 1,782 + 0,678X - 0,0428X^2; \quad R^2 = 0,98^{***}$$

Curves of  $\text{fitt-Y}$ , AGR and RGR are shown in Figure 1, 2 and 3. These figures demonstrate very well the variations of the grain filling processes determined by the genotypes.

Beside the classification of the hybrids the associations of the characteristics were investigated by correlations (Table 1). The strongest relationship was proved between  $\text{fitt-Y}_{\text{MAX}}$  and  $\text{AGR}_{\text{MAX}}$  ( $r = 0,889$ ). Considerable correlations were also found between  $\text{fitt-Y}_{\text{MAX}}$  and  $\text{AGR}_{\text{AVG}}$  ( $r = 0,820$ ),  $\text{AGR}_{\text{MAX}}$  and  $\text{AGR}_{\text{AVG}}$  ( $r = 0,709$ ),  $X_{\text{AGRMAX}}$  and  $\text{RGR}_{\text{AVG}}$  ( $r = 0,972$ ),  $X_{\text{AGRMAX}}$  and  $b_{\text{RGR}}$  ( $r = -0,509$ ),  $b_{\text{RGR}}$  and  $\text{RGR}_{\text{AVG}}$  ( $r = -0,678$ ). But these associations seem not to be of chief importance for our objective. Finally, data of  $\text{AGR}_{\text{MAX}}$  of the hybrids were analysed by ANOVA. The genotypes have been classified into three groups based on value of mean and  $\text{LSD}_{0,05}$  (Table 2).

Eleven hybrids produced high (13,0-15,43 grams/week), 23 showed medium (11,04-12,97 grams/week), and 14 have low (7,67-11,03 grams/week) levels of  $\text{AGR}_{\text{MAX}}$ . A presumption of an additive genetic effect is supposed due to the hybrids of the cross between lines LCMS8 and LR2 placed into the first group almost in all cases. It suggests that there is a good ability for inherits transmittance of the effective grain filling process determined by the genotype of the parental lines.

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