USE OF GROWTH ANALYSIS TO EVALUATE GENETIC MECHANISMS AFFECTING ACHENE YIELD FORMATION OF SUNFLOWER

A NÖVEKEDÉSANALÍZIS MÓDSZERÉNEK ALKALMAZÁSA A NAPRAFORGÓ KASZATTERMÉSÉT BEFOLYÁSOLÓ GENETIKAI HATÁSOK VIZSGÁLATÁBAN

CSIKÁSZ[1*] T., ALFÖLDI[2] Z., JÓZSA[2] S., TREITZ[1] M.

ÖSSZEFOGLALÁS

A kutatások során ötven napraforgó genotípus kaszattermés szárazanyag-felhalmozását (DMA) vizsgáltuk a növekedésanalízis funkcionális (függvények illesztésével kapott modellezés) módszerével, a Kaposvári Egyetem Takarmánytermesztési Kutató Intézetének bicsérdi kísérleti telepén, szántóföldi körülmények között. A függvény-illesztéseket az $\ln Y = P_0 + P_1*X + P_2*X^2$ egyenlet (Hunt-formula) alapján végeztük. Az illesztett függvények alapján meghatároztuk a kaszattermés maximális értékét (Ymax), az abszolút növekedési sebesség átlagos (AGRavg) és maximális (AGRmax) értékét, az abszolút növekedési sebesség legnagyobb értékének az idõpontját (Xagrmax), és a relatív növekedési sebesség átlagos értékét (RGRavg) a kísérleti hibridekre ismétlésenként. A hibridek között észlelhetõ, valamint a hibridek között a különbözõ mintavételi idõpontokban kimutatott szignifikáns különbségek arra utalnak, hogy a napraforgó kaszattermésének szárazanyag-felhalmozását a genotípus alapvetõen befolyásolja. A legszorosabb összefüggést az Ymax és AGRmax értékek között mértük.

KULCSSZAVAK: napraforgó, szárazanyag, növekedés analízis

ABSTRACT

The main objective of this study was to investigate the process of dry matter accumulation (DMA) in achenes during the grain-filling period of fifty sunflower genotypes by using the functional method of growth analysis in a field trial at Bicsérd, Hungary. The Hunt-formula of $\ln Y = P_0 + P_1*X + P_2*X^2$ was fitted to data. Maximum yield (Ymax), the average of the absolute growth rate (AGRavg), maximum growth rate (AGRmax), date of the maximum growth rate (Xagrmax), and the average of the relative growth rate (RGRavg) were calculated from growth curves for hybrids and replications. Significant differences among hybrids and their interaction with sampling dates indicate hybrid differences in the intensity of DMA accumulation. The strongest correlation was observed between the parameters of Ymax and AGRmax.

KEY WORDS: sunflower, dry matter, growth analysis

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DETAILED ABSTRACT

Achene yield as a phenotypic character of sunflower hybrids is the result of the interaction of the genotype and the environment. The evaluations of the basic processes involved in yield formation are of great importance. The main objective of this study was to investigate the process of dry matter accumulation (DMA) in achenes during the grain filling period of diverse sunflower genotypes by using the functional method of growth analysis. Fifty hybrids were planted in a field trial at Bicsérd Experimental Station, Research Institute of Forage Crops, University of Kaposvár, Hungary. Modeling the temporal changes the second-order polynomial of $\ln Y = P_0 + P_1*X + P_2*X^2$ employed earlier was used to fit to data of averages and replications of hybrids. The correctness of fitting was determined by the method of orthogonal polynomials. The following parameters of the growth curves were calculated for hybrids and replications: Ymax – maximum yield estimated, AGRavg – average of the absolute growth rate, AGRmax – maximum growth rate, Xagrmax – date of the maximum growth rate, RGRavg – average of the relative growth rate. Correlation analyses were completed among the calculated parameters. The analysis of variance (ANOVA) revealed strong differences among hybrids, sampling dates, and their interaction was proved also to be significant indicating the hybrid differences in the intensity of achene dry matter accumulation. Correlation analyses of calculated parameters showed the strongest correlation between Ymax and AGRmax (r = 0,936). Sunflower genotypes with intensive dry matter accumulation can be determined by this method.

INTRODUCTION

The effective selection of sunflower genotypes with high productivity potential is a considerable process of hybrid breeding. It is increasingly difficult to produce hybrids that overyield genotypes used in the production systems. Achene yield as a phenotypic trait is the result of the interaction between the genetic structure and the environment. As it is known, the effects of the environmental factors have increased relatively, and the yield level differences among the hybrids can be observed only in the particular production environment [4]. The interaction between the genotype and the environment may have a forceful influence also on the grain filling process [7]. Methods of hybrid breeding exploiting heterosis can be used effectively for diploid cross breeding species with their evolutionary predestination. Non-additive gene interactions can be exploited during the hybrid breeding process utilizing heterosis to achieve yield surplus. Most breeders, however, try to relate quantitative traits to genes inherited additively, since their effects are better predictable and they may assure reasonable backgrounds for parent selection [8].The question arose whether there is a reasonable chance to find significant additive genetic control for a quantitative trait like yield formation for a typical heterosis-species like sunflower. For investigating this, a research project for evaluating the basic processes of yield formation has been introduced. Increments of achene yield were characterized by measuring the achene dry matter content of samples of individual plants taken on consecutive sampling dates. The functional method of plant growth analysis [5,1] was employed to describe and model the temporal process of yield formation.

MATERIALS AND METHODS

The processes of dry matter accumulation (DMA) in achenes of fifty sunflower hybrids with different genetic constitutions were investigated in a field trial carried out at the Bicsérd Experimental Station, Research Institute of Forage Crops, University of Kaposvár, in 2000. Hybrids were planted in randomized block design using 4 replications without any fertilization. Plot sizes were 25.2 m^2, and plant density was 50000 · ha^{-1}. Soil type was brown forest soil. During the vegetation period the plots were protected against pathogens and pests by three fungicide and insecticide treatments.

Samples consisting of achenes of 3 plants per plots were taken at eleven occassions at 7-day intervals from the end of flowering until ripening. After hand threshing and drying the samples the dry matter content was determined. Data were processed and evaluated by analysis of variance (ANOVA). Modeling the temporal changes the second-order polynomial of $lnY = P_0 + P_1*X + P_2*X^2$ [6] was used to fit to data, where X denotes the period (in 6-day units) passed since the end of flowering and Y denotes the DMA value (g · 3 $plants^{-1}$) at time X. This method has earlier been adapted successfully for sunflower [2,3] (Csikász, 1998a; 1998b). The values of maximum yield estimated in the sampling interval (Ymax) were determined from fitted curves. By using the Hunt-formula, the genotype-specific parameters of DMA equations (P_0, P_1 and P_2) were obtained for both the averages of the replications and also for single replications making estimation of the influence of genotypes on different characteristics possible. The correctness of fitting was determined by the method of ortogonal polinomials.

The curves of absolute (AGR) and relative (RGR) growth rates were derived from DMA equations by differentiation [5], after which the three characteristics were computed for hybrids and replications using the following formulas:

- average increase in DMA during the sampling period (in dry matter · $week^{-1}$):

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

- maximum increase in DMA (in dry matter · $week^{-1}$):

$$AGR_{\max} = sqrt(-2P_2) \cdot \exp(P_0 - P_1^2/4P_2 - 0{,}5),$$

- time of maximal speed of growth (in 6-day units after the end of flowering):

$$X_{AGR_{\max}} = [P_1 - sqrt(-2P_2)]/(-2P_2)$$

Data were subjected to ANOVA. For describing associations of characteristics correlation analyses were completed among the calculated parameters and the Pearson product-movement correlation 'r' was determined. Finally, genotypes were classified based on the strongest correlation with Y_{MAX}.

Table 1: Average achene yield of sunflower genotypes in different sampling dates (g · 3 plants^{-1})

Code	1	2	3	4	5	6	7	8	9	10
H01	38,2	71,6	124,1	222,5	279,8	336,3	395,3	389,0	370,5	317,3
H02	46,6	106,3	124,5	230,0	278,8	330,5	424,0	418,0	396,3	381,0
H03	50,6	97,2	128,9	221,3	260,0	325,5	340,0	394,0	342,3	307,3
H04	58,2	139,2	137,8	216,0	274,8	319,0	371,3	396,0	346,3	338,8
H05	40,1	99,9	138,2	200,0	293,3	324,5	333,8	394,5	358,0	368,0
H06	49,5	121,6	160,2	255,0	277,8	367,0	358,8	395,8	365,5	362,5
H07	44,8	87,6	139,1	225,5	309,5	346,8	381,8	395,3	391,8	342,5
H08	39,7	93,9	135,7	217,5	274,5	302,8	321,0	341,8	307,0	305,3
H09	32,9	57,1	106,6	174,3	265,3	273,3	317,8	317,0	343,5	342,3
H10	67,1	119,8	151,0	200,5	285,8	309,8	328,0	371,5	351,8	332,0
H11	79,7	122,3	142,5	216,8	249,3	291,3	298,3	314,3	276,8	298,0
H12	41,0	92,4	122,6	204,5	260,0	286,0	309,0	302,0	314,8	316,0
H13	55,0	133,2	138,7	208,8	275,8	350,8	344,8	356,8	354,3	324,3
H14	39,4	74,8	116,5	187,0	224,0	287,5	344,5	332,3	367,5	340,5
H15	45,6	114,6	112,3	184,8	233,3	286,0	310,3	340,5	312,0	290,0
H16	60,7	120,2	170,8	221,3	271,5	316,5	344,8	375,0	373,0	339,5
H17	55,5	92,5	141,0	200,3	256,8	278,3	338,8	352,0	347,3	289,5
H18	70,2	114,1	170,5	233,8	270,3	292,0	329,0	324,3	326,8	315,5
H19	68,3	134,7	180,2	229,0	255,3	298,8	291,0	324,3	293,0	311,0
H20	45,0	123,5	150,1	242,0	323,5	366,8	421,0	377,8	359,0	383,8
H21	51,2	133,2	180,6	243,5	289,0	291,3	320,0	319,0	349,5	314,5
H22	37,9	86,1	122,7	194,5	245,0	271,3	320,5	334,5	289,5	318,3
H23	53,3	122,4	147,2	227,5	279,3	342,0	370,0	362,3	370,5	357,3
H24	41,5	112,6	139,5	219,5	255,3	313,8	342,8	354,8	323,0	319,3
H25	48,3	125,8	134,8	207,5	256,8	309,8	309,3	361,5	321,0	325,8
H26	51,2	84,2	142,6	189,8	248,0	305,5	335,3	332,5	364,8	328,5
H27	46,4	136,5	137,4	211,0	271,0	312,3	349,5	357,5	338,8	335,5
H28	57,5	167,4	162,4	213,8	282,5	324,0	316,3	347,8	323,3	315,8
H29	31,6	60,2	118,6	187,0	244,5	282,5	298,0	336,3	357,5	370,5
H30	60,3	124,7	137,8	218,3	270,8	310,0	354,8	348,8	347,3	334,0
H31	38,6	95,1	118,1	179,5	274,0	272,5	293,5	328,5	304,3	300,0
H32	40,7	97,9	148,0	198,3	258,5	287,3	305,0	337,5	311,3	336,0
H33	41,3	126,1	138,2	233,8	249,5	316,0	309,8	336,5	328,8	317,5
H34	48,6	130,8	142,4	225,0	267,8	338,5	348,5	363,8	383,5	332,0
H35	48,3	108,8	141,8	217,5	267,8	306,0	303,5	319,5	317,3	328,5
H36	33,1	55,6	91,2	194,0	244,8	311,0	329,5	386,8	390,8	366,0
H37	30,3	86,4	110,7	208,8	260,5	287,3	355,0	366,3	364,3	337,5
H38	51,4	116,7	122,9	186,3	241,3	339,5	364,8	360,3	385,5	375,3
H39	41,7	107,1	112,6	171,8	245,5	302,0	346,8	376,3	357,3	343,3
H40	48,0	97,2	139,6	217,3	275,8	307,5	343,0	358,8	355,0	325,5
H41	42,8	85,2	119,3	218,8	257,5	295,0	338,3	377,5	328,8	351,8
H42	24,1	70,7	99,5	173,0	224,5	259,3	310,8	348,0	352,3	338,8
H43	51,9	99,1	120,1	221,0	265,0	292,5	309,3	315,5	304,5	321,5
H44	25,2	70,3	90,5	209,5	286,8	355,8	409,5	438,3	423,3	412,5
H45	51,6	118,4	130,0	214,0	260,0	292,5	319,8	336,3	314,3	295,3
H46	26,6	80,5	116,6	205,5	311,0	318,3	421,0	403,8	423,3	401,8
H47	47,7	113,0	151,8	217,8	249,3	302,3	349,5	341,3	303,5	308,0
H48	49,2	116,6	132,0	214,5	252,8	313,3	329,0	323,3	330,8	313,3
H49	21,4	42,4	72,6	163,8	275,3	426,3	440,3	442,8	441,8	413,8
H50	37,6	74,1	89,8	198,5	275,3	342,5	390,0	402,3	369,5	379,5
Average:	46,1	103,2	132,1	209,4	266,1	312,3	342,7	358,6	347,4	336,4
$LSD_{0,05}$	14,8	31,5	29,8	38,5	41,4	54,2	46,1	48,2	45,5	50,9

Table 3: Parameters and R2 values of curves fitted to yield data of sunflower genotypes

Code	P_0	P_1	P_2	R^2	
H01	2,847	0,823	-0,0536	0,972	***
H02	3,279	0,680	-0,0418	0,948	***
H03	3,311	0,668	-0,0427	0,953	***
H04	3,654	0,569	-0,0355	0,920	***
H05	3,155	0,710	-0,0446	0,949	***
H06	3,422	0,673	-0,0437	0,942	***
H07	3,119	0,750	-0,0483	0,971	***
H08	3,108	0,734	-0,0484	0,946	***
H09	2,741	0,771	-0,0472	0,956	***
H10	3,754	0,524	-0,0321	0,955	***
H11	3,879	0,475	-0,0302	0,852	***
H12	3,191	0,673	-0,0429	0,942	***
H13	3,570	0,599	-0,0382	0,931	***
H14	3,064	0,678	-0,0405	0,964	***
H15	3,371	0,610	-0,0383	0,937	***
H16	3,656	0,573	-0,0359	0,946	***
H17	3,439	0,609	-0,0385	0,966	***
H18	3,824	0,516	-0,0330	0,962	***
H19	3,900	0,494	-0,0321	0,921	***
H20	3,310	0,714	-0,0465	0,931	***
H21	3,581	0,615	-0,0409	0,886	***
H22	2,993	0,711	-0,0452	0,933	***
H23	3,512	0,618	-0,0389	0,928	***
H24	3,171	0,714	-0,0465	0,890	***
H25	3,491	0,601	-0,0380	0,935	***
H26	3,333	0,621	-0,0378	0,924	***
H27	3,421	0,633	-0,0402	0,890	***
H28	3,745	0,528	-0,0365	0,852	***
H29	2,812	0,747	-0,0450	0,967	***
H30	3,653	0,559	-0,0348	0,949	***
H31	3,154	0,676	-0,0430	0,938	***
H32	3,254	0,663	-0,0421	0,942	***
H33	3,336	0,665	-0,0433	0,907	***
H34	3,451	0,637	-0,0407	0,916	***
H35	3,436	0,619	-0,0396	0,942	***
H36	2,583	0,817	-0,0489	0,935	***
H37	2,822	0,791	-0,0499	0,951	***
H38	3,452	0,585	-0,0341	0,930	***
H39	3,220	0,647	-0,0388	0,936	***
H40	3,332	0,659	-0,0419	0,963	***
H41	3,139	0,694	-0,0432	0,950	***
H42	2,623	0,796	-0,0485	0,967	***
H43	3,428	0,608	-0,0385	0,958	***
H44	2,364	0,938	-0,0582	0,944	***
H45	3,503	0,601	-0,0389	0,943	***
H46	2,542	0,894	-0,0558	0,923	***
H47	3,396	0,650	-0,0428	0,932	***
H48	3,448	0,617	-0,0394	0,940	***
H49	1,960	1,031	-0,0632	0,970	***
H50	2,848	0,772	-0,0469	0,961	***
Average	3,252	0,671	-0,0423		
$LSD_{0,05}$	0,400	0,116	0,0086	*** P<0,001	
SzD1%	0,5275011	0,1527986	0,01134		
SzD0,1%	0,6790818	0,1967062	0,0145987		

Table 4: Average values of calculated parameters for sunflower genotypes

Code	Y_{MAX} (g · 3 plants^{-1})	AGR_{AVG} (g · 6 d^{-1})	AGR_{MAX} (g · 6 d^{-1})	X_{AGRMAX}	RGR_{AVG}
H01	408,0	24,1	81,1	4,62	0,234
H02	424,2	30,0	74,5	4,68	0,220
H03	373,8	23,6	66,4	4,39	0,198
H04	379,8	25,4	61,5	4,27	0,178
H05	398,2	26,6	72,1	4,62	0,220
H06	411,1	25,1	73,7	4,32	0,193
H07	417,0	25,9	78,6	4,55	0,219
H08	361,7	20,6	68,4	4,36	0,201
H09	362,5	25,6	67,8	4,91	0,251
H10	363,8	25,0	55,8	4,22	0,171
H11	315,0	19,3	46,4	3,76	0,143
H12	343,1	22,0	60,8	4,45	0,201
H13	373,5	23,8	62,6	4,22	0,179
H14	370,3	27,5	64,1	4,91	0,232
H15	333,1	22,2	55,7	4,39	0,188
H16	386,3	25,3	62,5	4,32	0,178
H17	350,5	22,9	58,9	4,33	0,186
H18	346,4	21,5	54,0	3,94	0,153
H19	331,6	19,5	50,9	3,75	0,141
H20	430,3	25,9	79,6	4,43	0,203
H21	364,5	20,5	63,1	4,01	0,165
H22	328,6	21,1	59,5	4,52	0,214
H23	394,4	26,0	66,6	4,38	0,190
H24	370,8	22,0	68,4	4,35	0,203
H25	354,7	23,2	59,3	4,28	0,183
H26	365,0	26,0	60,9	4,59	0,205
H27	374,3	24,1	64,3	4,35	0,191
H28	306,4	15,9	49,6	3,54	0,126
H29	373,9	27,8	68,0	4,99	0,253
H30	366,1	24,5	58,6	4,23	0,177
H31	337,3	21,8	60,1	4,47	0,203
H32	354,0	22,9	62,2	4,44	0,200
H33	360,4	21,6	64,2	4,27	0,188
H34	385,7	24,5	66,7	4,33	0,190
H35	351,9	22,2	60,0	4,28	0,184
H36	401,9	29,8	76,1	5,14	0,278
H37	388,0	25,4	74,3	4,75	0,242
H38	395,5	30,5	62,5	4,82	0,211
H39	376,3	27,8	63,4	4,77	0,221
H40	375,8	24,2	66,1	4,41	0,198
H41	377,7	25,9	67,0	4,66	0,219
H42	364,0	26,4	68,6	5,02	0,263
H43	340,8	22,1	57,3	4,30	0,185
H44	467,1	31,2	96,9	5,11	0,298
H45	341,6	21,0	57,7	4,15	0,174
H46	456,2	30,3	92,4	5,01	0,280
H47	354,9	20,8	62,7	4,18	0,180
H48	352,0	22,3	60,0	4,26	0,183
H49	483,8	33,5	104,2	5,35	0,337
H50	418,2	30,3	77,7	5,00	0,256
Average	375,2	24,5	66,3	4,47	0,206
LSD0,05	39,4	4,3	10,9	0,33	0,033

RESULTS AND DISCUSSION

Table 1 shows the average DMA content of the different sunflower experimental hybrids in different sampling dates. Achene yield level achieved its maximum value in sampling dates 7 or 8 for most of the hybrids. However, there were some genotypes like that of code number H11 which peaked earlier in sampling date 6. Analysis of variance (ANOVA) showed considerable differences among DMA of diverse genotypes, sampling dates, and their interaction was proved also to be significant ($LSD_{0,05}$ = 43,6) indicating hybrid differences in the intensity of achene dry matter accumulation (Table 2).

Table 2. Table of analysis of variance (ANOVA) for data of achene dry matter content

Components	SS	df	MS	F	P-value	F critical
Sample	23988114	9	2665346	2687,39	0	1,89
Columns	477716	49	9749	9,83	3,41E-61	1,36
Interaction	1002532	441	2273	2,29	2,64E-31	1,13
Within	1487696	1500	992			
Total	26956058	1999				

The Hunt-formula fitted properly to experimental data of all hybrids, the R^2 values varied between 0,972 and 0,852 (P<0,001), and ANOVA proved the significant effects of the genotypes on the changes of the parameters (Table 3).

Using the appropriate mathematical formulas, parameters of Y_{MAX}, AGR_{AVG}, AGR_{MAX}, X_{AGRMAX}, and RGR_{AVG} were computed for hybrids and replications (Table 4). Significant differences among hybrids were recorded for each parameter evaluated. Correlation analyses of calculated indices showed in Table 5 revealed the strongest correlation between Ymax and AGRmax (r = 0,936). It indicates that the intensity of DMA is determined about 86 percent by AGR_{MAX}. Verifying this, AGR_{MAX} data were analyzed by ANOVA. Based on LSD(0,05) values hybrids were classified into three groups of showing low level (7,67-11,03 gram dry matter · $week^{-1}$), medium level (11,04-12,97 gram dry matter · $week^{-1}$), and high level (13,0-15,43 gram matter · $week^{-1}$) of AGR_{MAX} values. These results suggest that sunflower hybrids with intensive dry matter accumulation can be determined.

Table 5: Correlation analysis of calculated parameters

	Y_{MAX}	AGR_{AVG}	AGR_{MAX}	X_{AGRMAX}	RGR_{AVG}
Y_{MAX}	1				
AGR_{AVG}	0,8494	1			
AGR_{MAX}	0,9362	0,7535	1		
X_{AGRMAX}	0,6899	0,8735	0,7562	1	
RGR_{AVG}	0,7419	0,8199	0,8585	0,9620	1

r (kritikus, p=0,001) = 0,4648

Based on the average of the AGR_{MAX} values and the significant differences genotypes were classified into three groups of the following characteristic features:

- **high AGR_{MAX}** (AGR_{MAX} > average AGR_{MAX} + 0,5*$LSD_{0,05}$)
- **average AGR_{MAX}** (hybrids not belonging to categories number 1 and 3)
- **low AGR_{MAX}** (AGR_{MAX} < average AGR_{MAX} - 0,5*$LSD_{0,05}$)

Finally, hybrids were grouped based on the above categories and parental lines (Table 6), the fifty hybrids falling into the categories as follows: 12 were of „high", 22 belonged to „medium", and 16 were of „low" categories, respectively. There was significant difference revealed between the AGR_{MAX} values of hybrids of „low" and „high" categories. Evaluating the presence of parental lines in the different categories the following conclusions may be drawn: the inbred line coded LCMS19 is found only in Group 1, whereas inbred lines coded

LCMS05, LR01 and LR04 can be found both in Groups 1 and 2. The inbred lines coded LCMS08 and LR03 are represented only in Groups 2 and 3. It is worth noting that the parental lines of LCMS19 and LR01 proved to be superior even when crossing to parental lines with lower performance.

Figures 1 and 2 demonstrate the Y and AGR curves of six respective genotypes, three having high, whereas the other three having low AGR_{MAX} values. Genotypes with different intensity of DMA accumulation can be distinguished visually, as well.

Table 6: AGRMAX categories for hybrids and for parental lines

Code	A-code	R-code	AGR_{MAX} ($g \cdot 6\ d^{-1}$)	Category
H01	LCMS01	LR01	81,1	high
H02	LCMS02	LR01	74,5	high
H36	LCMS04	LR04	76,1	high
H05	LCMS05	LR01	72,1	high
H06	LCMS06	LR01	73,7	high
H07	LCMS07	LR01	78,6	high
H20	LCMS16	LR02	79,6	high
H37	LCMS17	LR04	74,3	high
H44	LCMS19	LR07	96,9	high
H46	LCMS19	LR09	92,4	high
H49	LCMS19	LR10	104,2	high
H50	LCMS19	LR11	77,7	high
H23	LCMS01	LR03	66,6	medium
H03	LCMS03	LR01	66,4	medium
H24	LCMS03	LR03	68,4	medium
H04	LCMS04	LR01	61,5	medium
H27	LCMS05	LR03	64,3	medium
H38	LCMS05	LR04	62,5	medium
H42	LCMS05	LR06	68,6	medium
H13	LCMS06	LR02	62,6	medium
H16	LCMS07	LR02	62,5	medium
H39	LCMS07	LR04	63,4	medium
H08	LCMS08	LR01	68,4	medium
H21	LCMS08	LR02	63,1	medium
H40	LCMS08	LR04	66,1	medium
H47	LCMS08	LR09	62,7	medium
H09	LCMS09	LR02	67,8	medium
H14	LCMS11	LR02	64,1	medium
H29	LCMS11	LR03	68,0	medium
H32	LCMS14	LR03	62,2	medium
H33	LCMS15	LR03	64,2	medium
H34	LCMS16	LR03	66,7	medium
H26	LCMS17	LR03	60,9	medium
H41	LCMS18	LR05	67,0	medium
H10	LCMS01	LR02	55,8	low
H11	LCMS03	LR02	46,4	low
H25	LCMS04	LR03	59,3	low
H28	LCMS06	LR03	49,6	low
H30	LCMS07	LR03	58,6	low
H35	LCMS08	LR03	60,0	low
H43	LCMS08	LR06	57,3	low
H45	LCMS08	LR08	57,7	low
H22	LCMS09	LR03	59,5	low
H12	LCMS10	LR02	60,8	low
H15	LCMS12	LR02	55,7	low
H17	LCMS13	LR02	58,9	low
H31	LCMS13	LR03	60,1	low
H18	LCMS14	LR02	54,0	low
H19	LCMS15	LR02	50,9	low
H48	LCMS18	LR09	60,0	low

Results of this experiment indicate additive genetic control of traits determining DMA accumulation, which, however, should further be investigated and proved in future trials.

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Figure 1: Curves characterizing the dynamics of dry matter accumulation of sunflower hybrids

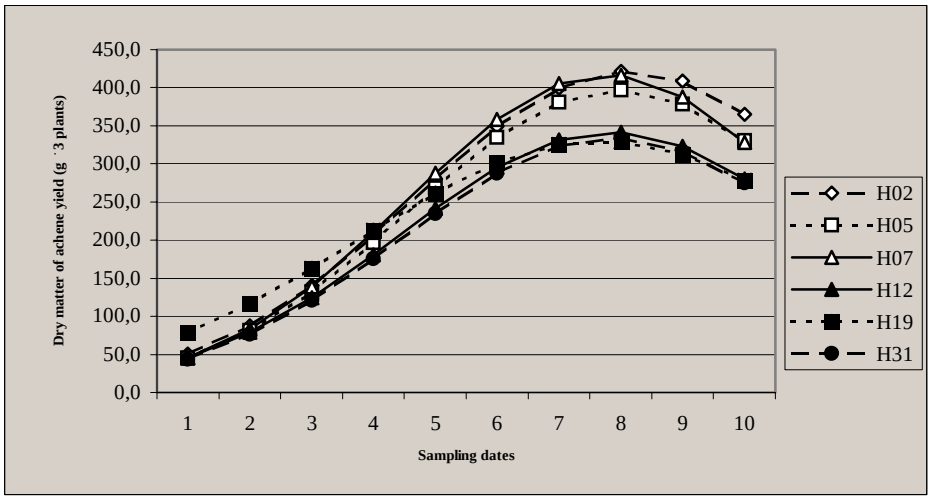
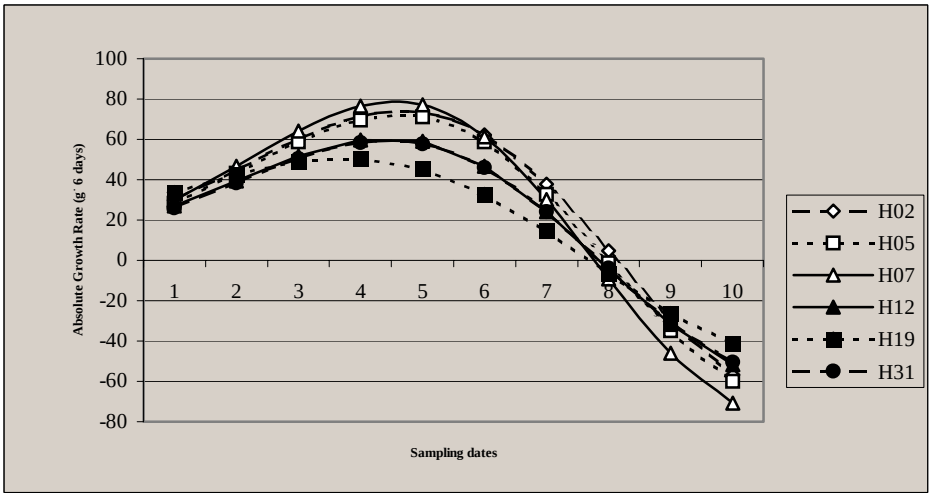


Figure 2: Curves of Absolute Growth Rates of sunflower hybrids of Figure 1.



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Tamás Csikász, tki.ireg@axelero.hu,
Mónika Treitz,
University of Kaposvár, Research Institute for Forage Crops, Iregszemcse, Hungary,
Phone: 36)-74 481 127,
Telefax: (36)-73-481 253,
Zoltán Alföldi,
Sándor Józsa,
University of Veszprém, Georgikon Faculty of Agriculture, Keszthely, Hungary,